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(21) International Application Number: PCT/US98/12764 (22) International Filing Date: 18 June 1998 (18.06.98) (30) Priority Data: 60/050,359 20 June 1997 (20.06.97) US 60/053,377 22 July 1997 (22.07.97) US 60/053,344 22 July 1997 (22.07.97) US 60/057,483 3 September 1997 (03.09.97) US (71) Applicants (for all designated States except US): HUMAN GENOME SCIENCES, INC. [US/US]; 9410 Key West Avenue, Rockville, MD 20850 (US). MEDIMMUNE, INC. [US/US]; 35 West Watkins Mill Road, Gaithersburg, MD 20878 (US). (72) Inventors; and (75) Inventors/Applicants (for US only): FRASER, Claire [US/US]; 11915 Glen Mill Road, Potomac, MD 20854 (US). WHITE, Owen, R. [US/US]; 886 Quince Orchard Boulevard #202, Gaithersburg, MD 20878 (US). CLAYTON, Rebecca [US/US]; 6706 B. Polor Avenue, Takoma Park, MD 20912 (US). DOUGHERTY, Brian, A. [US/US]; 10 Rosemary Lane, Killingworth, CT 06419 (US). LATHIGRA, Raju [IN/US]; 19051 Steeple Place, Germantown, MD 20874		(US). SMITH, Hamilton, O. [US/US]; 8222 Carrbridge Circle, Towson, MD 21204 (US). (74) Agents: HOOVER, Kenley, K. et al.; Human Genome Sciences, Inc., 9410 Key West Avenue, Rockville, MD 20850 (US). (81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG). Published <i>With international search report.</i> <i>Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i>	
(54) Title: BORRELIA BURGDORFERI POLYNUCLEOTIDES AND SEQUENCES			
(57) Abstract The present invention provides polynucleotide sequences of the genome of <i>Borrelia burgdorferi</i> , polypeptide sequences encoded by the polynucleotide sequences, corresponding polynucleotides and polypeptides, vectors and hosts comprising the polynucleotides, and assays and other uses thereof. The present invention further provides polynucleotide and polypeptide sequence information stored on computer readable media, and computer-based systems and methods which facilitate its use.			

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***Borrelia burgdorferi* Polynucleotides and Sequences**

5

Field of the Invention

The present invention relates to the field of molecular biology. In particular, it relates to, among other things, nucleotide sequences of *Borrelia burgdorferi*, contigs, ORFs, fragments, probes, primers and related polynucleotides thereof, peptides and polypeptides encoded by the sequences, and uses of the polynucleotides and sequences thereof, such as in fermentation, polypeptide production, assays and pharmaceutical development, among others.

15

Statement as to Rights to Inventions Made Under Federally-Sponsored Research and Development

Part of the work performed during development of this invention utilized U.S. Government funds. The U.S. Government may have certain rights in the invention - DE-FC02-95ER61962; DE-FC02-95ER61963; and NAGW 2554.

20

Background of the Invention

Spirochetes are a family of motile, unicellular, spiral-shaped bacteria which share a number of structural characteristics. Three genera of the spirochetes are pathogenic in humans: (a) *Treponema*, which includes the pathogens that cause syphilis (*T. pallidum*), yaws (*T. pertenue*), and pinta (*T. carateum*); (b) *Borrelia*, which includes the pathogens that cause epidemic and endemic relapsing fever and Lyme disease; and (c) *Leptospira*, which includes a wide variety of small spirochetes that cause mild to serious systemic human illness (Koff, A. B. and Rosen, T. *J. Am. Acad. Dermatol.* 29:519-535 (1993)).

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Lyme borreliosis, more commonly known as Lyme disease, is presently the most common human disease in the United States transmitted by an arthropod vector. Centers for Disease Control, Morbid. Mortal. Weekly Rep. 44:590-591 (1995). Further, infection of household pets, such as dogs, is a considerable problem. The causative agent of this affliction is the spirochete *Borrelia burgdorferi*, which is generally transmitted to mammalian hosts by feeding ticks. Barbour, A. and Fish, D. *Science* 260:1610-1616 (1993). Once the bacteria pass through the skin they disseminate and produce a variety of clinical manifestations. Diagnosis of this disease is often made serologically by the identification of antiborrelial antibodies. Hilton, E. et al., *J. Clin. Microbiol.* 35:774-776 (1997).

35

While initial symptoms often include a rash at the infection point, Lyme disease is a multisystemic disorder that may include arthritic, cardiac, and neurological manifestations. While antibiotics are currently used to treat active cases of Lyme disease, *B. burgdorferi* appears to be able to persist even after prolonged antibiotic treatment. Further, *B. burgdorferi* can persist for years in a mammalian host even in the presence of an active immune response. Straubinger, R. et al., J. Clin. Microbiol. 35:111-116 (1997); Steere, A., N. Engl. J. Med. 321:586-596 (1989).

Animal models have proven useful for studying the progression of Lyme disease, methods for preventing this disease, and immunological responses to antigenic challenges with *B. burgdorferi* proteins. Garcia-Monoco, J. et al., J. Infect. Dis. 175:1243-1245 (1997). Using a canine model, Starubinger, R. et al., Infect. Immun. 65:1273-1285 (1977), demonstrated that *B. burgdorferi* migrates into joints and induces up-regulation of interleukin-8 in synovial membranes. Similarly, *B. burgdorferi* induction of interleukin-8 production has been demonstrated in cultured human endothelial cells. Burns, M. et al., Infect. Immun. 65:1217-1222 (1997).

Antigenic heterogeneity has been postulated as a mechanism used by *B. burgdorferi* for evasion of host immune responses. Schwan, T. et al., Can. J. Microbiol. 37:450-454 (1991). In support of this mechanism, antigenic variation has been described with other pathogenic bacteria. Hagbloom, P. et al., Nature 315:156-158 (1985). Further, cassette type genetic recombination of genes encoding *B. burgdorferi* surface proteins has been shown to decrease the antigenicity of these organisms to antibodies generated against strains which have not undergone the same recombination. Zhang, J. et al., Cell 89:275-285 (1997).

A number of different types of Lyme disease vaccines have been tested and shown to induce immunological responses. Whole-cell *B. burgdorferi* vaccines have been shown to induce both immunological responses and protective immunity in several animal models. Reviewed in Wormser, G., Clin. Infect. Dis. 21:1267-1274 (1995). For example, dogs inoculated with a chemically inactivated whole-cell vaccine primarily develop antibodies to outer surface membrane proteins of the administered organism. Further, passive immunity has been also demonstrated in animals using *B. burgdorferi* specific antisera. Similarly, passive immunity is conferred human by the administration of sera obtained from Lyme disease patients.

While whole-cell Lyme disease vaccines confer protective immunity in animal models, use of such vaccines presents the risk that responsive antibodies will be generated which cross react with human antigens. Reviewed in Wormser, G., supra. This problem is at least partly the result of the production of *B. burgdorferi* specific antibodies which cross-react with hepatocytes and both muscle and nerve cells. *B. burgdorferi* heat shock proteins and the 41-kd flagellin subunit are believed to contain the antigens against which these cross-reactive antibodies are generated.

It is clear that the etiology of diseases mediated or exacerbated by *B. burgdorferi* genes, and that characterizing the genes and their patterns of expression would add dramatically to our

understanding of the organism and its host interactions. Knowledge of *B. burgdorferi* genes and genomic organization would dramatically improve understanding of disease etiology and lead to improved and new ways of preventing, ameliorating, arresting and reversing diseases. Moreover, characterized genes and genomic fragments of *B. burgdorferi* would provide reagents for, among other things, detecting, characterizing and controlling *B. burgdorferi* infections. There is a need therefore to characterize the genome of *B. burgdorferi* and for polynucleotides and sequences of this organism.

SUMMARY OF THE INVENTION

The present invention is based on the sequencing of fragments of the *Borrelia burgdorferi* genome. The primary nucleotide sequences which were generated are provided in SEQ ID NOS:1-155.

The present invention provides the complete nucleotide sequence of the *Borrelia burgdorferi* chromosome and 154 contigs representing the majority of the sequence of the *B. burgdorferi* extrachromosomal elements, all of which are listed in tables below and set out in the Sequence Listing submitted herewith, and representative fragments thereof, in a form which can be readily used, analyzed, and interpreted by a skilled artisan. In one embodiment, the present invention is provided as contiguous strings of primary sequence information corresponding to the nucleotide sequences depicted in SEQ ID NOS: 1-155.

The present invention further provides nucleotide sequences which are at least 95%, 96%, 97%, 98%, and 99%, identical to the nucleotide sequences of SEQ ID NOS:1-155, ORF IDs and corresponding ORFs.

The nucleotide sequences of SEQ ID NOS:1-155, ORF ID or ORF within, a representative fragment thereof, or a nucleotide sequence which is at least 95% identical to said nucleotide sequence may be provided in a variety of mediums to facilitate its use. In one application of this embodiment, the sequences of the present invention are recorded on computer readable media. Such media includes, but is not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media.

The present invention further provides systems, particularly computer-based systems which contain the sequence information herein described stored in a data storage means. Such systems are designed to identify commercially important fragments of the *Borrelia burgdorferi* genome.

Another embodiment of the present invention is directed to fragments of the *Borrelia burgdorferi* genome having particular structural or functional attributes. Such fragments of the *Borrelia burgdorferi* genome of the present invention include, but are not limited to, fragments which encode peptides, hereinafter referred to as open reading frames or ORFs, fragments which modulate the expression of an operably linked ORF, hereinafter referred to as expression

modulating fragments or EMFs, and fragments which can be used to diagnose the presence of *Borrelia burgdorferi* in a sample, hereinafter referred to as diagnostic fragments or DFs.

Each of the ORF IDs and ORFs in fragments of the *Borrelia burgdorferi* genome disclosed in Tables 1-6, and the EMFs found 5' prime of the initiation codon, can be used in numerous ways as polynucleotide reagents. For instance, the sequences can be used as diagnostic probes or amplification primers for detecting or determining the presence of a specific microbe in a sample, to selectively control gene expression in a host and in the production of polypeptides, such as polypeptides encoded by ORFs of the present invention, particular those polypeptides that have a pharmacological activity.

The present invention further includes recombinant constructs comprising one or more fragments of the *Borrelia burgdorferi* genome of the present invention. The recombinant constructs of the present invention comprise vectors, such as a plasmid or viral vector, into which a fragment of the *Borrelia burgdorferi* has been inserted.

The present invention further provides host cells containing any of the isolated fragments of the *Borrelia burgdorferi* genome of the present invention. The host cells can be a higher eukaryotic host cell, such as a mammalian cell, a lower eukaryotic cell, such as a yeast cell, or a procaryotic cell such as a bacterial cell.

The present invention is further directed to isolated polypeptides and proteins encoded by ORFs of the present invention. A variety of methods, well known to those of skill in the art, routinely may be utilized to obtain any of the polypeptides and proteins of the present invention. For instance, polypeptides and proteins of the present invention having relatively short, simple amino acid sequences readily can be synthesized using commercially available automated peptide synthesizers. Polypeptides and proteins of the present invention also may be purified from bacterial cells which naturally produce the protein. Yet another alternative is to purify polypeptide and proteins of the present invention from cells which have been altered to express them.

The invention further provides methods of obtaining homologs of the fragments of the *Borrelia burgdorferi* genome of the present invention and homologs of the proteins encoded by the ORFs of the present invention. Specifically, by using the nucleotide and amino acid sequences disclosed herein as a probe or as primers, and techniques such as PCR cloning and colony/plaque hybridization, one skilled in the art can obtain homologs.

The invention further provides antibodies which selectively bind polypeptides and proteins of the present invention. Such antibodies include both monoclonal and polyclonal antibodies.

The invention further provides hybridomas which produce the above-described antibodies. A hybridoma is an immortalized cell line which is capable of secreting a specific monoclonal antibody.

The present invention further provides methods of identifying test samples derived from cells which express one of the ORFs of the present invention, or a homolog thereof. Such

methods comprise incubating a test sample with one or more of the antibodies of the present invention, or one or more of the DFs of the present invention, under conditions which allow a skilled artisan to determine if the sample contains the ORF or product produced therefrom.

In another embodiment of the present invention, kits are provided which contain the necessary reagents to carry out the above-described assays.

Specifically, the invention provides a compartmentalized kit to receive, in close confinement, one or more containers which comprises: (a) a first container comprising one of the antibodies, or one of the DFs of the present invention; and (b) one or more other containers comprising one or more of the following: wash reagents, reagents capable of detecting presence of bound antibodies or hybridized DFs.

Using the isolated proteins of the present invention, the present invention further provides methods of obtaining and identifying agents capable of binding to a polypeptide or protein encoded by one of the ORFs of the present invention. Specifically, such agents include, as further described below, antibodies, peptides, carbohydrates, pharmaceutical agents and the like. Such methods comprise steps of: (a) contacting an agent with an isolated protein encoded by one of the ORFs of the present invention; and (b) determining whether the agent binds to said protein.

The present genomic sequences of *Borrelia burgdorferi* will be of great value to all laboratories working with this organism and for a variety of commercial purposes. Many fragments of the *Borrelia burgdorferi* genome will be immediately identified by similarity searches against GenBank or protein databases and will be of immediate value to *Borrelia burgdorferi* researchers and for immediate commercial value for the production of proteins or to control gene expression.

The methodology and technology for elucidating extensive genomic sequences of bacterial and other genomes has and will greatly enhance the ability to analyze and understand chromosomal organization. In particular, sequenced contigs and genomes will provide the models for developing tools for the analysis of chromosome structure and function, including the ability to identify genes within large segments of genomic DNA, the structure, position, and spacing of regulatory elements, the identification of genes with potential industrial applications, and the ability to do comparative genomic and molecular phylogeny.

DESCRIPTION OF THE FIGURES

FIGURE 1 is a block diagram of a computer system (102) that can be used to implement computer-based systems of present invention.

FIGURE 2 is a schematic diagram depicting the data flow and computer programs used to collect, assemble, edit and annotate the contigs of the *Borrelia burgdorferi* genome of the present invention. Both Macintosh and Unix platforms are used to handle the AB 373 and 377 sequence data files, largely as described in Kerlavage *et al.*, *Proceedings of the Twenty-Sixth*

Annual Hawaii International Conference on System Sciences, 585, IEEE Computer Society Press, Washington D.C. (1993). Factura (AB) is a Macintosh program designed for automatic vector sequence removal and end-trimming of sequence files. The program Loadis runs on a Macintosh platform and parses the feature data extracted from the sequence files by Factura to the Unix based *Borrelia burgdorferi* relational database. Assembly of contigs (and whole genome sequences) is accomplished by retrieving a specific set of sequence files and their associated features using Extrseq, a Unix utility for retrieving sequences from an SQL database. The resulting sequence file is processed to trim portions of the sequences with a high rate ambiguous nucleotides. The sequence files were assembled using TIGR Assembler, an assembly engine designed at The Institute for Genomic Research (TIGR) for rapid and accurate assembly of thousands of sequence fragments. The collection of contigs generated by the assembly step is loaded into the database with the lassie program. Identification of open reading frames (ORFs) is accomplished by processing contigs with zorf. The ORFs are searched against *B. burgdorferi* sequences from GenBank and against all protein sequences using the BLASTN and BLASTP programs, described in Altschul *et al.*, *J. Mol. Biol.* 215: 403-410 (1990). Results of the ORF determination and similarity searching steps were loaded into the database. As described below, some results of the determination and the searches are set out in Tables 1-6.

DETAILED DESCRIPTION OF ILLUSTRATIVE EMBODIMENTS

The present invention is based on the sequencing of fragments of the *Borrelia burgdorferi* genome and analysis of the sequences. The primary nucleotide sequences generated by sequencing the fragments are provided in SEQ ID NOS: 1-155. (As used herein, the "primary sequence" refers to the nucleotide sequence represented by the IUPAC nomenclature system.) SEQ ID NOS:1-155

In addition, the present invention provides the nucleotide sequences of SEQ ID NOS: 1-155, or representative fragments thereof, in a form which can be readily used, analyzed, and interpreted by a skilled artisan.

As used herein, a "representative fragment of the nucleotide sequence depicted in SEQ ID NOS:1-155" refers to any portion of the SEQ ID NOS: 1-155 which is not presently represented within a publicly available database. Preferred representative fragments of the present invention are *Borrelia burgdorferi* open reading frames (ORFs) represented by ORF IDs, expression modulating fragments (EMFs) and diagnostic fragments (DFs) which can be used to diagnose the presence of *Borrelia burgdorferi* in sample. A non-limiting identification of preferred representative portions are provided in Tables 1-6 as ORF IDs. As discussed in detail below, the information provided in SEQ ID NOS:1-155 and in Tables 1-6 together with routine cloning, synthesis, sequencing and assay methods will enable those skilled in the art to clone and sequence all "representative fragments" of interest, including ORFs encoding a large variety of *Borrelia burgdorferi* proteins.

The present invention is further directed to nucleic acid molecules encoding portions or fragments of the nucleotide sequences described herein. Fragments include portions of the nucleotide sequences of Table 1-6 (ORF IDs) and SEQ ID NOS:1-155, at least 10 contiguous nucleotides in length selected from any two integers, one of which representing a 5' nucleotide position and a second of which representing a 3' nucleotide position, where the first nucleotide for each nucleotide sequence in SEQ ID NOS:1-155 is position 1 (therefore, the sequence positions for each ORF ID is determined by the numbering of the SEQ ID comprising the ORF ID). That is, every combination of a 5' and 3' nucleotide position that a fragment at least 10 contiguous nucleotides in length could occupy is included in the invention. At least means a fragment may be 10 contiguous nucleotide bases in length or any integer between 10 and the length of an entire nucleotide sequence of SEQ ID NOS:1-155 minus 1. Therefore, included in the invention are contiguous fragments specified by any 5' and 3' nucleotide base positions of a nucleotide sequences of SEQ ID NOS:1-155 wherein the contiguous fragment is any integer between 10 and the length of an entire nucleotide sequence minus 1.

Further, the invention includes polynucleotides comprising fragments specified by size, in nucleotides, rather than by nucleotide positions. The invention includes any fragment size, in contiguous nucleotides, selected from integers between 10 and the length of an entire ORF ID or SEQ ID NO., minus 1. Preferred sizes of contiguous nucleotide fragments include 20 nucleotides, 30 nucleotides, 40 nucleotides, 50 nucleotides. Other preferred sizes of contiguous nucleotide fragments, which may be useful as diagnostic probes and primers, include fragments 50-300 nucleotides in length which include, as discussed above, fragment sizes representing each integer between 50-300. Larger fragments are also useful according to the present invention corresponding to most, if not all, of the nucleotide sequences shown in Tables 1-6 (ORF IDs) and SEQ ID NOS:1-155. The preferred sizes are, of course, meant to exemplify not limit the present invention as all size fragments, representing any integer between 10 and the length of an entire nucleotide sequence minus 1, of each ORF ID and SEQ ID NO., are included in the invention.

The present invention also provides for the exclusion of any fragment, specified by 5' and 3' base positions or by size in nucleotide bases as described above for any ORF ID or SEQ ID NOS:1-155. Any number of fragments of nucleotide sequences in ORF IDs or SEQ ID NOS:1-155, specified by 5' and 3' base positions or by size in nucleotides, as described above, may be excluded from the present invention.

While the presently disclosed sequences of SEQ ID NOS: 1-155 are highly accurate, sequencing techniques are not perfect and, in relatively rare instances, further investigation of a fragment or sequence of the invention may reveal a nucleotide sequence error present in a nucleotide sequence disclosed in SEQ ID NOS: 1-155. However, once the present invention is made available (*i.e.*, once the information in SEQ ID NOS: 1-155 and Tables 1-6 has been made available), resolving a rare sequencing error in SEQ ID NOS: 1-155 will be well within the skill

of the art. The present disclosure makes available sufficient sequence information to allow any of the described contigs or portions thereof to be obtained readily by straightforward application of routine techniques. Further sequencing of such polynucleotide may proceed in like manner using manual and automated sequencing methods which are employed ubiquitous in the art. Nucleotide sequence editing software is publicly available. For example, Applied Biosystem's (AB) AutoAssembler can be used as an aid during visual inspection of nucleotide sequences. By employing such routine techniques potential errors readily may be identified and the correct sequence then may be ascertained by targeting further sequencing effort, also of a routine nature, to the region containing the potential error.

Even if all of the very rare sequencing errors in SEQ ID NOS: 1-155 were corrected, the resulting nucleotide sequences would still be at least 95% identical, nearly all would be at least 99% identical, and the great majority would be at least 99.9% identical to the nucleotide sequences of SEQ ID NOS: 1-155.

As discussed elsewhere herein, polynucleotides of the present invention readily may be obtained by routine application of well known and standard procedures for cloning and sequencing DNA. Detailed methods for obtaining libraries and for sequencing are provided below, for instance. A wide variety of *Borrelia burgdorferi* strains that can be used to prepare *B. burgdorferi* genomic DNA for cloning and for obtaining polynucleotides of the present invention are available to the public from recognized depository institutions, such as the American Type Culture Collection (ATCC). While the present invention is enabled by the sequences and other information herein disclosed, the *B. burgdorferi* strain that provided the DNA of the present Sequence Listing, has been deposited with the ATCC, 10801 University Blvd. Manassas, VA 20110-2209, as Deposit No. 202012, on 8 August 1997. The ATCC Deposit is provided merely as a convenience to those of skill in the art. Reference to the deposit is not a waiver of any rights of the inventors or their assignees in the present subject matter.

The nucleotide sequences of the genomes from different strains of *Borrelia burgdorferi* differ somewhat. However, the nucleotide sequences of the genomes of all *Borrelia burgdorferi* strains will be at least 95% identical, in corresponding part, to the nucleotide sequences provided in SEQ ID NOS: 1-155 and the ORF IDs within. Nearly all will be at least 99% identical and the great majority will be 99.9% identical.

The present application is further directed to nucleic acid molecules at least 90%, 95%, 96%, 97%, 98% or 99% identical to a nucleic acid sequence shown in SEQ ID NOS: 1-155 and the ORF IDs within. The above nucleic acid sequences are included irrespective of whether they encode a polypeptide having *B. burgdorferi* activity. This is because even where a particular nucleic acid molecule does not encode a polypeptide having *B. burgdorferi* activity, one of skill in the art would still know how to use the nucleic acid molecule, for instance, as a hybridization probe. Uses of the nucleic acid molecules of the present invention that do not encode a polypeptide having *B. burgdorferi* activity include, *inter alia*, isolating a *B. burgdorferi* gene or allelic variants thereof from a DNA library, and detecting *B. burgdorferi* mRNA expression from

biological or environmental samples, suspected of containing *B. burgdorferi* by Northern Blot, PCR, or similar analysis.

Preferred, are nucleic acid molecules having sequences at least 90%, 95%, 96%, 97%, 98% or 99% identical to the nucleic acid sequence shown in SEQ ID NOS: 1-155, the ORF IDs, and the ORF within each ORF ID, which do, in fact, encode a polypeptide having *B. burgdorferi* protein activity. By "a polypeptide having *B. burgdorferi* activity" is intended polypeptides exhibiting activity similar, but not necessarily identical, to an activity of the *B. burgdorferi* protein of the invention, as measured in a particular biological assay suitable for measuring activity of the specified protein.

Due to the degeneracy of the genetic code, one of ordinary skill in the art will immediately recognize that a large number of the nucleic acid molecules having a sequence at least 90%, 95%, 96%, 97%, 98%, or 99% identical to the nucleic acid sequences shown in SEQ ID NOS: 1-155, the ORF IDs, and the ORF within each ORF ID, will encode a polypeptide having *B. burgdorferi* protein activity. In fact, since degenerate variants of these nucleotide sequences all encode the same polypeptide, this will be clear to the skilled artisan even without performing the above described comparison assay. It will be further recognized in the art that, for such nucleic acid molecules that are not degenerate variants, a reasonable number will also encode a polypeptide having *B. burgdorferi* protein activity. This is because the skilled artisan is fully aware of amino acid substitutions that are either less likely or not likely to significantly effect protein function (e.g., replacing one aliphatic amino acid with a second aliphatic amino acid), as further described below.

The biological activity or function of the polypeptides of the present invention are expected to be similar or identical to polypeptides from other bacteria that share a high degree of structural identity/similarity. Tables 1, 2, 4, and 5 lists accession numbers and descriptions for the closest matching sequences of polypeptides available through Genbank. It is therefore expected that the biological activity or function of the polypeptides of the present invention will be similar or identical to those polypeptides from other bacterial genuses, species, or strains listed in Tables 1, 2, 4, and 5.

By a polynucleotide having a nucleotide sequence at least, for example, 95% "identical" to a reference nucleotide sequence of the present invention, it is intended that the nucleotide sequence of the polynucleotide is identical to the reference sequence except that the polynucleotide sequence may include up to five point mutations per each 100 nucleotides of the reference nucleotide sequence encoding the *B. burgdorferi* polypeptide. In other words, to obtain a polynucleotide having a nucleotide sequence at least 95% identical to a reference nucleotide sequence, up to 5% of the nucleotides in the reference sequence may be deleted, inserted, or substituted with another nucleotide. The query sequence may be an entire sequence shown in SEQ ID NOS: 1-155, an ORF ID, or the ORF within each ORF ID, or any fragment specified as described herein.

As a practical matter, whether any particular nucleic acid molecule or polypeptide is at least 90%, 95%, 96%, 97%, 98% or 99% identical to a nucleotide sequence of the present invention can be determined conventionally using known computer programs. A preferred method for determining the best overall match between a query sequence (a sequence of the present invention) and a subject sequence, also referred to as a global sequence alignment, can be determined using the FASTDB computer program based on the algorithm of Brutlag et al. *See* Brutlag et al. (1990) *Comp. App. Biosci.* 6:237-245. In a sequence alignment the query and subject sequences are both DNA sequences. An RNA sequence can be compared by first converting U's to T's. The result of said global sequence alignment is in percent identity.

Preferred parameters used in a FASTDB alignment of DNA sequences to calculate percent identity are: Matrix=Unitary, k-tuple=4, Mismatch Penalty=1, Joining Penalty=30, Randomization Group Length=0, Cutoff Score=1, Gap Penalty=5, Gap Size Penalty=0.05, Window Size=500 or the length of the subject nucleotide sequence, whichever is shorter.

If the subject sequence is shorter than the query sequence because of 5' or 3' deletions, not because of internal deletions, a manual correction must be made to the results. This is because the FASTDB program does not account for 5' and 3' truncations of the subject sequence when calculating percent identity. For subject sequences truncated at the 5' or 3' ends, relative to the query sequence, the percent identity is corrected by calculating the number of bases of the query sequence that are 5' and 3' of the subject sequence, which are not matched/aligned, as a percent of the total bases of the query sequence. Whether a nucleotide is matched/aligned is determined by results of the FASTDB sequence alignment. This percentage is then subtracted from the percent identity, calculated by the above FASTDB program using the specified parameters, to arrive at a final percent identity score. This corrected score is what is used for the purposes of the present invention. Only nucleotides outside the 5' and 3' nucleotides of the subject sequence, as displayed by the FASTDB alignment, which are not matched/aligned with the query sequence, are calculated for the purposes of manually adjusting the percent identity score.

For example, a 90 nucleotide subject sequence is aligned to a 100 nucleotide query sequence to determine percent identity. The deletions occur at the 5' end of the subject sequence and therefore, the FASTDB alignment does not show a matched/alignment of the first 10 nucleotides at 5' end. The 10 unpaired nucleotides represent 10% of the sequence (number of nucleotides at the 5' and 3' ends not matched/total number of nucleotides in the query sequence) so 10% is subtracted from the percent identity score calculated by the FASTDB program. If the remaining 90 nucleotides were perfectly matched the final percent identity would be 90%. In another example, a 90 nucleotide subject sequence is compared with a 100 nucleotide query sequence. This time the deletions are internal deletions so that there are no nucleotides on the 5' or 3' of the subject sequence which are not matched/aligned with the query. In this case the percent identity calculated by FASTDB is not manually corrected. Once again, only nucleotides 5' and 3' of the

subject sequence which are not matched/aligned with the query sequence are manually corrected for. No other manual corrections are to be made for the purposes of the present invention.

COMPUTER RELATED EMBODIMENTS

5 The nucleotide sequences provided in SEQ ID NOS: 1-155, including ORF IDs and corresponding ORFs, a representative fragment thereof, or a nucleotide sequence at least 95%, preferably at least 96%, 97%, 98% or 99%, and most preferably at least 99.9% identical to said nucleotide sequences may be "provided" in a variety of mediums to facilitate use thereof. As used herein, provided refers to a manufacture, other than an isolated nucleic acid molecule,
10 which contains a nucleotide sequence of the present invention, a representative fragment thereof, or a nucleotide sequence at least 95%, preferably at least 99% and most preferably at least 99.9% identical to a polynucleotide of the present invention. Such a manufacture provides a large portion of the *Borrelia burgdorferi* genome and parts thereof (e.g., a *Borrelia burgdorferi* open reading frame (ORF)) in a form which allows a skilled artisan to examine the manufacture using
15 means not directly applicable to examining the *Borrelia burgdorferi* genome or a subset thereof as it exists in nature or in purified form.

 In one application of this embodiment, a nucleotide sequence of the present invention can be recorded on computer readable media. As used herein, "computer readable media" refers to any medium which can be read and accessed directly by a computer. Such media include, but are
20 not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories, such as magnetic/optical storage media. A skilled artisan can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising computer readable medium having recorded thereon a
25 nucleotide sequence of the present invention. Likewise, it will be clear to those of skill how additional computer readable media that may be developed also can be used to create analogous manufactures having recorded thereon a nucleotide sequence of the present invention.

 As used herein, "recorded" refers to a process for storing information on computer readable medium. A skilled artisan can readily adopt any of the presently known methods for
30 recording information on computer readable medium to generate manufactures comprising the nucleotide sequence information of the present invention.

 A variety of data storage structures are available to a skilled artisan for creating a computer readable medium having recorded thereon a nucleotide sequence of the present invention. The choice of the data storage structure will generally be based on the means chosen
35 to access the stored information. In addition, a variety of data processor programs and formats can be used to store the nucleotide sequence information of the present invention on computer readable medium. The sequence information can be represented in a word processing text file, formatted in commercially-available software such as WordPerfect and MicroSoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase,

Oracle, or the like. A skilled artisan can readily adapt any number of data-processor structuring formats (e.g., text file or database) in order to obtain computer readable medium having recorded thereon the nucleotide sequence information of the present invention.

Computer software is publicly available which allows a skilled artisan to access sequence information provided in a computer readable medium. Thus, by providing in computer readable form the nucleotide sequences of the present invention (e.g. SEQ ID NOS: 1-155); a representative fragment thereof, or a nucleotide sequence at least 95%, preferably at least 96%, 97%, 98%, 99% and most preferably at least 99.9% identical to a sequence of the present invention (e.g. SEQ ID NOS: 1-155) enables the skilled artisan routinely to access the provided sequence information for a wide variety of purposes.

The examples which follow demonstrate how software which implements the BLAST (Altschul *et al.*, *J. Mol. Biol.* 215:403-410 (1990)) and BLAZE (Brutlag *et al.*, *Comp. Chem.* 17:203-207 (1993)) search algorithms on a Sybase system was used to identify open reading frames (ORFs) within the *Borrelia burgdorferi* genome which contain homology to ORFs or proteins from both *Borrelia burgdorferi* and from other organisms. Among the ORFs discussed herein are protein encoding fragments of the *Borrelia burgdorferi* genome useful in producing commercially important proteins, such as enzymes used in fermentation reactions and in the production of commercially useful metabolites.

The present invention further provides systems, particularly computer-based systems, which contain the sequence information described herein. Such systems are designed to identify, among other things, commercially important fragments of the *Borrelia burgdorferi* genome.

As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware means of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based system are suitable for use in the present invention.

As stated above, the computer-based systems of the present invention comprise a data storage means having stored therein a nucleotide sequence of the present invention and the necessary hardware means and software means for supporting and implementing a search means.

As used herein, "data storage means" refers to memory which can store nucleotide sequence information of the present invention, or a memory access means which can access manufactures having recorded thereon the nucleotide sequence information of the present invention.

As used herein, "search means" refers to one or more programs which are implemented on the computer-based system to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of the present genomic sequences which match a particular target sequence or target motif. A variety of known algorithms are disclosed publicly and a variety of

commercially available software for conducting search means are and can be used in the computer-based systems of the present invention. Examples of such software includes, but is not limited to, MacPattern (EMBL), BLASTN and BLASTX (NCBIA). A skilled artisan can readily recognize that any one of the available algorithms or implementing software packages for conducting homology searches can be adapted for use in the present computer-based systems.

As used herein, a "target sequence" can be any DNA or amino acid sequence of six or more nucleotides or two or more amino acids. A skilled artisan can readily recognize that the longer a target sequence is, the less likely a target sequence will be present as a random occurrence in the database. The most preferred sequence length of a target sequence is from about 10 to 100 amino acids or from about 30 to 300 nucleotide residues. However, it is well recognized that searches for commercially important fragments, such as sequence fragments involved in gene expression and protein processing, may be of shorter length.

As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration which is formed upon the folding of the target motif. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzymic active sites and signal sequences. Nucleic acid target motifs include, but are not limited to, promoter sequences, hairpin structures and inducible expression elements (protein binding sequences).

A variety of structural formats for the input and output means can be used to input and output the information in the computer-based systems of the present invention. A preferred format for an output means ranks fragments of the *Borrelia burgdorferi* genomic sequences possessing varying degrees of homology to the target sequence or target motif. Such presentation provides a skilled artisan with a ranking of sequences which contain various amounts of the target sequence or target motif and identifies the degree of homology contained in the identified fragment.

A variety of comparing means can be used to compare a target sequence or target motif with the data storage means to identify sequence fragments of the *Borrelia burgdorferi* genome. In the present examples, implementing software which implement the BLAST and BLAZE algorithms, described in Altschul *et al.*, *J. Mol. Biol.* 215: 403-410 (1990), is used to identify open reading frames within the *Borrelia burgdorferi* genome. A skilled artisan can readily recognize that any one of the publicly available homology search programs can be used as the search means for the computer-based systems of the present invention. Of course, suitable proprietary systems that may be known to those of skill also may be employed in this regard.

Figure 1 provides a block diagram of a computer system illustrative of embodiments of this aspect of present invention. The computer system 102 includes a processor 106 connected to a bus 104. Also connected to the bus 104 are a main memory 108 (preferably implemented as random access memory, RAM) and a variety of secondary storage devices 110, such as a hard drive 112 and a removable medium storage device 114. The removable medium storage device

114 may represent, for example, a floppy disk drive, a CD-ROM drive, a magnetic tape drive, etc. A removable storage medium 116 (such as a floppy disk, a compact disk, a magnetic tape, etc.) containing control logic and/or data recorded therein may be inserted into the removable medium storage device 114. The computer system 102 includes appropriate software for reading the control logic and/or the data from the removable medium storage device 114, once it is inserted into the removable medium storage device 114.

A nucleotide sequence of the present invention may be stored in a well known manner in the main memory 108, any of the secondary storage devices 110, and/or a removable storage medium 116. During execution, software for accessing and processing the genomic sequence (such as search tools, comparing tools, etc.) reside in main memory 108, in accordance with the requirements and operating parameters of the operating system, the hardware system and the software program or programs.

BIOCHEMICAL EMBODIMENTS

Other embodiments of the present invention are directed to isolated fragments of the *Borrelia burgdorferi* genome. The fragments of the *Borrelia burgdorferi* genome of the present invention include, but are not limited to fragments which encode peptides, hereinafter open reading frames (ORFs), fragments which modulate the expression of an operably linked ORF, hereinafter expression modulating fragments (EMFs) and fragments which can be used to diagnose the presence of *Borrelia burgdorferi* in a sample, hereinafter diagnostic fragments (DFs).

As used herein, an "isolated nucleic acid molecule" or an "isolated fragment of the *Borrelia burgdorferi* genome" refers to a nucleic acid molecule possessing a specific nucleotide sequence which has been subjected to purification means to reduce, from the composition, the number of compounds which are normally associated with the composition. Particularly, the term refers to the nucleic acid molecules having the sequences set out in SEQ ID NOS: 1-155, to representative fragments thereof as described above including ORF IDs and ORFs, to polynucleotides at least 95%, preferably at least 96%, 97%, 98%, or 99% and especially preferably at least 99.9% identical in sequence thereto, also as set out above.

A variety of purification means can be used to generate the isolated fragments of the present invention. These include, but are not limited to methods which separate constituents of a solution based on charge, solubility, or size.

In one embodiment, *Borrelia burgdorferi* DNA can be enzymatically sheared to produce fragments of 15-20 kb in length. These fragments can then be used to generate a *Borrelia burgdorferi* library by inserting them into lambda clones as described in the Examples below. Primers flanking, for example, an ORF, such as those enumerated in Tables 1-6 can then be generated using nucleotide sequence information provided in SEQ ID NOS: 1-155. Well known and routine techniques of PCR cloning then can be used to isolate the ORF from the lambda DNA library or *Borrelia burgdorferi* genomic DNA. Thus, given the availability of SEQ ID NOS: 1-

155, the information in Tables 1-6, and the information that may be obtained readily by analysis of the sequences of SEQ ID NOS:1-155 using methods set out above, those of skill will be enabled by the present disclosure to isolate any ORF-containing or other nucleic acid fragment of the present invention.

5 The isolated nucleic acid molecules of the present invention include, but are not limited to single stranded and double stranded DNA, and single stranded RNA. For purposes of numbering and reference to polynucleotide and polypeptide sequences the entire sequence of each sequence of SEQ ID NOS:1-155 is included with the first nucleotide being position 1.

10 Therefore, for reference purposes the numbering used in the present invention is that provided in the sequence listing for SEQ ID NOS:1-155.

As used herein, an open reading frame (ORF), means a series of nucleotide triplets coding for amino acid residues without any termination codons and is a sequence translatable into protein. Further, unless specified, the term "ORF" for each ORF ID is defined by the termination codon at the 3' end and the 5' most methionine codon, at the 5' end; in frame with said 3' termination codon. Unless specified, the term "ORF" also refers to a particular polypeptide sequence defined by the ORF polynucleotide sequence, wherein the N-terminus is defined by the 5' most methionine codon in frame with the termination codon at the 3' end of the ORF ID and the C-terminus is defined by the last codon before the said 3' termination codon. As used herein, an ORF ID represents a sequence without any internal termination codons flanked by termination codons.

20 Tables 1-6 list ORF IDs in the *Borrelia burgdorferi* genomic contigs of the present invention that were identified as putative coding regions by the GeneMark software using organism-specific second-order Markov probability transition matrices. It will be appreciated that other criteria can be used, in accordance with well known analytical methods, such as those discussed herein, to generate more inclusive, more restrictive, or more selective lists.

25 The *B. burgdorferi* genome consists of one large linear chromosome containing approximately two thirds of its genetic material and multiple extrachromosomal elements (approximately 15) containing the remaining one third of its genetic material. SEQ ID NO:1 (Contig ID 1) is the complete sequence of the large linear *B. burgdorferi* chromosome. SEQ ID NOS:2-155 (Contig ID 2-155 respectively) are fragments (contigs) of the extrachromosomal elements. Tables 1-3 below relate only to SEQ ID NO:1. Tables 4-6 relate to the extrachromosomal elements (SEQ ID NOS:2-155).

30 Table 1 sets out ORF IDs in the *Borrelia burgdorferi* chromosome of the present invention that cover a continuous region of at least 50 bases are 95% or more identical (by BLAST analysis using default parameters) to a nucleotide sequence available through GenBank in July, 1997.

Table 2 sets out ORF IDs in the *Borrelia burgdorferi* chromosome of the present invention that are not in Table 1 and match, with a BLASTP probability score of 0.01 or less, a polypeptide sequence available through GenBank in July, 1997.

Table 3 sets out ORF IDs in the *Borrelia burgdorferi* chromosome of the present invention that do not match significantly, by BLASTP analysis, a polypeptide sequence available through GenBank in July, 1997.

Table 4 sets out ORF IDs in the *Borrelia burgdorferi* extrachromosomal element contigs of the present invention that over a continuous region of at least 50 bases are 95% or more identical (by BLAST analysis) to a nucleotide sequence available through GenBank in July, 1997.

Table 5 sets out ORF IDs in the *Borrelia burgdorferi* extrachromosomal element contigs of the present invention that are not in Table 1 and match, with a BLASTP probability score of 0.01 or less, a polypeptide sequence available through GenBank in July, 1997.

Table 6 sets out ORF IDs in the *Borrelia burgdorferi* extrachromosomal element contigs of the present invention that do not match significantly, by BLASTP analysis, a polypeptide sequence available through GenBank in July, 1997.

In each table, the first and second columns identify the ORF ID by, respectively, contig number and ORF ID number within the contig; the third column indicates the first nucleotide of the ORF ID, counting from the 5' end of the contig strand; and the fourth column indicates the last nucleotide of the ORF ID, counting from the 5' end of the contig strand.

In Tables 1, 2, 4 and 5, column five, lists the Reference for the closest matching sequence available through GenBank. These reference numbers are the database accession numbers commonly used by those of skill in the art, who will be familiar with their denominators. Descriptions of the nomenclature are available from the National Center for Biotechnology Information. Column seven provides the BLAST identity score from the comparison of the ORF ID and the homologous gene; and column nine indicates the length in nucleotides of the highest scoring segment pair identified by the BLAST identity analysis.

The concepts of percent identity and percent similarity of two polypeptide sequences is well understood in the art. For example, two polypeptides 10 amino acids in length which differ at three amino acid positions (*e.g.*, at positions 1, 3 and 5) are said to have a percent identity of 70%. However, the same two polypeptides would be deemed to have a percent similarity of 80% if, for example at position 5, the amino acids moieties, although not identical, were "similar" (*i.e.*, possessed similar biochemical characteristics). As is known in the art, substitution of one amino acid for a "similar" amino acid is a conservative substitution.

Generally, proteins are highly tolerant of conservative substitutions. Many programs for analysis of nucleotide or amino acid sequence similarity, such as fasta and BLAST specifically list percent identity of a matching region as an output parameter. Thus, for instance, Tables 1, 2, 4 and 5 herein enumerate the percent identity and similarity of the highest scoring segment pair in each ORF and its listed relative. Further details concerning the algorithms and criteria used for homology searches are provided below and are described in the pertinent literature highlighted by the citations provided below.

It will be appreciated that other criteria can be used to generate more inclusive and more exclusive listings of the types set out in the tables. As those of skill will appreciate, narrow and broad searches both are useful. Thus, a skilled artisan can readily identify ORFs in contigs of the *Borrelia burgdorferi* genome other than those listed in Tables 1-6, such as ORFs which are overlapping or encoded by the opposite strand of an identified ORF in addition to those ascertainable using the computer-based systems of the present invention.

As used herein, an "expression modulating fragment," EMF, means a series of nucleotide molecules which modulates the expression of an operably linked ORF or EMF.

As used herein, a sequence is said to "modulate the expression of an operably linked sequence" when the expression of the sequence is altered by the presence of the EMF. EMFs include, but are not limited to, promoters, and promoter modulating sequences (inducible elements). One class of EMFs are fragments which induce the expression of an operably linked ORF in response to a specific regulatory factor or physiological event.

EMF sequences can be identified within the contigs of the *Borrelia burgdorferi* genome by their proximity to the ORFs provided in Tables 1-6. An intergenic segment, or a fragment of the intergenic segment, from about 10 to 200 nucleotides in length, taken from any one of the ORFs of Tables 1-6 will modulate the expression of an operably linked ORF in a fashion similar to that found with the naturally linked ORF sequence. As used herein, an "intergenic segment" refers to fragments of the *Borrelia burgdorferi* genome which are between two ORF(s) herein described. EMFs also can be identified using known EMFs as a target sequence or target motif in the computer-based systems of the present invention. Further, the two methods can be combined and used together.

The presence and activity of an EMF can be confirmed using an EMF trap vector. An EMF trap vector contains a cloning site linked to a marker sequence. A marker sequence encodes an identifiable phenotype, such as antibiotic resistance or a complementing nutrition auxotrophic factor, which can be identified or assayed when the EMF trap vector is placed within an appropriate host under appropriate conditions. As described above, a EMF will modulate the expression of an operably linked marker sequence. A more detailed discussion of various marker sequences is provided below. A sequence which is suspected as being an EMF is cloned in all three reading frames in one or more restriction sites upstream from the marker sequence in the EMF trap vector. The vector is then transformed into an appropriate host using known procedures and the phenotype of the transformed host is examined under appropriate conditions. As described above, an EMF will modulate the expression of an operably linked marker sequence.

As used herein, a "diagnostic fragment," DF, means a series of nucleotide molecules which selectively hybridize to *Borrelia burgdorferi* sequences. DFs can be readily identified by identifying unique sequences within contigs of the *Borrelia burgdorferi* genome, such as by using well-known computer analysis software, and by generating and testing probes or

amplification primers consisting of the DF sequence in an appropriate diagnostic format which determines amplification or hybridization selectivity.

The sequences falling within the scope of the present invention are not limited to the specific sequences herein described, but also include allelic and species variations thereof. Allelic and species variations can be routinely determined by comparing the sequences provided in SEQ ID NOS:1-155, ORF IDs and ORFs within, a representative fragment thereof, or a nucleotide sequence at least 99% and preferably 99.9% identical to SEQ ID NOS: 1-155, ORF IDs and ORFs within, with a sequence from another isolate of the same species. Furthermore, to accommodate codon variability, the invention includes nucleic acid molecules coding for the same amino acid sequences as do the specific ORFs disclosed herein. In other words, in the coding region of an ORF, substitution of one codon for another which encodes the same amino acid is expressly contemplated.

Any specific sequence disclosed herein can be readily screened for errors by resequencing a particular fragment, such as an ORF, in both directions (*i.e.*, sequence both strands).

Alternatively, error screening can be performed by sequencing corresponding polynucleotides of *Borrelia burgdorferi* origin isolated by using part or all of the fragments in question as a probe or primer.

Each of the ORF IDs and ORFs of the *Borrelia burgdorferi* genome disclosed in Tables 1-6, and the EMFs found 5' to the ORF IDs, can be used as polynucleotide reagents in numerous ways. For example, the sequences can be used as diagnostic probes or diagnostic amplification primers to detect the presence of a specific microbe in a sample, particularly *Borrelia burgdorferi*. Especially preferred in this regard are ORF IDs and ORFs such as those of Tables 3 and 6, which do not match previously characterized sequences from other organisms and thus are most likely to be highly selective for *Borrelia burgdorferi*. Also particularly preferred are ORF IDs and ORFs that can be used to distinguish between strains of *Borrelia burgdorferi*, particularly those that distinguish medically important strain, such as drug-resistant strains.

In addition, the fragments of the present invention, as broadly described, can be used to control gene expression through triple helix formation or antisense DNA or RNA, both of which methods are based on the binding of a polynucleotide sequence to DNA or RNA. Triple helix formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Information from the sequences of the present invention can be used to design antisense and triple helix-forming oligonucleotides. Polynucleotides suitable for use in these methods are usually 20 to 40 bases in length and are designed to be complementary to a region of the gene involved in transcription, for triple-helix formation, or to the mRNA itself, for antisense inhibition. Both techniques have been demonstrated to be effective in model systems, and the requisite techniques are well known and involve routine procedures. Triple helix techniques are discussed in, for example, Lee *et al.*, *Nucl. Acids Res.* 6:3073 (1979); Cooney *et al.*, *Science* 241:456 (1988); and Dervan *et al.*, *Science* 251:1360 (1991). Antisense techniques in general are discussed in, for instance, Okano,

J. Neurochem. 56:560 (1991) and *Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression*, CRC Press, Boca Raton, FL (1988)).

The present invention further provides recombinant constructs comprising one or more fragments of the *Borrelia burgdorferi* genomic fragments and contigs of the present invention.

- 5 Certain preferred recombinant constructs of the present invention comprise a vector, such as a plasmid or viral vector, into which a fragment of the *Borrelia burgdorferi* genome has been inserted, in a forward or reverse orientation. In the case of a vector comprising one of the ORF IDs or ORFs of the present invention, the vector may further comprise regulatory sequences, including for example, a promoter, operably linked to the ORF ID or ORF. For vectors
- 10 comprising the EMFs of the present invention, the vector may further comprise a marker sequence or heterologous ORF ID or ORF operably linked to the EMF.

Large numbers of suitable vectors and promoters are known to those of skill in the art and are commercially available for generating the recombinant constructs of the present invention.

The following vectors are provided by way of example. Useful bacterial vectors include

- 15 phagescript, PsiX174, pBluescript SK, pBS KS, pNH8a, pNH16a, pNH18a, pNH46a (available from Stratagene); pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (available from Pharmacia); pQE vectors (available from Promega). Useful eukaryotic vectors include pWLneo, pSV2cat, pOG44, pXT1, pSG (available from Stratagene) pSVK3, pBPV, pMSG, pSVL (available from Pharmacia).

- 20 Promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers. Two appropriate vectors are pKK232-8 and pCM7. Particular named bacterial promoters include lacI, lacZ, T3, T7, gpt, lambda PR, and trc. Eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein- I. Selection of
- 25 the appropriate vector and promoter is well within the level of ordinary skill in the art.

The present invention further provides host cells containing any one of the isolated fragments of the *Borrelia burgdorferi* genomic fragments and contigs of the present invention, wherein the fragment has been introduced into the host cell using known methods. The host cell can be a higher eukaryotic host cell, such as a mammalian cell, a lower eukaryotic host cell, such

30 as a yeast cell, or a procaryotic cell, such as a bacterial cell.

A polynucleotide of the present invention, such as a recombinant construct comprising an ORF of the present invention, may be introduced into the host by a variety of well established techniques that are standard in the art, such as calcium phosphate transfection, DEAE, dextran mediated transfection and electroporation, which are described in, for instance, Davis, L. *et al.*,

35 BASIC METHODS IN MOLECULAR BIOLOGY (1986).

A host cell containing one of the fragments of the *Borrelia burgdorferi* genomic fragments and contigs of the present invention, can be used in conventional manners to produce the gene product encoded by the isolated fragment (in the case of an ORF) or can be used to produce a heterologous protein under the control of the EMF.

The present invention further provides isolated polypeptides encoded by the nucleic acid fragments of the present invention or by degenerate variants of the nucleic acid fragments of the present invention. By "degenerate variant" is intended nucleotide fragments which differ from a nucleic acid fragment of the present invention (*e.g.*, an ORF) by nucleotide sequence but, due to the degeneracy of the Genetic Code, encode an identical polypeptide sequence.

Preferred nucleic acid fragments of the present invention are the ORF IDs depicted in Tables 2, 3, 5 and 6, and ORFs within, which encode proteins.

A variety of methodologies known in the art can be utilized to obtain any one of the isolated polypeptides or proteins of the present invention. At the simplest level, the amino acid sequence can be synthesized using commercially available peptide synthesizers. This is particularly useful in producing small peptides and fragments of larger polypeptides. Such short fragments as may be obtained most readily by synthesis are useful, for example, in generating antibodies against the native polypeptide, as discussed further below.

In an alternative method, the polypeptide or protein is purified from bacterial cells which naturally produce the polypeptide or protein. One skilled in the art can readily employ well-known methods for isolating polypeptides and proteins to isolate and purify polypeptides or proteins of the present invention produced naturally by a bacterial strain, or by other methods. Methods for isolation and purification that can be employed in this regard include, but are not limited to, immunochromatography, HPLC, size-exclusion chromatography, ion-exchange chromatography, and immuno-affinity chromatography.

The polypeptides and proteins of the present invention also can be purified from cells which have been altered to express the desired polypeptide or protein. As used herein, a cell is said to be altered to express a desired polypeptide or protein when the cell, through genetic manipulation, is made to produce a polypeptide or protein which it normally does not produce or which the cell normally produces at a lower level. Those skilled in the art can readily adapt procedures for introducing and expressing either recombinant or synthetic sequences into eukaryotic or prokaryotic cells in order to generate a cell which produces one of the polypeptides or proteins of the present invention.

The polypeptides of the present invention are preferably provided in an isolated form, and preferably are substantially purified. A recombinantly produced version of the *B. burgdorferi* polypeptide can be substantially purified by the one-step method described by Smith et al. (1988) Gene 67:31-40. Polypeptides of the invention also can be purified from natural or recombinant sources using antibodies directed against the polypeptides of the invention in methods which are well known in the art of protein purification.

The invention further provides for isolated *B. burgdorferi* polypeptides comprising an amino acid sequence selected from the group including: (a) the amino acid sequence of a full-length *B. burgdorferi* polypeptide having the complete amino acid sequence from the first methionine codon to the termination codon of each sequence listed in SEQ ID NOS:1-155, wherein said termination codon is at the end of each SEQ ID NO: and said first methionine is the

first methionine in frame with said termination codon; and (b) the amino acid sequence of a full-length *B. burgdorferi* polypeptide having the complete amino acid sequence in (a) excepting the N-terminal methionine.

The polypeptides of the present invention also include polypeptides having an amino acid sequence at least 80% identical, more preferably at least 90% identical, and still more preferably 95%, 96%, 97%, 98% or 99% identical to those described in (a) and (b) above.

The present invention is further directed to polynucleotides encoding portions or fragments of the amino acid sequences described herein as well as to portions or fragments of the isolated amino acid sequences described herein. Fragments include portions of the amino acid sequences described herein at least 5 contiguous amino acid in length and selected from any two integers, one of which representing an N-terminal position and another representing a C-terminal position. The initiation codon of the ORFs of the present invention is position 1. The initiation codon (position 1) for purposes of the present invention is the first methionine codon of each ORF ID which is in frame with the termination codon at the end of each said sequence. Every combination of a N-terminal and C-terminal position that a fragment at least 5 contiguous amino acid residues in length could occupy, on any given ORF is included in the invention, i.e., from initiation codon up to the termination codon. "At least" means a fragment may be 5 contiguous amino acid residues in length or any integer between 5 and the number of residues in an ORF, minus 1. Therefore, included in the invention are contiguous fragments specified by any N-terminal and C-terminal positions of amino acid sequence set forth in SEQ ID NOS:1-155 or Tables 1-6 wherein the contiguous fragment is any integer between 5 and the number of residues in an ORF minus 1.

Further, the invention includes polypeptides comprising fragments specified by size, in amino acid residues, rather than by N-terminal and C-terminal positions. The invention includes any fragment size, in contiguous amino acid residues, selected from integers between 5 and the number of residues in an ORF, minus 1. Preferred sizes of contiguous polypeptide fragments include about 5 amino acid residues, about 10 amino acid residues, about 20 amino acid residues, about 30 amino acid residues, about 40 amino acid residues, about 50 amino acid residues, about 100 amino acid residues, about 200 amino acid residues, about 300 amino acid residues, and about 400 amino acid residues. The preferred sizes are, of course, meant to exemplify, not limit, the present invention as all size fragments representing any integer between 5 and the number of residues in a full length sequence minus 1 are included in the invention. The present invention also provides for the exclusion of any fragments specified by N-terminal and C-terminal positions or by size in amino acid residues as described above. Any number of fragments specified by N-terminal and C-terminal positions or by size in amino acid residues as described above may be excluded.

The above fragments need not be active since they would be useful, for example, in immunoassays, in epitope mapping, epitope tagging, to generate antibodies to a particular portion of the protein, as vaccines, and as molecular weight markers.

Further polypeptides of the present invention include polypeptides which have at least 90% similarity, more preferably at least 95% similarity, and still more preferably at least 96%, 97%, 98% or 99% similarity to those described above.

5 A further embodiment of the invention relates to a polypeptide which comprises the amino acid sequence of a *B. burgdorferi* polypeptide having an amino acid sequence which contains at least one conservative amino acid substitution, but not more than 50 conservative amino acid substitutions, not more than 40 conservative amino acid substitutions, not more than 30 conservative amino acid substitutions, and not more than 20 conservative amino acid substitutions. Also provided are polypeptides which comprise the amino acid sequence of a *B.*
10 *burgdorferi* polypeptide, having at least one, but not more than 10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 conservative amino acid substitutions.

By a polypeptide having an amino acid sequence at least, for example, 95% "identical" to a query amino acid sequence of the present invention, it is intended that the amino acid sequence of the subject polypeptide is identical to the query sequence except that the subject polypeptide
15 sequence may include up to five amino acid alterations per each 100 amino acids of the query amino acid sequence. In other words, to obtain a polypeptide having an amino acid sequence at least 95% identical to a query amino acid sequence, up to 5% of the amino acid residues in the subject sequence may be inserted, deleted, (indels) or substituted with another amino acid. These alterations of the reference sequence may occur at the amino or carboxy terminal positions of the
20 reference amino acid sequence or anywhere between those terminal positions, interspersed either individually among residues in the reference sequence or in one or more contiguous groups within the reference sequence.

As a practical matter, whether any particular polypeptide is at least 90%, 95%, 96%, 97%, 98% or 99% identical to the ORF amino acid sequences encoded by the sequences of SEQ
25 ID NOS:1-155, as described hererin, can be determined conventionally using known computer programs. A preferred method for determining the best overall match between a query sequence (a sequence of the present invention) and a subject sequence, also referred to as a global sequence alignment, can be determined using the FASTDB computer program based on the algorithm of Brutlag et al., (1990) Comp. App. Biosci. 6:237-245. In a sequence alignment the query and
30 subject sequences are both amino acid sequences. The result of said global sequence alignment is in percent identity. Preferred parameters used in a FASTDB amino acid alignment are: Matrix=PAM 0, k-tuple=2, Mismatch Penalty=1, Joining Penalty=20, Randomization Group Length=0, Cutoff Score=1, Window Size=sequence length, Gap Penalty=5, Gap Size Penalty=0.05, Window Size=500 or the length of the subject amino acid sequence, whichever is
35 shorter.

If the subject sequence is shorter than the query sequence due to N- or C-terminal deletions, not because of internal deletions, the results, in percent identity, must be manually corrected. This is because the FASTDB program does not account for N- and C-terminal truncations of the subject sequence when calculating global percent identity. For subject

sequences truncated at the N- and C-termini, relative to the query sequence, the percent identity is corrected by calculating the number of residues of the query sequence that are N- and C-terminal of the subject sequence, which are not matched/aligned with a corresponding subject residue, as a percent of the total bases of the query sequence. Whether a residue is matched/aligned is
5 determined by results of the FASTDB sequence alignment. This percentage is then subtracted from the percent identity, calculated by the above FASTDB program using the specified parameters, to arrive at a final percent identity score. This final percent identity score is what is used for the purposes of the present invention. Only residues to the N- and C-termini of the subject sequence, which are not matched/aligned with the query sequence, are considered for the
10 purposes of manually adjusting the percent identity score. That is, only query amino acid residues outside the farthest N- and C-terminal residues of the subject sequence.

For example, a 90 amino acid residue subject sequence is aligned with a 100 residue query sequence to determine percent identity. The deletion occurs at the N-terminus of the subject sequence and therefore, the FASTDB alignment does not match/align with the first 10
15 residues at the N-terminus. The 10 unpaired residues represent 10% of the sequence (number of residues at the N- and C-termini not matched/total number of residues in the query sequence) so 10% is subtracted from the percent identity score calculated by the FASTDB program. If the remaining 90 residues were perfectly matched the final percent identity would be 90%. In another example, a 90 residue subject sequence is compared with a 100 residue query sequence.
20 This time the deletions are internal so there are no residues at the N- or C-termini of the subject sequence which are not matched/aligned with the query. In this case the percent identity calculated by FASTDB is not manually corrected. Once again, only residue positions outside the N- and C-terminal ends of the subject sequence, as displayed in the FASTDB alignment, which are not matched/aligned with the query sequence are manually corrected. No other manual
25 corrections are to be made for the purposes of the present invention.

The above polypeptide sequences are included irrespective of whether they have their normal biological activity. This is because even where a particular polypeptide molecule does not have biological activity, one of skill in the art would still know how to use the polypeptide, for instance, as a vaccine or to generate antibodies. Other uses of the polypeptides of the present
30 invention that do not have *B. burgdorferi* activity include, *inter alia*, as epitope tags, in epitope mapping, and as molecular weight markers on SDS-PAGE gels or on molecular sieve gel filtration columns using methods known to those of skill in the art.

As described below, the polypeptides of the present invention can also be used to raise polyclonal and monoclonal antibodies, which are useful in assays for detecting *B. burgdorferi* protein
35 expression or as agonists and antagonists capable of enhancing or inhibiting *B. burgdorferi* protein function. Further, such polypeptides can be used in the yeast two-hybrid system to "capture" *B. burgdorferi* protein binding proteins which are also candidate agonists and antagonists according to the present invention. See, e.g., Fields et al. (1989) Nature 340:245-246.

Any host/vector system can be used to express one or more of the ORFs of the present invention. These include, but are not limited to, eukaryotic hosts such as HeLa cells, CV-1 cell, COS cells, and Sf9 cells, as well as prokaryotic host such as *E. coli* and *B. subtilis*. The most preferred cells are those which do not normally express the particular polypeptide or protein or which expresses the polypeptide or protein at low natural level.

"Recombinant," as used herein, means that a polypeptide or protein is derived from recombinant (*e.g.*, microbial or mammalian) expression systems. "Microbial" refers to recombinant polypeptides or proteins made in bacterial or fungal (*e.g.*, yeast) expression systems. As a product, "recombinant microbial" defines a polypeptide or protein essentially free of native endogenous substances and unaccompanied by associated native glycosylation. Polypeptides or proteins expressed in most bacterial cultures, *e.g.*, *E. coli*, will be free of glycosylation modifications; polypeptides or proteins expressed in yeast will have a glycosylation pattern different from that expressed in mammalian cells.

"Nucleotide sequence" refers to a heteropolymer of deoxyribonucleotides. Generally, DNA segments encoding the polypeptides and proteins provided by this invention are assembled from fragments of the *Borrelia burgdorferi* genome and short oligonucleotide linkers, or from a series of oligonucleotides, to provide a synthetic gene which is capable of being expressed in a recombinant transcriptional unit comprising regulatory elements derived from a microbial or viral operon.

Recombinant expression vehicle or vector" refers to a plasmid or phage or virus or vector, for expressing a polypeptide from a DNA (RNA) sequence. The expression vehicle can comprise a transcriptional unit comprising an assembly of (1) a genetic regulatory elements necessary for gene expression in the host, including elements required to initiate and maintain transcription at a level sufficient for suitable expression of the desired polypeptide, including, for example, promoters and, where necessary, an enhancer and a polyadenylation signal; (2) a structural or coding sequence which is transcribed into mRNA and translated into protein, and (3) appropriate signals to initiate translation at the beginning of the desired coding region and terminate translation at its end. Structural units intended for use in yeast or eukaryotic expression systems preferably include a leader sequence enabling extracellular secretion of translated protein by a host cell. Alternatively, where recombinant protein is expressed without a leader or transport sequence, it may include an N-terminal methionine residue. This residue may or may not be subsequently cleaved from the expressed recombinant protein to provide a final product.

"Recombinant expression system" means host cells which have stably integrated a recombinant transcriptional unit into chromosomal DNA or carry the recombinant transcriptional unit extra chromosomally. The cells can be prokaryotic or eukaryotic. Recombinant expression systems as defined herein will express heterologous polypeptides or proteins upon induction of the regulatory elements linked to the DNA segment or synthetic gene to be expressed.

Mature proteins can be expressed in mammalian cells, yeast, bacteria, or other cells under the control of appropriate promoters. Cell-free translation systems can also be employed to

produce such proteins using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described in Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual*, 2nd Edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York (1989), the disclosure of which is hereby incorporated by reference in its entirety.

Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transformation of the host cell, *e.g.*, the ampicillin resistance gene of *E. coli* and *S. cerevisiae* TRP1 gene, and a promoter derived from a highly expressed gene to direct transcription of a downstream structural sequence. Such promoters can be derived from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK), alpha-factor, acid phosphatase, or heat shock proteins, among others. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein into the periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an N-terminal identification peptide imparting desired characteristics, *e.g.*, stabilization or simplified purification of expressed recombinant product.

Useful expression vectors for bacterial use are constructed by inserting a structural DNA sequence encoding a desired protein together with suitable translation initiation and termination signals in operable reading phase with a functional promoter. The vector will comprise one or more phenotypic selectable markers and an origin of replication to ensure maintenance of the vector and, when desirable, provide amplification within the host.

Suitable prokaryotic hosts for transformation include strains of *E. coli*, *B. subtilis*, *Salmonella typhimurium* and various species within the genera *Pseudomonas* and *Streptomyces*. Others may, also be employed as a matter of choice.

As a representative but non-limiting example, useful expression vectors for bacterial use can comprise a selectable marker and bacterial origin of replication derived from commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017). Such commercial vectors include, for example, pKK223-3 (available from Pharmacia Fine Chemicals, Uppsala, Sweden) and GEM 1 (available from Promega Biotec, Madison, WI, USA). These pBR322 "backbone" sections are combined with an appropriate promoter and the structural sequence to be expressed.

Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter, where it is inducible, is derepressed or induced by appropriate means (*e.g.*, temperature shift or chemical induction) and cells are cultured for an additional period to provide for expression of the induced gene product. Thereafter cells are typically harvested, generally by centrifugation, disrupted to release expressed protein, generally by physical or chemical means, and the resulting crude extract is retained for further purification.

Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7 lines of monkey kidney

fibroblasts, described in Gluzman, *Cell* 23:175 (1981), and other cell lines capable of expressing a compatible vector, for example, the C127, 3T3, CHO, HeLa and BHK cell lines.

Mammalian expression vectors will comprise an origin of replication, a suitable promoter and enhancer, and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5' flanking nontranscribed sequences. DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early promoter, enhancer, splice, and polyadenylation sites may be used to provide the required nontranscribed genetic elements.

Recombinant polypeptides and proteins produced in bacterial culture is usually isolated by initial extraction from cell pellets, followed by one or more salting-out, aqueous ion exchange or size exclusion chromatography steps. Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents. Protein refolding steps can be used, as necessary, in completing configuration of the mature protein. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps.

The present invention further includes isolated polypeptides, proteins and nucleic acid molecules which are substantially equivalent to those herein described. As used herein, substantially equivalent can refer both to nucleic acid and amino acid sequences, for example a mutant sequence, that varies from a reference sequence by one or more substitutions, deletions, or additions, the net effect of which does not result in an adverse functional dissimilarity between reference and subject sequences. Particularly preferred in this regard are conservative substitutions, known to those of skill in the art. For purposes of the present invention, sequences having equivalent biological activity, and equivalent expression characteristics are considered substantially equivalent. For purposes of determining equivalence, truncation of the mature sequence (e.g., removal of leader sequence(s)) should be disregarded.

The invention further provides methods of obtaining homologs from other strains of *Borrelia burgdorferi*, of the fragments of the *Borrelia burgdorferi* genome of the present invention and homologs of the proteins encoded by the ORFs of the present invention. As used herein, a sequence or protein of *Borrelia burgdorferi* is defined as a homolog of a fragment of the *Borrelia burgdorferi* fragments or contigs or a protein encoded by one of the ORFs of the present invention, if it shares significant homology to one of the fragments of the *Borrelia burgdorferi* genome of the present invention or a protein encoded by one of the ORFs of the present invention. Specifically, by using the sequence disclosed herein as a probe or as primers, and techniques such as PCR cloning and colony/plaque hybridization, one skilled in the art can obtain homologs.

As used herein, two nucleic acid molecules or proteins are said to "share significant homology" if the two contain regions which possess greater than 85% sequence (amino acid or nucleic acid) homology. Preferred homologs in this regard are those with more than 90% homology. Especially preferred are those with 95% or more homology. Among especially

preferred homologs those with 96, 97%, 98%, 99% or more homology are particularly preferred. The most preferred homologs among these are those with 99.9% homology or more. It will be understood that, among measures of homology, identity is particularly preferred in this regard.

5 Region specific primers or probes derived from the nucleotide sequence provided in SEQ ID NOS: 1-155 or from a nucleotide sequence at least 95%, particularly at least 96%, 97%, 98% or 99%, especially at least 99.5% identical to a sequence of SEQ ID NOS: 1-155 can be used to prime DNA synthesis and PCR amplification, as well as to identify colonies containing cloned DNA encoding a homolog. Methods suitable to this aspect of the present invention are well
10 known and have been described in great detail in many publications such as, for example, Innis *et al.*, *PCR Protocols*, Academic Press, San Diego, CA (1990)).

 When using primers derived from SEQ ID NOS: 1-155 or from a nucleotide sequence having an aforementioned identity to a sequence of SEQ ID NOS:1-155, one skilled in the art will recognize that by employing high stringency conditions (*e.g.*, annealing at 50-60°C in 6X SSPC and 50% formamide, and washing at 50- 65°C in 0.5X SSPC) only sequences which are greater
15 than 75% homologous to the primer will be amplified. By employing lower stringency conditions (*e.g.*, hybridizing at 35-37°C in 5X SSPC and 40-45% formamide, and washing at 42°C in 0.5X SSPC), sequences which are greater than 40-50% homologous to the primer will also be amplified.

20 When using DNA probes derived from SEQ ID NOS:1-155, or from a nucleotide sequence having an aforementioned identity to a sequence of SEQ ID NOS: 1-155 , for colony/plaque hybridization, one skilled in the art will recognize that by employing high stringency conditions (*e.g.*, hybridizing at 50- 65°C in 5X SSPC and 50% formamide, and washing at 50- 65°C in 0.5X SSPC), sequences having regions which are greater than 90%
25 homologous to the probe can be obtained, and that by employing lower stringency conditions (*e.g.*, hybridizing at 35-37°C in 5X SSPC and 40-45% formamide, and washing at 42°C in 0.5X SSPC), sequences having regions which are greater than 35-45% homologous to the probe will be obtained.

 Any organism can be used as the source for homologs of the present invention so long as
30 the organism naturally expresses such a protein or contains genes encoding the same. The most preferred organism for isolating homologs are bacteria which are closely related to *Borrelia burgdorferi*.

ILLUSTRATIVE USES OF COMPOSITIONS OF THE INVENTION

35 Each ORF of the ORF IDs provided in Tables 1, 2, 4 and 5 is identified with a function by homology to a known gene or polypeptide. As a result, one skilled in the art can use the polypeptides of the present invention for commercial, therapeutic and industrial purposes consistent with the type of putative identification of the polypeptide. Such identifications permit one skilled in the art to use the *Borrelia burgdorferi* ORFs in a manner similar to the known type

of sequences for which the identification is made; for example, to ferment a particular sugar source or to produce a particular metabolite. A variety of reviews illustrative of this aspect of the invention are available, including the following reviews on the industrial use of enzymes, for example, BIOCHEMICAL ENGINEERING AND BIOTECHNOLOGY HANDBOOK, 2nd Ed., MacMillan Publications, Ltd. NY (1991) and BIOCATALYSTS IN ORGANIC SYNTHESIS, Tramper *et al.*, Eds., Elsevier Science Publishers, Amsterdam, The Netherlands (1985). A variety of exemplary uses that illustrate this and similar aspects of the present invention are discussed below.

1. Biosynthetic Enzymes

Open reading frames encoding proteins involved in mediating the catalytic reactions involved in intermediary and macromolecular metabolism, the biosynthesis of small molecules, cellular processes and other functions includes enzymes involved in the degradation of the intermediary products of metabolism, enzymes involved in central intermediary metabolism, enzymes involved in respiration, both aerobic and anaerobic, enzymes involved in fermentation, enzymes involved in ATP proton motor force conversion, enzymes involved in broad regulatory function, enzymes involved in amino acid synthesis, enzymes involved in nucleotide synthesis, enzymes involved in cofactor and vitamin synthesis, can be used for industrial biosynthesis.

The various metabolic pathways present in *Borrelia burgdorferi* can be identified based on absolute nutritional requirements as well as by examining the various enzymes identified in Table 1-6 and SEQ ID NOS:1-155.

Of particular interest are polypeptides involved in the degradation of intermediary metabolites as well as non-macromolecular metabolism. Such enzymes include amylases, glucose oxidases, and catalase.

Proteolytic enzymes are another class of commercially important enzymes. Proteolytic enzymes find use in a number of industrial processes including the processing of flax and other vegetable fibers, in the extraction, clarification and depectinization of fruit juices, in the extraction of vegetables' oil and in the maceration of fruits and vegetables to give unicellular fruits. A detailed review of the proteolytic enzymes used in the food industry is provided in Rombouts *et al.*, *Symbiosis* 21:79 (1986) and Voragen *et al.* in *Biocatalysts In Agricultural Biotechnology*, Whitaker *et al.*, Eds., *American Chemical Society Symposium Series* 389:93 (1989).

The metabolism of sugars is an important aspect of the primary metabolism of *Borrelia burgdorferi*. Enzymes involved in the degradation of sugars, such as, particularly, glucose, galactose, fructose and xylose, can be used in industrial fermentation. Some of the important sugar transforming enzymes, from a commercial viewpoint, include sugar isomerases such as glucose isomerase. Other metabolic enzymes have found commercial use such as glucose oxidases which produces ketogulonic acid (KGA). KGA is an intermediate in the commercial production of ascorbic acid using the Reichstein's procedure, as described in Krueger *et al.*, *Biotechnology* 6(A), Rhine *et al.*, Eds., Verlag Press, Weinheim, Germany (1984).

Glucose oxidase (GOD) is commercially available and has been used in purified form as well as in an immobilized form for the deoxygenation of beer. See, for instance, Hartmeir *et al.*, *Biotechnology Letters* 1:21 (1979). The most important application of GOD is the industrial scale fermentation of gluconic acid. Market for gluconic acids which are used in the detergent, textile, leather, photographic, pharmaceutical, food, feed and concrete industry, as described, for example, in Bigelis *et al.*, beginning on page 357 in GENE MANIPULATIONS AND FUNGI; Benett *et al.*, Eds., Academic Press, New York (1985). In addition to industrial applications, GOD has found applications in medicine for quantitative determination of glucose in body fluids recently in biotechnology for analyzing syrups from starch and cellulose hydrosylates. This application is described in Owusu *et al.*, *Biochem. et Biophysica. Acta.* 872:83 (1986), for instance.

The main sweetener used in the world today is sugar which comes from sugar beets and sugar cane. In the field of industrial enzymes, the glucose isomerase process shows the largest expansion in the market today. Initially, soluble enzymes were used and later immobilized enzymes were developed (Krueger *et al.*, *Biotechnology, The Textbook of Industrial Microbiology*, Sinauer Associated Incorporated, Sunderland, Massachusetts (1990)). Today, the use of glucose- produced high fructose syrups is by far the largest industrial business using immobilized enzymes. A review of the industrial use of these enzymes is provided by Jorgensen, *Starch* 40:307 (1988).

Proteinases, such as alkaline serine proteinases, are used as detergent additives and thus represent one of the largest volumes of microbial enzymes used in the industrial sector. Because of their industrial importance, there is a large body of published and unpublished information regarding the use of these enzymes in industrial processes. (See Faultman *et al.*, *Acid Proteases Structure Function and Biology*, Tang, J., ed., Plenum Press, New York (1977) and Godfrey *et al.*, *Industrial Enzymes*, MacMillan Publishers, Surrey, UK (1983) and Hepner *et al.*, *Report Industrial Enzymes by 1990*, Hel Hepner & Associates, London (1986)).

Another class of commercially usable proteins of the present invention are the microbial lipases, described by, for instance, Macrae *et al.*, *Philosophical Transactions of the Chiral Society of London* 310:227 (1985) and Poserke, *Journal of the American Oil Chemist Society* 61:1758 (1984). A major use of lipases is in the fat and oil industry for the production of neutral glycerides using lipase catalyzed inter-esterification of readily available triglycerides. Application of lipases include the use as a detergent additive to facilitate the removal of fats from fabrics in the course of the washing procedures.

The use of enzymes, and in particular microbial enzymes, as catalyst for key steps in the synthesis of complex organic molecules is gaining popularity at a great rate. One area of great interest is the preparation of chiral intermediates. Preparation of chiral intermediates is of interest to a wide range of synthetic chemists particularly those scientists involved with the preparation of new pharmaceuticals, agrochemicals, fragrances and flavors. (See Davies *et al.*, *Recent Advances in the Generation of Chiral Intermediates Using Enzymes*, CRC Press, Boca Raton,

Florida (1990)). The following reactions catalyzed by enzymes are of interest to organic chemists: hydrolysis of carboxylic acid esters, phosphate esters, amides and nitriles, esterification reactions, trans-esterification reactions, synthesis of amides, reduction of alkanones and oxoalkanates, oxidation of alcohols to carbonyl compounds, oxidation of sulfides to sulfoxides, and carbon bond forming reactions such as the aldol reaction.

When considering the use of an enzyme encoded by one of the ORFs of the present invention for biotransformation and organic synthesis it is sometimes necessary to consider the respective advantages and disadvantages of using a microorganism as opposed to an isolated enzyme. Pros and cons of using a whole cell system on the one hand or an isolated partially purified enzyme on the other hand, has been described in detail by Bud *et al.*, Chemistry in Britain (1987), p. 127.

Amino transferases, enzymes involved in the biosynthesis and metabolism of amino acids, are useful in the catalytic production of amino acids. The advantages of using microbial based enzyme systems is that the amino transferase enzymes catalyze the stereo- selective synthesis of only L-amino acids and generally possess uniformly high catalytic rates. A description of the use of amino transferases for amino acid production is provided by Roselle-David, *Methods of Enzymology* 136:479 (1987).

Another category of useful proteins encoded by the ORFs of the present invention include enzymes involved in nucleic acid synthesis, repair, and recombination.

2. Generation of Antibodies

As described here, the proteins of the present invention, as well as homologs thereof, can be used in a variety of procedures and methods known in the art which are currently applied to other proteins. The proteins of the present invention can further be used to generate an antibody which selectively binds the protein.

B. burgdorferi protein-specific antibodies for use in the present invention can be raised against the intact *B. burgdorferi* protein or an antigenic polypeptide fragment thereof, which may be presented together with a carrier protein, such as an albumin, to an animal system (such as rabbit or mouse) or, if it is long enough (at least about 25 amino acids), without a carrier.

As used herein, the term "antibody" (Ab) or "monoclonal antibody" (Mab) is meant to include intact molecules, single chain whole antibodies, and antibody fragments. Antibody fragments of the present invention include Fab and F(ab')₂ and other fragments including single-chain Fvs (scFv) and disulfide-linked Fvs (sdFv). Also included in the present invention are chimeric and humanized monoclonal antibodies and polyclonal antibodies specific for the polypeptides of the present invention. The antibodies of the present invention may be prepared by any of a variety of methods. For example, cells expressing a polypeptide of the present invention or an antigenic fragment thereof can be administered to an animal in order to induce the production of sera containing polyclonal antibodies. For example, a preparation of *B. burgdorferi* polypeptide or fragment thereof is prepared and purified to render it substantially free

of natural contaminants. Such a preparation is then introduced into an animal in order to produce polyclonal antisera of greater specific activity.

In a preferred method, the antibodies of the present invention are monoclonal antibodies or binding fragments thereof. Such monoclonal antibodies can be prepared using hybridoma technology. *See, e.g.*, Harlow et al., ANTIBODIES: A LABORATORY MANUAL, (Cold Spring Harbor Laboratory Press, 2nd ed. 1988); Hammerling, et al., in: MONOCLONAL ANTIBODIES AND T-CELL HYBRIDOMAS 563-681 (Elsevier, N.Y., 1981). Fab and F(ab')₂ fragments may be produced by proteolytic cleavage, using enzymes such as papain (to produce Fab fragments) or pepsin (to produce F(ab')₂ fragments). Alternatively, *B. burgdorferi* polypeptide-binding fragments, chimeric, and humanized antibodies can be produced through the application of recombinant DNA technology or through synthetic chemistry using methods known in the art.

Alternatively, additional antibodies capable of binding to the polypeptide antigen of the present invention may be produced in a two-step procedure through the use of anti-idiotypic antibodies. Such a method makes use of the fact that antibodies are themselves antigens, and that, therefore, it is possible to obtain an antibody which binds to a second antibody. In accordance with this method, *B. burgdorferi* polypeptide-specific antibodies are used to immunize an animal, preferably a mouse. The splenocytes of such an animal are then used to produce hybridoma cells, and the hybridoma cells are screened to identify clones which produce an antibody whose ability to bind to the *B. burgdorferi* polypeptide-specific antibody can be blocked by the *B. burgdorferi* polypeptide antigen. Such antibodies comprise anti-idiotypic antibodies to the *B. burgdorferi* polypeptide-specific antibody and can be used to immunize an animal to induce formation of further *B. burgdorferi* polypeptide-specific antibodies.

Antibodies and fragments thereof of the present invention may be described by the portion of a polypeptide of the present invention recognized or specifically bound by the antibody. Antibody binding fragments of a polypeptide of the present invention may be described or specified in the same manner as for polypeptide fragments discussed above, i.e., by N-terminal and C-terminal positions or by size in contiguous amino acid residues. Any number of antibody binding fragments, of a polypeptide of the present invention, specified by N-terminal and C-terminal positions or by size in amino acid residues, as described above, may also be excluded from the present invention. Therefore, the present invention includes antibodies that specifically bind a particularly described fragment of a polypeptide of the present invention and allows for the exclusion of the same.

Antibodies and fragments thereof of the present invention may also be described or specified in terms of their cross-reactivity. Antibodies and fragments that do not bind polypeptides of any other species of *Borrelia* other than *B. burgdorferi* are included in the present invention. Likewise, antibodies and fragments that bind only species of *Borrelia*, i.e. antibodies and fragments that do not bind bacteria from any genus other than *Borrelia*, are included in the present invention.

3. Epitope-Bearing Portions

In another aspect, the invention provides peptides and polypeptides comprising epitope-bearing portions of the *B. burgdorferi* polypeptides of the present invention. These epitopes are immunogenic or antigenic epitopes of the polypeptides of the present invention. An "immunogenic epitope" is defined as a part of a protein that elicits an antibody response when the whole protein or polypeptide is the immunogen. These immunogenic epitopes are believed to be confined to a few loci on the molecule. On the other hand, a region of a protein molecule to which an antibody can bind is defined as an "antigenic determinant" or "antigenic epitope." The number of immunogenic epitopes of a protein generally is less than the number of antigenic epitopes. See, e.g., Geysen, et al. (1983) Proc. Natl. Acad. Sci. USA 81:3998- 4002. Amino acid residues comprising antigenic epitopes may be determined by algorithms such as the Jameson-Wolf analysis or similar algorithms or by *in vivo* testing for an antigenic response using the methods described herein or those known in the art.

As to the selection of peptides or polypeptides bearing an antigenic epitope (*i.e.*, that contain a region of a protein molecule to which an antibody can bind), it is well known in that art that relatively short synthetic peptides that mimic part of a protein sequence are routinely capable of eliciting an antiserum that reacts with the partially mimicked protein. See, e.g., Sutcliffe, et al., (1983) Science 219:660-666. Peptides capable of eliciting protein-reactive sera are frequently represented in the primary sequence of a protein, can be characterized by a set of simple chemical rules, and are confined neither to immunodominant regions of intact proteins (*i.e.*, immunogenic epitopes) nor to the amino or carboxyl terminals. Peptides that are extremely hydrophobic and those of six or fewer residues generally are ineffective at inducing antibodies that bind to the mimicked protein; longer, peptides, especially those containing proline residues, usually are effective. See, Sutcliffe, et al., *supra*, p. 661. For instance, 18 of 20 peptides designed according to these guidelines, containing 8-39 residues covering 75% of the sequence of the influenza virus hemagglutinin HA1 polypeptide chain, induced antibodies that reacted with the HA1 protein or intact virus; and 12/12 peptides from the MuLV polymerase and 18/18 from the rabies glycoprotein induced antibodies that precipitated the respective proteins.

Antigenic epitope-bearing peptides and polypeptides of the invention are therefore useful to raise antibodies, including monoclonal antibodies, that bind specifically to a polypeptide of the invention. Thus, a high proportion of hybridomas obtained by fusion of spleen cells from donors immunized with an antigen epitope-bearing peptide generally secrete antibody reactive with the native protein. See Sutcliffe, et al., *supra*, p. 663. The antibodies raised by antigenic epitope-bearing peptides or polypeptides are useful to detect the mimicked protein, and antibodies to different peptides may be used for tracking the fate of various regions of a protein precursor which undergoes post-translational processing. The peptides and anti-peptide antibodies may be used in a variety of qualitative or quantitative assays for the mimicked protein, for instance in competition assays since it has been shown that even short peptides (*e.g.*, about 9 amino acids)

can bind and displace the larger peptides in immunoprecipitation assays. *See, e.g.,* Wilson, et al., (1984) Cell 37:767-778. The anti-peptide antibodies of the invention also are useful for purification of the mimicked protein, for instance, by adsorption chromatography using methods known in the art.

5 Antigenic epitope-bearing peptides and polypeptides of the invention designed according to the above guidelines preferably contain a sequence of at least seven, more preferably at least nine and most preferably between about 10 to about 50 amino acids (i.e. any integer between 7 and 50) contained within the amino acid sequence of a polypeptide of the invention. However, peptides or polypeptides comprising a larger portion of an amino acid sequence of a polypeptide
10 of the invention, containing about 50 to about 100 amino acids, or any length up to and including the entire amino acid sequence of a polypeptide of the invention, also are considered epitope-bearing peptides or polypeptides of the invention and also are useful for inducing antibodies that react with the mimicked protein. Preferably, the amino acid sequence of the epitope-bearing peptide is selected to provide substantial solubility in aqueous solvents (i.e., the
15 sequence includes relatively hydrophilic residues and highly hydrophobic sequences are preferably avoided); and sequences containing proline residues are particularly preferred.

The epitope-bearing peptides and polypeptides of the present invention may be produced by any conventional means for making peptides or polypeptides including recombinant means using nucleic acid molecules of the invention. For instance, an epitope-bearing amino acid
20 sequence of the present invention may be fused to a larger polypeptide which acts as a carrier during recombinant production and purification, as well as during immunization to produce anti-peptide antibodies. Epitope-bearing peptides also may be synthesized using known methods of chemical synthesis. For instance, Houghten has described a simple method for synthesis of large numbers of peptides, such as 10-20 mg of 248 different 13 residue peptides representing
25 single amino acid variants of a segment of the HA1 polypeptide which were prepared and characterized (by ELISA-type binding studies) in less than four weeks (Houghten, R. A. Proc. Natl. Acad. Sci. USA 82:5131-5135 (1985)). This "Simultaneous Multiple Peptide Synthesis (SMPS)" process is further described in U.S. Patent No. 4,631,211 to Houghten and coworkers (1986). In this procedure the individual resins for the solid-phase synthesis of various peptides
30 are contained in separate solvent-permeable packets, enabling the optimal use of the many identical repetitive steps involved in solid-phase methods. A completely manual procedure allows 500-1000 or more syntheses to be conducted simultaneously (Houghten et al. (1985) Proc. Natl. Acad. Sci. 82:5131-5135 at 5134.

Epitope-bearing peptides and polypeptides of the invention are used to induce antibodies
35 according to methods well known in the art. *See, e.g.,* Sutcliffe, et al., *supra*;; Wilson, et al., *supra*;; and Bittle, et al. (1985) J. Gen. Virol. 66:2347-2354. Generally, animals may be immunized with free peptide; however, anti-peptide antibody titer may be boosted by coupling of the peptide to a macromolecular carrier, such as keyhole limpet hemacyanin (KLH) or tetanus toxoid. For instance, peptides containing cysteine may be coupled to carrier using a linker such

as m-maleimidobenzoyl-N-hydroxysuccinimide ester (MBS), while other peptides may be coupled to carrier using a more general linking agent such as glutaraldehyde. Animals such as rabbits, rats and mice are immunized with either free or carrier-coupled peptides, for instance, by intraperitoneal and/or intradermal injection of emulsions containing about 100 µg peptide or carrier protein and Freund's adjuvant. Several booster injections may be needed, for instance, at intervals of about two weeks, to provide a useful titer of anti-peptide antibody which can be detected, for example, by ELISA assay using free peptide adsorbed to a solid surface. The titer of anti-peptide antibodies in serum from an immunized animal may be increased by selection of anti-peptide antibodies, for instance, by adsorption to the peptide on a solid support and elution of the selected antibodies according to methods well known in the art.

Immunogenic epitope-bearing peptides of the invention, *i.e.*, those parts of a protein that elicit an antibody response when the whole protein is the immunogen, are identified according to methods known in the art. For instance, Geysen, *et al.*, *supra*, discloses a procedure for rapid concurrent synthesis on solid supports of hundreds of peptides of sufficient purity to react in an ELISA. Interaction of synthesized peptides with antibodies is then easily detected without removing them from the support. In this manner a peptide bearing an immunogenic epitope of a desired protein may be identified routinely by one of ordinary skill in the art. For instance, the immunologically important epitope in the coat protein of foot-and-mouth disease virus was located by Geysen *et al. supra* with a resolution of seven amino acids by synthesis of an overlapping set of all 208 possible hexapeptides covering the entire 213 amino acid sequence of the protein. Then, a complete replacement set of peptides in which all 20 amino acids were substituted in turn at every position within the epitope were synthesized, and the particular amino acids conferring specificity for the reaction with antibody were determined. Thus, peptide analogs of the epitope-bearing peptides of the invention can be made routinely by this method. U.S. Patent No. 4,708,781 to Geysen (1987) further describes this method of identifying a peptide bearing an immunogenic epitope of a desired protein.

Further still, U.S. Patent No. 5,194,392, to Geysen (1990), describes a general method of detecting or determining the sequence of monomers (amino acids or other compounds) which is a topological equivalent of the epitope (*i.e.*, a "mimotope") which is complementary to a particular paratope (antigen binding site) of an antibody of interest. More generally, U.S. Patent No. 4,433,092, also to Geysen (1989), describes a method of detecting or determining a sequence of monomers which is a topographical equivalent of a ligand which is complementary to the ligand binding site of a particular receptor of interest. Similarly, U.S. Patent No. 5,480,971 to Houghten, R. A. *et al.* (1996) discloses linear C₁-C₇-alkyl peralkylated oligopeptides and sets and libraries of such peptides, as well as methods for using such oligopeptide sets and libraries for determining the sequence of a peralkylated oligopeptide that preferentially binds to an acceptor molecule of interest. Thus, non-peptide analogs of the epitope-bearing peptides of the invention also can be made routinely by these methods. The entire disclosure of each document cited in this section on "Polypeptides and Fragments" is

hereby incorporated herein by reference.

As one of skill in the art will appreciate, the polypeptides of the present invention and the epitope-bearing fragments thereof described above can be combined with parts of the constant domain of immunoglobulins (IgG), resulting in chimeric polypeptides. These fusion proteins facilitate purification and show an increased half-life *in vivo*. This has been shown, *e.g.*, for chimeric proteins consisting of the first two domains of the human CD4-polypeptide and various domains of the constant regions of the heavy or light chains of mammalian immunoglobulins. (EPA 0,394,827; Traunecker et al. (1988) Nature 331:84-86. Fusion proteins that have a disulfide-linked dimeric structure due to the IgG part can also be more efficient in binding and neutralizing other molecules than a monomeric *B. burgdorferi* polypeptide or fragment thereof alone. See Fountoulakis et al. (1995) J. Biochem. 270:3958-3964. Nucleic acids encoding the above epitopes of *B. burgdorferi* polypeptides can also be recombined with a gene of interest as an epitope tag to aid in detection and purification of the expressed polypeptide.

4. Diagnostic Assays and Kits

The present invention further relates to methods for assaying *Borrelia* infection in an animal by detecting the expression of genes encoding *Borrelia* polypeptides of the present invention. The methods comprise analyzing tissue or body fluid from the animal for *Borrelia*-specific antibodies, nucleic acids, or proteins. Analysis of nucleic acid specific to *Borrelia* is assayed by PCR or hybridization techniques using nucleic acid sequences of the present invention as either hybridization probes or primers. See, *e.g.*, Sambrook et al. Molecular cloning: A Laboratory Manual (Cold Spring Harbor Laboratory Press, 2nd ed., 1989, page 54 reference); Ereemeeva et al. (1994) J. Clin. Microbiol. 32:803-810 (describing differentiation among spotted fever group *Rickettsiae* species by analysis of restriction fragment length polymorphism of PCR-amplified DNA) and Chen et al. 1994 J. Clin. Microbiol. 32:589-595 (detecting *B. burgdorferi* nucleic acids via PCR).

Where diagnosis of a disease state related to infection with *Borrelia* has already been made, the present invention is useful for monitoring progression or regression of the disease state whereby patients exhibiting enhanced *Borrelia* gene expression will experience a worse clinical outcome relative to patients expressing these gene(s) at a lower level.

By "biological sample" is intended any biological sample obtained from an animal, cell line, tissue culture, or other source which contains *Borrelia* polypeptide, mRNA, or DNA. Biological samples include body fluids (such as saliva, blood, plasma, urine, mucus, synovial fluid, etc.) tissues (such as muscle, skin, and cartilage) and any other biological source suspected of containing *Borrelia* polypeptides or nucleic acids. Methods for obtaining biological samples such as tissue are well known in the art.

The present invention is useful for detecting diseases related to *Borrelia* infections in animals. Preferred animals include monkeys, apes, cats, dogs, birds, cows, pigs, mice, horses, rabbits and humans. Particularly preferred are humans.

Total RNA can be isolated from a biological sample using any suitable technique such as the single-step guanidinium-thiocyanate-phenol-chloroform method described in Chomczynski et al. (1987) Anal. Biochem. 162:156-159. mRNA encoding *Borrelia* polypeptides having sufficient homology to the nucleic acid sequences identified in SEQ ID NOS:1-155 to allow for hybridization between complementary sequences are then assayed using any appropriate method. These include Northern blot analysis, S1 nuclease mapping, the polymerase chain reaction (PCR), reverse transcription in combination with the polymerase chain reaction (RT-PCR), and reverse transcription in combination with the ligase chain reaction (RT-LCR).

Northern blot analysis can be performed as described in Harada et al. (1990) Cell 63:303-312. Briefly, total RNA is prepared from a biological sample as described above. For the Northern blot, the RNA is denatured in an appropriate buffer (such as glyoxal/dimethyl sulfoxide/sodium phosphate buffer), subjected to agarose gel electrophoresis, and transferred onto a nitrocellulose filter. After the RNAs have been linked to the filter by a UV linker, the filter is prehybridized in a solution containing formamide, SSC, Denhardt's solution, denatured salmon sperm, SDS, and sodium phosphate buffer. A *B. burgdorferi* polynucleotide sequence shown in SEQ ID NOS:1-155 labeled according to any appropriate method (such as the ³²P-multiprimer DNA labeling system (Amersham)) is used as probe. After hybridization overnight, the filter is washed and exposed to x-ray film. DNA for use as probe according to the present invention is described in the sections above and will preferably at least 15 nucleotides in length.

S1 mapping can be performed as described in Fujita et al. (1987) Cell 49:357-367. To prepare probe DNA for use in S1 mapping, the sense strand of an above-described *B. burgdorferi* DNA sequence of the present invention is used as a template to synthesize labeled antisense DNA. The antisense DNA can then be digested using an appropriate restriction endonuclease to generate further DNA probes of a desired length. Such antisense probes are useful for visualizing protected bands corresponding to the target mRNA (i.e., mRNA encoding *Borrelia* polypeptides).

Levels of mRNA encoding *Borrelia* polypeptides are assayed, for e.g., using the RT-PCR method described in Makino et al. (1990) Technique 2:295-301. By this method, the radioactivities of the "amplicons" in the polyacrylamide gel bands are linearly related to the initial concentration of the target mRNA. Briefly, this method involves adding total RNA isolated from a biological sample in a reaction mixture containing a RT primer and appropriate buffer. After incubating for primer annealing, the mixture can be supplemented with a RT buffer, dNTPs, DTT, RNase inhibitor and reverse transcriptase. After incubation to achieve reverse transcription of the RNA, the RT products are then subject to PCR using labeled primers. Alternatively, rather than labeling the primers, a labeled dNTP can be included in the PCR reaction mixture. PCR amplification can be performed in a DNA thermal cycler according to conventional techniques. After a suitable number of rounds to achieve amplification, the PCR reaction mixture is electrophoresed on a polyacrylamide gel. After drying the gel, the radioactivity of the appropriate

bands (corresponding to the mRNA encoding the *Borrelia* polypeptides of the present invention) are quantified using an imaging analyzer. RT and PCR reaction ingredients and conditions, reagent and gel concentrations, and labeling methods are well known in the art. Variations on the RT-PCR method will be apparent to the skilled artisan. Other PCR methods that can detect the nucleic acid of the present invention can be found in PCR PRIMER: A LABORATORY MANUAL (C.W. Dieffenbach et al. eds., Cold Spring Harbor Lab Press, 1995).

The polynucleotides of the present invention, including both DNA and RNA, may be used to detect polynucleotides of the present invention or *Borrelia* species including *B. burgdorferi* using bio chip technology. The present invention includes both high density chip arrays (>1000 oligonucleotides per cm²) and low density chip arrays (<1000 oligonucleotides per cm²). Bio chips comprising arrays of polynucleotides of the present invention may be used to detect *Borrelia* species, including *B. burgdorferi*, in biological and environmental samples and to diagnose an animal, including humans, with an *B. burgdorferi* or other *Borrelia* infection. The bio chips of the present invention may comprise polynucleotide sequences of other pathogens including bacteria, viral, parasitic, and fungal polynucleotide sequences, in addition to the polynucleotide sequences of the present invention, for use in rapid differential pathogenic detection and diagnosis. The bio chips can also be used to monitor an *B. burgdorferi* or other *Borrelia* infections and to monitor the genetic changes (deletions, insertions, mismatches, etc.) in response to drug therapy in the clinic and drug development in the laboratory. The bio chip technology comprising arrays of polynucleotides of the present invention may also be used to simultaneously monitor the expression of a multiplicity of genes, including those of the present invention. The polynucleotides used to comprise a selected array may be specified in the same manner as for the fragments, i.e., by their 5' and 3' positions or length in contiguous base pairs and include from. Methods and particular uses of the polynucleotides of the present invention to detect *Borrelia* species, including *B. burgdorferi*, using bio chip technology include those known in the art and those of: U.S. Patent Nos. 5510270, 5545531, 5445934, 5677195, 5532128, 5556752, 5527681, 5451683, 5424186, 5607646, 5658732 and World Patent Nos. WO/9710365, WO/9511995, WO/9743447, WO/9535505, each incorporated herein in their entireties.

Biosensors using the polynucleotides of the present invention may also be used to detect, diagnose, and monitor *B. burgdorferi* or other *Borrelia* species and infections thereof. Biosensors using the polynucleotides of the present invention may also be used to detect particular polynucleotides of the present invention. Biosensors using the polynucleotides of the present invention may also be used to monitor the genetic changes (deletions, insertions, mismatches, etc.) in response to drug therapy in the clinic and drug development in the laboratory. Methods and particular uses of the polynucleotides of the present invention to detect *Borrelia* species, including *B. burgdorferi*, using biosensors include those known in the art and those of: U.S. Patent Nos. 5721102, 5658732, 5631170, and World Patent Nos. WO/9735011, WO/9720203, each incorporated herein in their entireties.

Thus, the present invention includes both bio chips and biosensors comprising polynucleotides of the present invention and methods of their use.

Assaying *Borrelia* polypeptide levels in a biological sample can occur using any art-known method, such as antibody-based techniques. For example, *Borrelia* polypeptide expression in tissues can be studied with classical immunohistological methods. In these, the specific recognition is provided by the primary antibody (polyclonal or monoclonal) but the secondary detection system can utilize fluorescent, enzyme, or other conjugated secondary antibodies. As a result, an immunohistological staining of tissue section for pathological examination is obtained. Tissues can also be extracted, *e.g.*, with urea and neutral detergent, for the liberation of *Borrelia* polypeptides for Western-blot or dot/slot assay. *See, e.g.*, Jalkanen, M. et al. (1985) J. Cell. Biol. 101:976-985; Jalkanen, M. et al. (1987) J. Cell. Biol. 105:3087-3096. In this technique, which is based on the use of cationic solid phases, quantitation of a *Borrelia* polypeptide can be accomplished using an isolated *Borrelia* polypeptide as a standard. This technique can also be applied to body fluids.

Other antibody-based methods useful for detecting *Borrelia* polypeptide gene expression include immunoassays, such as the ELISA and the radioimmunoassay (RIA). For example, a *Borrelia* polypeptide-specific monoclonal antibodies can be used both as an immunoabsorbent and as an enzyme-labeled probe to detect and quantify a *Borrelia* polypeptide. The amount of a *Borrelia* polypeptide present in the sample can be calculated by reference to the amount present in a standard preparation using a linear regression computer algorithm. Such an ELISA is described in Iacobelli et al. (1988) Breast Cancer Research and Treatment 11:19-30. In another ELISA assay, two distinct specific monoclonal antibodies can be used to detect *Borrelia* polypeptides in a body fluid. In this assay, one of the antibodies is used as the immunoabsorbent and the other as the enzyme-labeled probe.

The above techniques may be conducted essentially as a "one-step" or "two-step" assay. The "one-step" assay involves contacting the *Borrelia* polypeptide with immobilized antibody and, without washing, contacting the mixture with the labeled antibody. The "two-step" assay involves washing before contacting the mixture with the labeled antibody. Other conventional methods may also be employed as suitable. It is usually desirable to immobilize one component of the assay system on a support, thereby allowing other components of the system to be brought into contact with the component and readily removed from the sample. Variations of the above and other immunological methods included in the present invention can also be found in Harlow et al., ANTIBODIES: A LABORATORY MANUAL, (Cold Spring Harbor Laboratory Press, 2nd ed. 1988).

Suitable enzyme labels include, for example, those from the oxidase group, which catalyze the production of hydrogen peroxide by reacting with substrate. Glucose oxidase is particularly preferred as it has good stability and its substrate (glucose) is readily available. Activity of an oxidase label may be assayed by measuring the concentration of hydrogen peroxide formed by the enzyme-labeled antibody/substrate reaction. Besides enzymes, other suitable

labels include radioisotopes, such as iodine (^{125}I , ^{121}I), carbon (^{14}C), sulphur (^{35}S), tritium (^3H), indium (^{112}In), and technetium ($^{99\text{m}}\text{Tc}$), and fluorescent labels, such as fluorescein and rhodamine, and biotin.

Further suitable labels for the *Borrelia* polypeptide-specific antibodies of the present invention are provided below. Examples of suitable enzyme labels include malate dehydrogenase, *Borrelia* nuclease, delta-5-steroid isomerase, yeast-alcohol dehydrogenase, alpha-glycerol phosphate dehydrogenase, triose phosphate isomerase, peroxidase, alkaline phosphatase, asparaginase, glucose oxidase, beta-galactosidase, ribonuclease, urease, catalase, glucose-6-phosphate dehydrogenase, glucoamylase, and acetylcholine esterase.

Examples of suitable radioisotopic labels include ^3H , ^{111}In , ^{125}I , ^{131}I , ^{32}P , ^{35}S , ^{14}C , ^{51}Cr , ^{57}To , ^{58}Co , ^{59}Fe , ^{75}Se , ^{152}Eu , ^{90}Y , ^{67}Cu , ^{217}Ci , ^{211}At , ^{212}Pb , ^{47}Sc , ^{109}Pd , etc. ^{111}In is a preferred isotope where *in vivo* imaging is used since it avoids the problem of dehalogenation of the ^{125}I or ^{131}I -labeled monoclonal antibody by the liver. In addition, this radionucleotide has a more favorable gamma emission energy for imaging. See, e.g., Perkins et al. (1985) Eur. J. Nucl. Med. 10:296-301; Carasquillo et al. (1987) J. Nucl. Med. 28:281-287. For example, ^{111}In coupled to monoclonal antibodies with 1-(P-isothiocyanatobenzyl)-DPTA has shown little uptake in non-tumors tissues, particularly the liver, and therefore enhances specificity of tumor localization. See, Esteban et al. (1987) J. Nucl. Med. 28:861-870.

Examples of suitable non-radioactive isotopic labels include ^{157}Gd , ^{55}Mn , ^{162}Dy , ^{52}Tr , and ^{56}Fe .

Examples of suitable fluorescent labels include an ^{152}Eu label, a fluorescein label, an isothiocyanate label, a rhodamine label, a phycoerythrin label, a phycocyanin label, an allophycocyanin label, an o-phthaldehyde label, and a fluorescamine label.

Examples of suitable toxin labels include, *Pseudomonas* toxin, diphtheria toxin, ricin, and cholera toxin.

Examples of chemiluminescent labels include a luminal label, an isoluminal label, an aromatic acridinium ester label, an imidazole label, an acridinium salt label, an oxalate ester label, a luciferin label, a luciferase label, and an aequorin label.

Examples of nuclear magnetic resonance contrasting agents include heavy metal nuclei such as Gd, Mn, and iron.

Typical techniques for binding the above-described labels to antibodies are provided by Kennedy et al. (1976) Clin. Chim. Acta 70:1-31, and Schurs et al. (1977) Clin. Chim. Acta 81:1-40. Coupling techniques mentioned in the latter are the glutaraldehyde method, the periodate method, the dimaleimide method, the m-maleimidobenzyl-N-hydroxy-succinimide ester method, all of which methods are incorporated by reference herein.

In a related aspect, the invention includes a diagnostic kit for use in screening serum containing antibodies specific against *B. burgdorferi* infection. Such a kit may include an isolated *B. burgdorferi* antigen comprising an epitope which is specifically immunoreactive with at least one anti-*B. burgdorferi* antibody. Such a kit also includes means for detecting the

binding of said antibody to the antigen. In specific embodiments, the kit may include a recombinantly produced or chemically synthesized peptide or polypeptide antigen. The peptide or polypeptide antigen may be attached to a solid support.

5 In a more specific embodiment, the detecting means of the above-described kit includes a solid support to which said peptide or polypeptide antigen is attached. Such a kit may also include a non-attached reporter-labeled anti-human antibody. In this embodiment, binding of the antibody to the *B. burgdorferi* antigen can be detected by binding of the reporter labeled antibody to the anti-*B. burgdorferi* polypeptide antibody.

10 In a related aspect, the invention includes a method of detecting *B. burgdorferi* infection in a subject. This detection method includes reacting a body fluid, preferably serum, from the subject with an isolated *B. burgdorferi* antigen, and examining the antigen for the presence of bound antibody. In a specific embodiment, the method includes a polypeptide antigen attached to a solid support, and serum is reacted with the support. Subsequently, the support is reacted with a reporter-labeled anti-human antibody. The support is then examined for the presence of
15 reporter-labeled antibody.

The solid surface reagent employed in the above assays and kits is prepared by known techniques for attaching protein material to solid support material, such as polymeric beads, dip sticks, 96-well plates or filter material. These attachment methods generally include non-specific adsorption of the protein to the support or covalent attachment of the protein, typically through a
20 free amine group, to a chemically reactive group on the solid support, such as an activated carboxyl, hydroxyl, or aldehyde group. Alternatively, streptavidin coated plates can be used in conjunction with biotinylated antigen(s).

The polypeptides and antibodies of the present invention, including fragments thereof, may be used to detect *Borrelia* species including *B. burgdorferi* using bio chip and biosensor
25 technology. Bio chip and biosensors of the present invention may comprise the polypeptides of the present invention to detect antibodies, which specifically recognize *Borrelia* species, including *B. burgdorferi*. Bio chip and biosensors of the present invention may also comprise antibodies which specifically recognize the polypeptides of the present invention to detect *Borrelia* species, including *B. burgdorferi* or specific polypeptides of the present invention. Bio chips or
30 biosensors comprising polypeptides or antibodies of the present invention may be used to detect *Borrelia* species, including *B. burgdorferi*, in biological and environmental samples and to diagnose an animal, including humans, with an *B. burgdorferi* or other *Borrelia* infection. Thus, the present invention includes both bio chips and biosensors comprising polypeptides or antibodies of the present invention and methods of their use.

35 The bio chips of the present invention may further comprise polypeptide sequences of other pathogens including bacteria, viral, parasitic, and fungal polypeptide sequences, in addition to the polypeptide sequences of the present invention, for use in rapid differential pathogenic detection and diagnosis. The bio chips of the present invention may further comprise antibodies or fragments thereof specific for other pathogens including bacteria, viral, parasitic, and fungal

polypeptide sequences, in addition to the antibodies or fragments thereof of the present invention, for use in rapid differential pathogenic detection and diagnosis. The bio chips and biosensors of the present invention may also be used to monitor an *B. burgdorferi* or other *Borrelia* infection and to monitor the genetic changes (amino acid deletions, insertions, substitutions, etc.) in response to drug therapy in the clinic and drug development in the laboratory. The bio chip and biosensors comprising polypeptides or antibodies of the present invention may also be used to simultaneously monitor the expression of a multiplicity of polypeptides, including those of the present invention. The polypeptides used to comprise a bio chip or biosensor of the present invention may be specified in the same manner as for the fragments, i.e., by their N-terminal and C-terminal positions or length in contiguous amino acid residue. Methods and particular uses of the polypeptides and antibodies of the present invention to detect *Borrelia* species, including *B. burgdorferi*, or specific polypeptides using bio chip and biosensor technology include those known in the art, those of the U.S. Patent Nos. and World Patent Nos. listed above for bio chips and biosensors using polynucleotides of the present invention, and those of: U.S. Patent Nos. 5658732, 5135852, 5567301, 5677196, 5690894 and World Patent Nos. WO9729366, WO9612957, each incorporated herein in their entireties.

5. Screening Assay for Binding Agents

Using the isolated proteins of the present invention, the present invention further provides methods of obtaining and identifying agents which bind to a protein encoded by one of the ORFs of the present invention or to one of the fragments and the *Borrelia burgdorferi* fragment and contigs herein described.

In general, such methods comprise steps of:

- (a) contacting an agent with an isolated protein encoded by one of the ORFs of the present invention, or an isolated fragment of the *Borrelia burgdorferi* genome; and
- (b) determining whether the agent binds to said protein or said fragment.

The agents screened in the above assay can be, but are not limited to, peptides, carbohydrates, vitamin derivatives, or other pharmaceutical agents. The agents can be selected and screened at random or rationally selected or designed using protein modeling techniques.

For random screening, agents such as peptides, carbohydrates, pharmaceutical agents and the like are selected at random and are assayed for their ability to bind to the protein encoded by the ORF of the present invention.

Alternatively, agents may be rationally selected or designed. As used herein, an agent is said to be "rationally selected or designed" when the agent is chosen based on the configuration of the particular protein. For example, one skilled in the art can readily adapt currently available procedures to generate peptides, pharmaceutical agents and the like capable of binding to a specific peptide sequence in order to generate rationally designed antipeptide peptides, for example see Hurby *et al.*, "Application of Synthetic Peptides: Antisense Peptides," in *Synthetic*

Peptides, A User's Guide, W. H. Freeman, NY. (1992), pp. 289-307, and Kaspiczak *et al.*, *Biochemistry* 28:9230-8 (1989), or pharmaceutical agents, or the like.

In addition to the foregoing, one class of agents of the present invention, as broadly described, can be used to control gene expression through binding to one of the ORFs or EMFs of the present invention. As described above, such agents can be randomly screened or rationally designed/selected. Targeting the ORF or EMF allows a skilled artisan to design sequence specific or element specific agents, modulating the expression of either a single ORF or multiple ORFs which rely on the same EMF for expression control.

One class of DNA binding agents are agents which contain base residues which hybridize or form a triple helix by binding to DNA or RNA. Such agents can be based on the classic phosphodiester, ribonucleic acid backbone, or can be a variety of sulfhydryl or polymeric derivatives which have base attachment capacity.

Agents suitable for use in these methods usually contain 20 to 40 bases and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee *et al.*, *Nucl. Acids Res.* 6:3073 (1979); Cooney *et al.*, *Science* 241:456 (1988); and Dervan *et al.*, *Science* 251:1360 (1991)) or to the mRNA itself (antisense - Okano, *J. Neurochem.* 56:560 (1991); *Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression*, CRC Press, Boca Raton, FL (1988)). Triple helix- formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention can be used to design antisense and triple helix-forming oligonucleotides, and other DNA binding agents.

6. Pharmaceutical Compositions and Vaccines

The present invention further provides pharmaceutical agents which can be used to modulate the growth or pathogenicity of *Borrelia burgdorferi*, or another related organism, *in vivo* or *in vitro*. As used herein, a "pharmaceutical agent" is defined as a composition of matter which can be formulated using known techniques to provide a pharmaceutical compositions. As used herein, the "pharmaceutical agents of the present invention" refers the pharmaceutical agents which are derived from the proteins encoded by the ORFs of the present invention or are agents which are identified using the herein described assays.

As used herein, a pharmaceutical agent is said to "modulate the growth pathogenicity of *Borrelia burgdorferi* or a related organism, *in vivo* or *in vitro*," when the agent reduces the rate of growth, rate of division, or viability of the organism in question. The pharmaceutical agents of the present invention can modulate the growth or pathogenicity of an organism in many fashions, although an understanding of the underlying mechanism of action is not needed to practice the use of the pharmaceutical agents of the present invention. Some agents will modulate the growth by binding to an important protein thus blocking the biological activity of the protein, while other agents may bind to a component of the outer surface of the organism blocking attachment or

rendering the organism more prone to act the bodies nature immune system. Alternatively, the agent may comprise a protein encoded by one of the ORFs of the present invention and serve as a vaccine. The development and use of a vaccine based on outer membrane components are well known in the art.

5 As used herein, a "related organism" is a broad term which refers to any organism whose growth can be modulated by one of the pharmaceutical agents of the present invention. In general, such an organism will contain a homolog of the protein which is the target of the pharmaceutical agent or the protein used as a vaccine. As such, related organisms do not need to be bacterial but may be fungal or viral pathogens.

10 The pharmaceutical agents and compositions of the present invention may be administered in a convenient manner, such as by the oral, topical, intravenous, intraperitoneal, intramuscular, subcutaneous, intranasal or intradermal routes. The pharmaceutical compositions are administered in an amount which is effective for treating and/or prophylaxis of the specific indication. In general, they are administered in an amount of at least about 1 mg/kg body weight
15 and in most cases they will be administered in an amount not in excess of about 1 g/kg body weight per day. In most cases, the dosage is from about 0.1 mg/kg to about 10 g/kg body weight daily, taking into account the routes of administration, symptoms, *etc.*

The agents of the present invention can be used in native form or can be modified to form a chemical derivative. As used herein, a molecule is said to be a "chemical derivative" of another
20 molecule when it contains additional chemical moieties not normally a part of the molecule. Such moieties may improve the molecule's solubility, absorption, biological half life, *etc.* The moieties may alternatively decrease the toxicity of the molecule, eliminate or attenuate any undesirable side effect of the molecule, *etc.* Moieties capable of mediating such effects are disclosed in, among other sources, REMINGTON'S PHARMACEUTICAL SCIENCES (1980)
25 cited elsewhere herein.

For example, such moieties may change an immunological character of the functional derivative, such as affinity for a given antibody. Such changes in immunomodulation activity are measured by the appropriate assay, such as a competitive type immunoassay. Modifications of such protein properties as redox or thermal stability, biological half-life, hydrophobicity,
30 susceptibility to proteolytic degradation or the tendency to aggregate with carriers or into multimers also may be effected in this way and can be assayed by methods well known to the skilled artisan.

The therapeutic effects of the agents of the present invention may be obtained by providing the agent to a patient by any suitable means (*e.g.*, inhalation, intravenously,
35 intramuscularly, subcutaneously, enterally, or parenterally). It is preferred to administer the agent of the present invention so as to achieve an effective concentration within the blood or tissue in which the growth of the organism is to be controlled. To achieve an effective blood concentration, the preferred method is to administer the agent by injection. The administration may be by continuous infusion, or by single or multiple injections.

In providing a patient with one of the agents of the present invention, the dosage of the administered agent will vary depending upon such factors as the patient's age, weight, height, sex, general medical condition, previous medical history, *etc.* In general, it is desirable to provide the recipient with a dosage of agent which is in the range of from about 1 pg/kg to 10 mg/kg (body weight of patient), although a lower or higher dosage may be administered. The therapeutically effective dose can be lowered by using combinations of the agents of the present invention or another agent.

As used herein, two or more compounds or agents are said to be administered "in combination" with each other when either (1) the physiological effects of each compound, or (2) the serum concentrations of each compound can be measured at the same time. The composition of the present invention can be administered concurrently with, prior to, or following the administration of the other agent.

The agents of the present invention are intended to be provided to recipient subjects in an amount sufficient to decrease the rate of growth (as defined above) of the target organism.

The administration of the agent(s) of the invention may be for either a "prophylactic" or "therapeutic" purpose. When provided prophylactically, the agent(s) are provided in advance of any symptoms indicative of the organisms growth. The prophylactic administration of the agent(s) serves to prevent, attenuate, or decrease the rate of onset of any subsequent infection. When provided therapeutically, the agent(s) are provided at (or shortly after) the onset of an indication of infection. The therapeutic administration of the compound(s) serves to attenuate the pathological symptoms of the infection and to increase the rate of recovery.

The agents of the present invention are administered to a subject, such as a mammal, or a patient, in a pharmaceutically acceptable form and in a therapeutically effective concentration. A composition is said to be "pharmacologically acceptable" if its administration can be tolerated by a recipient patient. Such an agent is said to be administered in a "therapeutically effective amount" if the amount administered is physiologically significant. An agent is physiologically significant if its presence results in a detectable change in the physiology of a recipient patient.

The agents of the present invention can be formulated according to known methods to prepare pharmaceutically useful compositions, whereby these materials, or their functional derivatives, are combined in a mixture with a pharmaceutically acceptable carrier vehicle. Suitable vehicles and their formulation, inclusive of other human proteins, *e.g.*, human serum albumin, are described, for example, in REMINGTON'S PHARMACEUTICAL SCIENCES, 16th Ed., Osol, A., Ed., Mack Publishing, Easton PA (1980). In order to form a pharmaceutically acceptable composition suitable for effective administration, such compositions will contain an effective amount of one or more of the agents of the present invention, together with a suitable amount of carrier vehicle.

Additional pharmaceutical methods may be employed to control the duration of action. Control release preparations may be achieved through the use of polymers to complex or absorb one or more of the agents of the present invention. The controlled delivery may be effectuated by

a variety of well known techniques, including formulation with macromolecules such as, for example, polyesters, polyamino acids, polyvinyl, pyrrolidone, ethylenevinylacetate, methylcellulose, carboxymethylcellulose, or protamine, sulfate, adjusting the concentration of the macromolecules and the agent in the formulation, and by appropriate use of methods of incorporation, which can be manipulated to effectuate a desired time course of release. Another possible method to control the duration of action by controlled release preparations is to incorporate agents of the present invention into particles of a polymeric material such as polyesters, polyamino acids, hydrogels, poly(lactic acid) or ethylene vinylacetate copolymers. Alternatively, instead of incorporating these agents into polymeric particles, it is possible to entrap these materials in microcapsules prepared, for example, by coacervation techniques or by interfacial polymerization with, for example, hydroxymethylcellulose or gelatine-microcapsules and poly(methylmethacrylate) microcapsules, respectively, or in colloidal drug delivery systems, for example, liposomes, albumin microspheres, microemulsions, nanoparticles, and nanocapsules or in macroemulsions. Such techniques are disclosed in REMINGTON'S PHARMACEUTICAL SCIENCES (1980).

The invention further provides a pharmaceutical pack or kit comprising one or more containers filled with one or more of the ingredients of the pharmaceutical compositions of the invention. Associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use or sale for human administration.

In addition, the agents of the present invention may be employed in conjunction with other therapeutic compounds.

7. Shot-Gun Approach to Megabase DNA Sequencing

The present invention further demonstrates that a large sequence can be sequenced using a random shotgun approach. This procedure, described in detail in the examples that follow, has eliminated the up front cost of isolating and ordering overlapping or contiguous subclones prior to the start of the sequencing protocols.

Certain aspects of the present invention are described in greater detail in the examples that follow. The examples are provided by way of illustration. Other aspects and embodiments of the present invention are contemplated by the inventors, as will be clear to those of skill in the art from reading the present disclosure.

ILLUSTRATIVE EXAMPLES

LIBRARIES AND SEQUENCING

1. Shotgun Sequencing Probability Analysis

The overall strategy for a shotgun approach to whole genome sequencing follows from the Lander and Waterman (Landerman and Waterman, *Genomics* 2:231 (1988)) application of the equation for the Poisson distribution. According to this treatment, the probability, P_0 , that any given base in a sequence of size L , in nucleotides, is not sequenced after a certain amount, n , in nucleotides, of random sequence has been determined can be calculated by the equation $P_0 = e^{-m}$, where m is L/n , the fold coverage. For instance, for a genome of 2.8 Mb, $m=1$ when 2.8 Mb of sequence has been randomly generated (1X coverage). At that point, $P_0 = e^{-1} = 0.37$. The probability that any given base has not been sequenced is the same as the probability that any region of the whole sequence L has not been determined and, therefore, is equivalent to the fraction of the whole sequence that has yet to be determined. Thus, at one-fold coverage, approximately 37% of a polynucleotide of size L , in nucleotides has not been sequenced. When 14 Mb of sequence has been generated, coverage is 5X for a 2.8 Mb and the unsequenced fraction drops to .0067 or 0.67%. 5X coverage of a 2.8 Mb sequence can be attained by sequencing approximately 17,000 random clones from both insert ends with an average sequence read length of 410 bp.

Similarly, the total gap length, G , is determined by the equation $G = Le^{-m}$, and the average gap size, g , follows the equation, $g = L/n$. Thus, 5X coverage leaves about 240 gaps averaging about 82 bp in size in a sequence of a polynucleotide 2.8 Mb long.

The treatment above is essentially that of Lander and Waterman, *Genomics* 2: 231 (1988).

2. Random Library Construction

In order to approximate the random model described above during actual sequencing, a nearly ideal library of cloned genomic fragments is required. The following library construction procedure was developed to achieve this end.

Borrelia burgdorferi DNA is prepared by phenol extraction. A mixture containing 200 µg DNA in 1.0 ml of 300 mM sodium acetate, 10 mM Tris-HCl, 1 mM Na-EDTA, 50% glycerol is processed through a nebulizer (IPI Medical Products) with a stream of nitrogen adjusted to 35 Kpa for 2 minutes. The sonicated DNA is ethanol precipitated and redissolved in 500 µl TE buffer.

To create blunt-ends, a 100 µl aliquot of the resuspended DNA is digested with 5 units of BAL31 nuclease (New England BioLabs) for 10 min at 30°C in 200 µl BAL31 buffer. The digested DNA is phenol-extracted, ethanol-precipitated, redissolved in 100 µl TE buffer, and then size-fractionated by electrophoresis through a 1.0% low melting temperature agarose gel. The section containing DNA fragments 1.6-2.0 kb in size is excised from the gel, and the LGT agarose is melted and the resulting solution is extracted with phenol to separate the agarose from the DNA. DNA is ethanol precipitated and redissolved in 20 µl of TE buffer for ligation to vector.

A two-step ligation procedure is used to produce a plasmid library with 97% inserts, of which >99% were single inserts. The first ligation mixture (50 μ l) contains 2 μ g of DNA fragments, 2 μ g pUC18 DNA (Pharmacia) cut with SmaI and dephosphorylated with bacterial alkaline phosphatase, and 10 units of T4 ligase (GIBCO/BRL) and is incubated at 14°C for 4 hr.

- 5 The ligation mixture then is phenol extracted and ethanol precipitated, and the precipitated DNA is dissolved in 20 μ l TE buffer and electrophoresed on a 1.0% low melting agarose gel. Discrete bands in a ladder are visualized by ethidium bromide-staining and UV illumination and identified by size as insert (I), vector (v), v+I, v+2i, v+3i, etc. The portion of the gel containing v+I DNA is excised and the v+I DNA is recovered and resuspended into 20 μ l TE. The v+I DNA then is
- 10 blunt-ended by T4 polymerase treatment for 5 min. at 37°C in a reaction mixture (50 μ l) containing the v+I linears, 500 μ M each of the 4 dNTPs, and 9 units of T4 polymerase (New England BioLabs), under recommended buffer conditions. After phenol extraction and ethanol precipitation the repaired v+I linears are dissolved in 20 μ l TE. The final ligation to produce circles is carried out in a 50 μ l reaction containing 5 μ l of v+I linears and 5 units of T4 ligase at
- 15 14°C overnight. After 10 min. at 70°C the following day, the reaction mixture is stored at -20°C.

This two-stage procedure results in a molecularly random collection of single-insert plasmid recombinants with minimal contamination from double-insert chimeras (<1%) or free vector (<3%).

- Since deviation from randomness can arise from propagation the DNA in the host, *E. coli*
- 20 host cells deficient in all recombination and restriction functions (A. Greener, *Strategies* 3 (1):5 (1990)) are used to prevent rearrangements, deletions, and loss of clones by restriction. Furthermore, transformed cells are plated directly on antibiotic diffusion plates to avoid the usual broth recovery phase which allows multiplication and selection of the most rapidly growing cells.

- Plating is carried out as follows. A 100 μ l aliquot of Epicurian Coli SURE II
- 25 Supercompetent Cells (Stratagene 200152) is thawed on ice and transferred to a chilled Falcon 2059 tube on ice. A 1.7 μ l aliquot of 1.42 M beta-mercaptoethanol is added to the aliquot of cells to a final concentration of 25 mM. Cells are incubated on ice for 10 min. A 1 μ l aliquot of the final ligation is added to the cells and incubated on ice for 30 min. The cells are heat pulsed for 30 sec. at 42°C and placed back on ice for 2 min. The outgrowth period in liquid culture is
- 30 eliminated from this protocol in order to minimize the preferential growth of any given transformed cell. Instead the transformation mixture is plated directly on a nutrient rich SOB plate containing a 5 ml bottom layer of SOB agar (5% SOB agar: 20 g tryptone, 5 g yeast extract, 0.5 g NaCl, 1.5% Difco Agar per liter of media). The 5 ml bottom layer is supplemented with 0.4 ml of 50 mg/ml ampicillin per 100 ml SOB agar. The 15 ml top layer of SOB agar is
- 35 supplemented with 1 ml X-Gal (2%), 1 ml MgCl₂ (1 M), and 1 ml MgSO₄/100 ml SOB agar. The 15 ml top layer is poured just prior to plating. Our titer is approximately 100 colonies/10 μ l aliquot of transformation.

All colonies are picked for template preparation regardless of size. Thus, only clones lost due to "poison" DNA or deleterious gene products are deleted from the library, resulting in a slight increase in gap number over that expected.

3. Random DNA Sequencing

High quality double stranded DNA plasmid templates are prepared using a "boiling bead" method developed in collaboration with Advanced Genetic Technology Corp. (Gaithersburg, MD) (Adams *et al.*, *Science* 252:1651 (1991); Adams *et al.*, *Nature* 355:632 (1992)). Plasmid preparation is performed in a 96-well format for all stages of DNA preparation from bacterial growth through final DNA purification. Template concentration is determined using Hoechst Dye and a Millipore Cytofluor. DNA concentrations are not adjusted, but low-yielding templates are identified where possible and not sequenced.

Templates are also prepared from two *Borrelia burgdorferi* lambda genomic libraries. An amplified library is constructed in the vector Lambda GEM-12 (Promega) and an unamplified library is constructed in Lambda DASH II (Stratagene). In particular, for the unamplified lambda library, *Borrelia burgdorferi* DNA (> 100 kb) is partially digested in a reaction mixture (200 ul) containing 50 µg DNA, 1X Sau3AI buffer, 20 units Sau3AI for 6 min. at 23°C. The digested DNA was phenol-extracted and electrophoresed on a 0.5% low melting agarose gel at 2V/cm for 7 hours. Fragments from 15 to 25 kb are excised and recovered in a final volume of 6 ul. One µl of fragments is used with 1 µl of DASHII vector (Stratagene) in the recommended ligation reaction. One µl of the ligation mixture is used per packaging reaction following the recommended protocol with the Gigapack II XL Packaging Extract (Stratagene, #227711). Phage are plated directly without amplification from the packaging mixture (after dilution with 500 µl of recommended SM buffer and chloroform treatment). Yield is about 2.5x10³ pfu/ul. The amplified library is prepared essentially as above except the lambda GEM-12 vector is used. After packaging, about 3.5x10⁴ pfu are plated on the restrictive NM539 host. The lysate is harvested in 2 ml of SM buffer and stored frozen in 7% dimethylsulfoxide. The phage titer is approximately 1x10⁹ pfu/ml.

Liquid lysates (100 µl) are prepared from randomly selected plaques (from the unamplified library) and template is prepared by long-range PCR using T7 and T3 vector-specific primers.

Sequencing reactions are carried out on plasmid and/or PCR templates using the AB Catalyst LabStation with Applied Biosystems PRISM Ready Reaction Dye Primer Cycle Sequencing Kits for the M13 forward (M13-21) and the M13 reverse (M13RP1) primers (Adams *et al.*, *Nature* 368:474 (1994)). Dye terminator sequencing reactions are carried out on the lambda templates on a Perkin-Elmer 9600 Thermocycler using the Applied Biosystems Ready Reaction Dye Terminator Cycle Sequencing kits. T7 and SP6 primers are used to sequence the ends of the inserts from the Lambda GEM-12 library and T7 and T3 primers are used to sequence the ends of the inserts from the Lambda DASH II library. Sequencing reactions are performed

by eight individuals using an average of fourteen AB 373 DNA Sequencers per day. All sequencing reactions are analyzed using the Stretch modification of the AB 373, primarily using a 34 cm well-to-read distance. The overall sequencing success rate very approximately is about 85% for M13-21 and M13RP1 sequences and 65% for dye-terminator reactions. The average usable read length is 485 bp for M13-21 sequences, 445bp for M13RP1 sequences, and 375 bp for dye-terminator reactions.

Richards *et al.*, Chapter 28 in AUTOMATED DNA SEQUENCING AND ANALYSIS, M. D. Adams, C. Fields, J. C. Venter, Eds., Academic Press, London, (1994) described the value of using sequence from both ends of sequencing templates to facilitate ordering of contigs in shotgun assembly projects of lambda and cosmid clones. We balance the desirability of both-end sequencing (including the reduced cost of lower total number of templates) against shorter read-lengths for sequencing reactions performed with the M13RP1 (reverse) primer compared to the M13-21 (forward) primer. Approximately one-half of the templates are sequenced from both ends. Random reverse sequencing reactions are done based on successful forward sequencing reactions. Some M13RP1 sequences are obtained in a semi-directed fashion: M13-21: sequences pointing outward at the ends of contigs are chosen for M13RP1 sequencing in an effort to specifically order contigs.

4. Protocol for Automated Cycle Sequencing

The sequencing is carried out using ABI Catalyst robots and AB 373 Automated DNA Sequencers. The Catalyst robot is a publicly available sophisticated pipetting and temperature control robot which has been developed specifically for DNA sequencing reactions. The Catalyst combines pre-aliquoted templates and reaction mixes consisting of deoxy- and dideoxynucleotides, the thermostable Taq DNA polymerase, fluorescently-labelled sequencing primers, and reaction buffer. Reaction mixes and templates are combined in the wells of an aluminum 96-well thermocycling plate. Thirty consecutive cycles of linear amplification (*i.e.*, one primer synthesis) steps are performed including denaturation, annealing of primer and template, and extension; *i.e.*, DNA synthesis. A heated lid with rubber gaskets on the thermocycling plate prevents evaporation without the need for an oil overlay.

Two sequencing protocols are used: one for dye-labelled primers and a second for dye-labelled dideoxy chain terminators. The shotgun sequencing involves use of four dye-labelled sequencing primers, one for each of the four terminator nucleotide. Each dye-primer is labelled with a different fluorescent dye, permitting the four individual reactions to be combined into one lane of the 373 DNA Sequencer for electrophoresis, detection, and base-calling. ABI currently supplies pre-mixed reaction mixes in bulk packages containing all the necessary non-template reagents for sequencing. Sequencing can be done with both plasmid and PCR-generated templates with both dye-primers and dye-terminators with approximately equal fidelity, although plasmid templates generally give longer usable sequences.

Thirty-two reactions are loaded per AB373 Sequencer each day, for a total of 960 samples. Electrophoresis is run overnight following the manufacturer's protocols, and the data is collected for twelve hours. Following electrophoresis and fluorescence detection, the ABI 373 performs automatic lane tracking and base-calling. The lane-tracking is confirmed visually. Each sequence electropherogram (or fluorescence lane trace) is inspected visually and assessed for quality. Trailing sequences of low quality are removed and the sequence itself is loaded via software to a Sybase database (archived daily to 8mm tape). Leading vector polylinker sequence is removed automatically by a software program. Average edited lengths of sequences from the standard ABI 373 are around 400 bp and depend mostly on the quality of the template used for the sequencing reaction. ABI 373 Sequencers converted to Stretch Liners provide a longer electrophoresis path prior to fluorescence detection and increase the average number of usable bases to 500-600 bp.

INFORMATICS

1. Data Management

A number of information management systems for a large-scale sequencing lab have been developed. (For review see, for instance, Kerlavage *et al.*, *Proceedings of the Twenty-Sixth Annual Hawaii International Conference on System Sciences*, IEEE Computer Society Press, Washington D. C., 585 (1993)) The system used to collect and assemble the sequence data was developed using the Sybase relational database management system and was designed to automate data flow wherever possible and to reduce user error. The database stores and correlates all information collected during the entire operation from template preparation to final analysis of the genome. Because the raw output of the ABI 373 Sequencers was based on a Macintosh platform and the data management system chosen was based on a Unix platform, it was necessary to design and implement a variety of multi-user, client-server applications which allow the raw data as well as analysis results to flow seamlessly into the database with a minimum of user effort.

2. Assembly

An assembly engine (TIGR Assembler) developed for the rapid and accurate assembly of thousands of sequence fragments was employed to generate contigs. The TIGR assembler simultaneously clusters and assembles fragments of the genome. In order to obtain the speed necessary to assemble more than 104 fragments, the algorithm builds a hash table of 12 bp oligonucleotide subsequences to generate a list of potential sequence fragment overlaps. The number of potential overlaps for each fragment determines which fragments are likely to fall into repetitive elements. Beginning with a single seed sequence fragment, TIGR Assembler extends the current contig by attempting to add the best matching fragment based on oligonucleotide content. The contig and candidate fragment are aligned using a modified version of the Smith-Waterman algorithm which provides for optimal gapped alignments (Waterman, M. S., *Methods*

in *Enzymology* 164:765 (1988)). The contig is extended by the fragment only if strict criteria for the quality of the match are met. The match criteria include the minimum length of overlap, the maximum length of an unmatched end, and the minimum percentage match. These criteria are automatically lowered by the algorithm in regions of minimal coverage and raised in regions with a possible repetitive element. The number of potential overlaps for each fragment determines which fragments are likely to fall into repetitive elements. Fragments representing the boundaries of repetitive elements and potentially chimeric fragments are often rejected based on partial mismatches at the ends of alignments and excluded from the current contig. TIGR Assembler is designed to take advantage of clone size information coupled with sequencing from both ends of each template. It enforces the constraint that sequence fragments from two ends of the same template point toward one another in the contig and are located within a certain range of base pairs (definable for each clone based on the known clone size range for a given library). The process resulted in 155 contigs as represented by SEQ ID NOs:1-155.

3. Identifying Genes

The predicted coding regions of the *Borrelia burgdorferi* genome were initially defined with the program GeneMark, which finds ORFs using a probabilistic classification technique. The predicted coding region sequences were used in searches against a database of all nucleotide sequences from GenBank (July, 1997), using the BLASTN search method to identify overlaps of 50 or more nucleotides with at least a 95% identity (using default parameters). Those ORFs with nucleotide sequence matches are shown in Table 1. The ORFs without such matches were translated to protein sequences and compared to a non-redundant database of known proteins generated by combining the Swiss-prot, PIR and GenPept databases. ORFs that matched a database protein with BLASTP probability less than or equal to 0.01 are shown in Table 2. The table also lists assigned functions based on the closest match in the databases. ORFs that did not match protein or nucleotide sequences in the databases at these levels are shown in Table 3.

ILLUSTRATIVE APPLICATIONS

1. Production of an Antibody to a *Borrelia burgdorferi* Protein

Substantially pure protein or polypeptide is isolated from the transfected or transformed cells using any one of the methods known in the art. The protein can also be produced in a recombinant prokaryotic expression system, such as *E. coli*, or can be chemically synthesized. Concentration of protein in the final preparation is adjusted, for example, by concentration on an Amicon filter device, to the level of a few micrograms/ml. Monoclonal or polyclonal antibody to the protein can then be prepared as follows.

2. Monoclonal Antibody Production by Hybridoma Fusion

Monoclonal antibody to epitopes of any of the peptides identified and isolated as described can be prepared from murine hybridomas according to the classical method of Kohler, G. and Milstein, C., *Nature* 256:495 (1975) or modifications of the methods thereof. Briefly, a mouse is repetitively inoculated with a few micrograms of the selected protein over a period of a few weeks. The mouse is then sacrificed, and the antibody producing cells of the spleen isolated. The spleen cells are fused by means of polyethylene glycol with mouse myeloma cells, and the excess unfused cells destroyed by growth of the system on selective media comprising aminopterin (HAT media). The successfully fused cells are diluted and aliquots of the dilution placed in wells of a microtiter plate where growth of the culture is continued. Antibody-producing clones are identified by detection of antibody in the supernatant fluid of the wells by immunoassay procedures, such as ELISA, as originally described by Engvall, E., *Meth. Enzymol.* 70:419 (1980), and modified methods thereof. Selected positive clones can be expanded and their monoclonal antibody product harvested for use. Detailed procedures for monoclonal antibody production are described in Davis, L. *et al.*, *Basic Methods in Molecular Biology*, Elsevier, New York. Section 21-2 (1989).

3. Polyclonal Antibody Production by Immunization

Polyclonal antiserum containing antibodies to heterogenous epitopes of a single protein can be prepared by immunizing suitable animals with the expressed protein described above, which can be unmodified or modified to enhance immunogenicity. Effective polyclonal antibody production is affected by many factors related both to the antigen and the host species. For example, small molecules tend to be less immunogenic than others and may require the use of carriers and adjuvant. Also, host animals vary in response to site of inoculations and dose, with both inadequate or excessive doses of antigen resulting in low titer antisera. Small doses (ng level) of antigen administered at multiple intradermal sites appears to be most reliable. An effective immunization protocol for rabbits can be found in Vaitukaitis, J. *et al.*, *J. Clin. Endocrinol. Metab.* 33:988-991 (1971).

Booster injections can be given at regular intervals, and antiserum harvested when antibody titer thereof, as determined semi-quantitatively, for example, by double immunodiffusion in agar against known concentrations of the antigen, begins to fall. See, for example, Ouchterlony, O. *et al.*, Chap. 19 in: *Handbook of Experimental Immunology*, Wier, D., ed, Blackwell (1973). Plateau concentration of antibody is usually in the range of 0.1 to 0.2 mg/ml of serum (about 12M). Affinity of the antisera for the antigen is determined by preparing competitive binding curves, as described, for example, by Fisher, D., Chap. 42 in: *Manual of Clinical Immunology*, second edition, Rose and Friedman, eds., Amer. Soc. For Microbiology, Washington, D. C. (1980)

Antibody preparations prepared according to either protocol are useful in quantitative immunoassays which determine concentrations of antigen-bearing substances in biological

samples; they are also used semi- quantitatively or qualitatively to identify the presence of antigen in a biological sample. In addition, antibodies are useful in various animal models of pneumococcal disease as a means of evaluating the protein used to make the antibody as a potential vaccine target or as a means of evaluating the antibody as a potential immunotherapeutic or immunoprophylactic reagent.

4. Preparation of PCR Primers and Amplification of DNA

Various fragments of the *Borrelia burgdorferi* genome, such as those of Tables 1-6 and SEQ ID NOS: 1-155 can be used, in accordance with the present invention, to prepare PCR primers for a variety of uses. The PCR primers are preferably at least 15 bases, and more preferably at least 18 bases in length. When selecting a primer sequence, it is preferred that the primer pairs have approximately the same G/C ratio, so that melting temperatures are approximately the same. The PCR primers and amplified DNA of this Example find use in the Examples that follow.

5. Isolation of a Selected DNA Clone From *B. burgdorferi*

Three approaches are used to isolate a *B. burgdorferi* clone comprising a polynucleotide of the present invention from any *B. burgdorferi* genomic DNA library. The *B. burgdorferi* strain B31PU has been deposited as a convenient source for obtaining a *B. burgdorferi* strain although a wide variety of strains *B. burgdorferi* strains can be used which are known in the art.

B. burgdorferi genomic DNA is prepared using the following method. A 20ml overnight bacterial culture grown in a rich medium (e.g., Trypticase Soy Broth, Brain Heart Infusion broth or Super broth), pelleted, washed two times with TES (30mM Tris-pH 8.0, 25mM EDTA, 50mM NaCl), and resuspended in 5ml high salt TES (2.5M NaCl). Lysostaphin is added to final concentration of approx 50ug/ml and the mixture is rotated slowly 1 hour at 37C to make protoplast cells. The solution is then placed in incubator (or place in a shaking water bath) and warmed to 55C. Five hundred micro liter of 20% sarcosyl in TES (final concentration 2%) is then added to lyse the cells. Next, guanidine HCl is added to a final concentration of 7M (3.69g in 5.5 ml). The mixture is swirled slowly at 55C for 60-90 min (solution should clear). A CsCl gradient is then set up in SW41 ultra clear tubes using 2.0ml 5.7M CsCl and overlaying with 2.85M CsCl. The gradient is carefully overlayed with the DNA-containing GuHCl solution. The gradient is spun at 30,000 rpm, 20C for 24 hr and the lower DNA band is collected. The volume is increased to 5 ml with TE buffer. The DNA is then treated with protease K (10 ug/ml) overnight at 37 C, and precipitated with ethanol. The precipitated DNA is resuspended in a desired buffer.

In the first method, a plasmid is directly isolated by screening a plasmid *B. burgdorferi* genomic DNA library using a polynucleotide probe corresponding to a polynucleotide of the present invention. Particularly, a specific polynucleotide with 30-40 nucleotides is synthesized using an Applied Biosystems DNA synthesizer according to the sequence reported. The

oligonucleotide is labeled, for instance, with ^{32}P - γ -ATP using T4 polynucleotide kinase and purified according to routine methods. (See, e.g., Maniatis et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Press, Cold Spring, NY (1982).) The library is transformed into a suitable host, as indicated above (such as XL-1 Blue (Stratagene)) using techniques known to those of skill in the art. See, e.g., Sambrook et al. *MOLECULAR CLONING: A LABORATORY MANUAL* (Cold Spring Harbor, N.Y. 2nd ed. 1989); Ausubel et al., *CURRENT PROTOCOLS IN MOLECULAR BIOLOGY* (John Wiley and Sons, N.Y. 1989). The transformants are plated on 1.5% agar plates (containing the appropriate selection agent, e.g., ampicillin) to a density of about 150 transformants (colonies) per plate. These plates are screened using Nylon membranes according to routine methods for bacterial colony screening. See, e.g., Sambrook et al. *MOLECULAR CLONING: A LABORATORY MANUAL* (Cold Spring Harbor, N.Y. 2nd ed. 1989); Ausubel et al., *CURRENT PROTOCOLS IN MOLECULAR BIOLOGY* (John Wiley and Sons, N.Y. 1989) or other techniques known to those of skill in the art.

Alternatively, two primers of 15-25 nucleotides derived from the 5' and 3' ends of a polynucleotide of SEQ ID NOS:1-155 are synthesized and used to amplify the desired DNA by PCR using a *B. burgdorferi* genomic DNA prep as a template. PCR is carried out under routine conditions, for instance, in 25 μl of reaction mixture with 0.5 μg of the above DNA template. A convenient reaction mixture is 1.5-5 mM MgCl_2 , 0.01% (w/v) gelatin, 20 μM each of dATP, dCTP, dGTP, dTTP, 25 pmol of each primer and 0.25 Unit of Taq polymerase. Thirty five cycles of PCR (denaturation at 94°C for 1 min; annealing at 55°C for 1 min; elongation at 72°C for 1 min) are performed with a Perkin-Elmer Cetus automated thermal cycler. The amplified product is analyzed by agarose gel electrophoresis and the DNA band with expected molecular weight is excised and purified. The PCR product is verified to be the selected sequence by subcloning and sequencing the DNA product.

Finally, overlapping oligos of the DNA sequences of SEQ ID NOS:1-155 can be chemically synthesized and used to generate a nucleotide sequence of desired length using PCR methods known in the art.

6(a). Expression and Purification *Borrelia* polypeptides in *E. coli*

The bacterial expression vector pQE60 is used for bacterial expression of some of the polypeptide fragments of the present invention. (QIAGEN, Inc., 9259 Eton Avenue, Chatsworth, CA, 91311). pQE60 encodes ampicillin antibiotic resistance ("Amp^r") and contains a bacterial origin of replication ("ori"), an IPTG inducible promoter, a ribosome binding site ("RBS"), six codons encoding histidine residues that allow affinity purification using nickel-nitrilo-tri-acetic acid ("Ni-NTA") affinity resin (QIAGEN, Inc., *supra*) and suitable single restriction enzyme cleavage sites. These elements are arranged such that an inserted DNA fragment encoding a polypeptide expresses that polypeptide with the six His residues (i.e., a "6

X His tag") covalently linked to the carboxyl terminus of that polypeptide.

The DNA sequence encoding the desired portion of a *B. burgdorferi* protein of the present invention is amplified from *B. burgdorferi* genomic DNA using PCR oligonucleotide primers which anneal to the 5' and 3' sequences coding for the portions of the *B. burgdorferi* polynucleotide shown in SEQ ID NOS:1-155. Additional nucleotides containing restriction sites to facilitate cloning in the pQE60 vector are added to the 5' and 3' sequences, respectively.

For cloning the mature protein, the 5' primer has a sequence containing an appropriate restriction site followed by nucleotides of the amino terminal coding sequence of the desired *B. burgdorferi* polynucleotide sequence in SEQ ID NOS:1-155. One of ordinary skill in the art would appreciate that the point in the protein coding sequence where the 5' and 3' primers begin may be varied to amplify a DNA segment encoding any desired portion of the complete protein shorter or longer than the mature form. The 3' primer has a sequence containing an appropriate restriction site followed by nucleotides complementary to the 3' end of the polypeptide coding sequence of SEQ ID NOS:1-155, excluding a stop codon, with the coding sequence aligned with the restriction site so as to maintain its reading frame with that of the six His codons in the pQE60 vector.

The amplified *B. burgdorferi* DNA fragment and the vector pQE60 are digested with restriction enzymes which recognize the sites in the primers and the digested DNAs are then ligated together. The *B. burgdorferi* DNA is inserted into the restricted pQE60 vector in a manner which places the *B. burgdorferi* protein coding region downstream from the IPTG-inducible promoter and in-frame with an initiating AUG and the six histidine codons.

The ligation mixture is transformed into competent *E. coli* cells using standard procedures such as those described by Sambrook et al., *supra*. *E. coli* strain M15/rep4, containing multiple copies of the plasmid pREP4, which expresses the lac repressor and confers kanamycin resistance ("Kanr"), is used in carrying out the illustrative example described herein. This strain, which is only one of many that are suitable for expressing a *B. burgdorferi* polypeptide, is available commercially (QIAGEN, Inc., *supra*). Transformants are identified by their ability to grow on LB agar plates in the presence of ampicillin and kanamycin. Plasmid DNA is isolated from resistant colonies and the identity of the cloned DNA confirmed by restriction analysis, PCR and DNA sequencing.

Clones containing the desired constructs are grown overnight ("O/N") in liquid culture in LB media supplemented with both ampicillin (100 µg/ml) and kanamycin (25 µg/ml). The O/N culture is used to inoculate a large culture, at a dilution of approximately 1:25 to 1:250. The cells are grown to an optical density at 600 nm ("OD600") of between 0.4 and 0.6. Isopropyl-β-D-thiogalactopyranoside ("IPTG") is then added to a final concentration of 1 mM to induce transcription from the lac repressor sensitive promoter, by inactivating the lacI repressor. Cells subsequently are incubated further for 3 to 4 hours. Cells then are harvested by centrifugation.

The cells are then stirred for 3-4 hours at 4°C in 6M guanidine-HCl, pH 8. The cell

debris is removed by centrifugation, and the supernatant containing the *B. burgdorferi* polypeptide is loaded onto a nickel-nitrilo-tri-acetic acid ("Ni-NTA") affinity resin column (QIAGEN, Inc., *supra*). Proteins with a 6 x His tag bind to the Ni-NTA resin with high affinity are purified in a simple one-step procedure (for details see: The QIAexpressionist, 1995, QIAGEN, Inc., *supra*). Briefly the supernatant is loaded onto the column in 6 M guanidine-HCl, pH 8, the column is first washed with 10 volumes of 6 M guanidine-HCl, pH 8, then washed with 10 volumes of 6 M guanidine-HCl pH 6, and finally the *B. burgdorferi* polypeptide is eluted with 6 M guanidine-HCl, pH 5.

The purified protein is then renatured by dialyzing it against phosphate-buffered saline (PBS) or 50 mM Na-acetate, pH 6 buffer plus 200 mM NaCl. Alternatively, the protein could be successfully refolded while immobilized on the Ni-NTA column. The recommended conditions are as follows: renature using a linear 6M-1M urea gradient in 500 mM NaCl, 20% glycerol, 20 mM Tris/HCl pH 7.4, containing protease inhibitors. The renaturation should be performed over a period of 1.5 hours or more. After renaturation the proteins can be eluted by the addition of 250 mM imidazole. Imidazole is removed by a final dialyzing step against PBS or 50 mM sodium acetate pH 6 buffer plus 200 mM NaCl. The purified protein is stored at 4°C or frozen at -80°C.

The polypeptide of the present invention are also prepared using a non-denaturing protein purification method. For these polypeptides, the cell pellet from each liter of culture is resuspended in 25 mls of Lysis Buffer A at 4°C (Lysis Buffer A = 50 mM Na-phosphate, 300 mM NaCl, 10 mM 2-mercaptoethanol, 10% Glycerol, pH 7.5 with 1 tablet of Complete EDTA-free protease inhibitor cocktail (Boehringer Mannheim #1873580) per 50 ml of buffer). Absorbance at 550 nm is approximately 10-20 O.D./ml. The suspension is then put through three freeze/thaw cycles from -70°C (using a ethanol-dry ice bath) up to room temperature. The cells are lysed via sonication in short 10 sec bursts over 3 minutes at approximately 80W while kept on ice. The sonicated sample is then centrifuged at 15,000 RPM for 30 minutes at 4°C. The supernatant is passed through a column containing 1.0 ml of CL-4B resin to pre-clear the sample of any proteins that may bind to agarose non-specifically, and the flow-through fraction is collected.

The pre-cleared flow-through is applied to a nickel-nitrilo-tri-acetic acid ("Ni-NTA") affinity resin column (Quiagen, Inc., *supra*). Proteins with a 6 X His tag bind to the Ni-NTA resin with high affinity and can be purified in a simple one-step procedure. Briefly, the supernatant is loaded onto the column in Lysis Buffer A at 4°C, the column is first washed with 10 volumes of Lysis Buffer A until the A280 of the eluate returns to the baseline. Then, the column is washed with 5 volumes of 40 mM Imidazole (92% Lysis Buffer A / 8% Buffer B) (Buffer B = 50 mM Na-Phosphate, 300 mM NaCl, 10% Glycerol, 10 mM 2-mercaptoethanol, 500 mM Imidazole, pH of the final buffer should be 7.5). The protein is eluted off of the column with a series of increasing Imidazole solutions made by adjusting the ratios of Lysis Buffer A to Buffer B. Three different concentrations are used: 3 volumes of 75 mM Imidazole, 3 volumes of

150 mM Imidazole, 5 volumes of 500 mM Imidazole. The fractions containing the purified protein are analyzed using 8 %, 10 % or 14% SDS-PAGE depending on the protein size. The purified protein is then dialyzed 2X against phosphate-buffered saline (PBS) in order to place it into an easily workable buffer. The purified protein is stored at 4°C or frozen at -80°.

- 5 The following alternative method may be used to purify *B. burgdorferi* expressed in *E. coli* when it is present in the form of inclusion bodies. Unless otherwise specified, all of the following steps are conducted at 4-10°C.

Upon completion of the production phase of the *E. coli* fermentation, the cell culture is cooled to 4-10°C and the cells are harvested by continuous centrifugation at 15,000 rpm

- 10 (Heraeus Sepatech). On the basis of the expected yield of protein per unit weight of cell paste and the amount of purified protein required, an appropriate amount of cell paste, by weight, is suspended in a buffer solution containing 100 mM Tris, 50 mM EDTA, pH 7.4. The cells are dispersed to a homogeneous suspension using a high shear mixer.

- The cells are then lysed by passing the solution through a microfluidizer (Microfluidics, Corp. or APV Gaulin, Inc.) twice at 4000-6000 psi. The homogenate is then mixed with NaCl solution to a final concentration of 0.5 M NaCl, followed by centrifugation at 7000 x g for 15 min. The resultant pellet is washed again using 0.5M NaCl, 100 mM Tris, 50 mM EDTA, pH 7.4.

- 20 The resulting washed inclusion bodies are solubilized with 1.5 M guanidine hydrochloride (GuHCl) for 2-4 hours. After 7000 x g centrifugation for 15 min., the pellet is discarded and the *B. burgdorferi* polypeptide-containing supernatant is incubated at 4°C overnight to allow further GuHCl extraction.

- Following high speed centrifugation (30,000 x g) to remove insoluble particles, the GuHCl solubilized protein is refolded by quickly mixing the GuHCl extract with 20 volumes of buffer containing 50 mM sodium, pH 4.5, 150 mM NaCl, 2 mM EDTA by vigorous stirring. The refolded diluted protein solution is kept at 4°C without mixing for 12 hours prior to further purification steps.

- To clarify the refolded *B. burgdorferi* polypeptide solution, a previously prepared tangential filtration unit equipped with 0.16 µm membrane filter with appropriate surface area (e.g., Filtron), equilibrated with 40 mM sodium acetate, pH 6.0 is employed. The filtered sample is loaded onto a cation exchange resin (e.g., Poros HS-50, Perseptive Biosystems). The column is washed with 40 mM sodium acetate, pH 6.0 and eluted with 250 mM, 500 mM, 1000 mM, and 1500 mM NaCl in the same buffer, in a stepwise manner. The absorbance at 280 nm of the effluent is continuously monitored. Fractions are collected and further analyzed by SDS-PAGE.

Fractions containing the *B. burgdorferi* polypeptide are then pooled and mixed with 4

volumes of water. The diluted sample is then loaded onto a previously prepared set of tandem columns of strong anion (Poros HQ-50, Perseptive Biosystems) and weak anion (Poros CM-20, Perseptive Biosystems) exchange resins. The columns are equilibrated with 40 mM sodium acetate, pH 6.0. Both columns are washed with 40 mM sodium acetate, pH 6.0, 200 mM NaCl.

5 The CM-20 column is then eluted using a 10 column volume linear gradient ranging from 0.2 M NaCl, 50 mM sodium acetate, pH 6.0 to 1.0 M NaCl, 50 mM sodium acetate, pH 6.5. Fractions are collected under constant A_{280} monitoring of the effluent. Fractions containing the *B. burgdorferi* polypeptide (determined, for instance, by 16% SDS-PAGE) are then pooled.

The resultant *B. burgdorferi* polypeptide exhibits greater than 95% purity after the above
10 refolding and purification steps. No major contaminant bands are observed from Commassie blue stained 16% SDS-PAGE gel when 5 μ g of purified protein is loaded. The purified protein is also tested for endotoxin/LPS contamination, and typically the LPS content is less than 0.1 ng/ml according to LAL assays.

15 6(b). Alternative Expression and Purification *Borrelia* polypeptides in *E. coli*

The vector pQE10 is alternatively used to clone and express some of the polypeptides of the present invention for use in the soft tissue and systemic infection models discussed below. The difference being such that an inserted DNA fragment encoding a polypeptide expresses that
20 polypeptide with the six His residues (i.e., a "6 X His tag") covalently linked to the amino terminus of that polypeptide. The bacterial expression vector pQE10 (QIAGEN, Inc., 9259 Eton Avenue, Chatsworth, CA, 91311) was used in this example. The components of the pQE10 plasmid are arranged such that the inserted DNA sequence encoding a polypeptide of the present invention expresses the polypeptide with the six His residues (i.e., a "6 X His tag")) covalently
25 linked to the amino terminus.

The DNA sequences encoding the desired portions of a polypeptide of SEQ ID NOS:1-155 were amplified using PCR oligonucleotide primers from genomic *B. burgdorferi* DNA. The PCR primers anneal to the nucleotide sequences encoding the desired amino acid sequence of a polypeptide of the present invention. Additional nucleotides containing restriction sites to
30 facilitate cloning in the pQE10 vector were added to the 5' and 3' primer sequences, respectively.

For cloning a polypeptide of the present invention, the 5' and 3' primers were selected to amplify their respective nucleotide coding sequences. One of ordinary skill in the art would appreciate that the point in the protein coding sequence where the 5' and 3' primers begins may be varied to amplify a DNA segment encoding any desired portion of a polypeptide of the present
35 invention. The 5' primer was designed so the coding sequence of the 6 X His tag is aligned with the restriction site so as to maintain its reading frame with that of *B. burgdorferi* polypeptide. The 3' was designed to include an stop codon. The amplified DNA fragment was then cloned, and the protein expressed, as described above for the pQE60 plasmid.

The DNA sequences of SEQ ID NOS:1-155 encoding amino acid sequences may also be cloned and expressed as fusion proteins by a protocol similar to that described directly above, wherein the pET-32b(+) vector (Novagen, 601 Science Drive, Madison, WI 53711) is preferentially used in place of pQE10.

5 The above methods are not limited to the polypeptide fragments actually produced. The above method, like the methods below, can be used to produce either full length polypeptides or desired fragments thereof.

10 6(c). Alternative Expression and Purification of *Borrelia* polypeptides in *E. coli*

The bacterial expression vector pQE60 is used for bacterial expression in this example (QIAGEN, Inc., 9259 Eton Avenue, Chatsworth, CA, 91311). However, in this example, the polypeptide coding sequence is inserted such that translation of the six His codons is prevented and, therefore, the polypeptide is produced with no 6 X His tag.

15 The DNA sequence encoding the desired portion of the *B. burgdorferi* amino acid sequence is amplified from an *B. burgdorferi* genomic DNA prep the deposited DNA clones using PCR oligonucleotide primers which anneal to the 5' and 3' nucleotide sequences corresponding to the desired portion of the *B. burgdorferi* polypeptides. Additional nucleotides containing restriction sites to facilitate cloning in the pQE60 vector are added to the 5' and 3' primer sequences.

20 For cloning a *B. burgdorferi* polypeptides of the present invention, 5' and 3' primers are selected to amplify their respective nucleotide coding sequences. One of ordinary skill in the art would appreciate that the point in the protein coding sequence where the 5' and 3' primers begin may be varied to amplify a DNA segment encoding any desired portion of a polypeptide of the present invention. The 3' and 5' primers contain appropriate restriction sites followed by nucleotides complementary to the 5' and 3' ends of the coding sequence respectively. The 3' primer is additionally designed to include an in-frame stop codon.

25 The amplified *B. burgdorferi* DNA fragments and the vector pQE60 are digested with restriction enzymes recognizing the sites in the primers and the digested DNAs are then ligated together. Insertion of the *B. burgdorferi* DNA into the restricted pQE60 vector places the *B. burgdorferi* protein coding region including its associated stop codon downstream from the IPTG-inducible promoter and in-frame with an initiating AUG. The associated stop codon prevents translation of the six histidine codons downstream of the insertion point.

35 The ligation mixture is transformed into competent *E. coli* cells using standard procedures such as those described by Sambrook et al. *E. coli* strain M15/rep4, containing multiple copies of the plasmid pREP4, which expresses the lac repressor and confers kanamycin resistance ("Kan^r"), is used in carrying out the illustrative example described herein. This strain, which is only one of many that are suitable for expressing *B. burgdorferi* polypeptide, is available commercially (QIAGEN, Inc., *supra*). Transformants are identified by their ability to grow on

LB plates in the presence of ampicillin and kanamycin. Plasmid DNA is isolated from resistant colonies and the identity of the cloned DNA confirmed by restriction analysis, PCR and DNA sequencing.

Clones containing the desired constructs are grown overnight ("O/N") in liquid culture in LB media supplemented with both ampicillin (100 µg/ml) and kanamycin (25 µg/ml). The O/N culture is used to inoculate a large culture, at a dilution of approximately 1:25 to 1:250. The cells are grown to an optical density at 600 nm ("OD600") of between 0.4 and 0.6. isopropyl-b-D-thiogalactopyranoside ("IPTG") is then added to a final concentration of 1 mM to induce transcription from the *lac* repressor sensitive promoter, by inactivating the *lacI* repressor. Cells subsequently are incubated further for 3 to 4 hours. Cells then are harvested by centrifugation.

To purify the *B. burgdorferi* polypeptide, the cells are then stirred for 3-4 hours at 4°C in 6M guanidine-HCl, pH 8. The cell debris is removed by centrifugation, and the supernatant containing the *B. burgdorferi* polypeptide is dialyzed against 50 mM Na-acetate buffer pH 6, supplemented with 200 mM NaCl. Alternatively, the protein can be successfully refolded by dialyzing it against 500 mM NaCl, 20% glycerol, 25 mM Tris/HCl pH 7.4, containing protease inhibitors. After renaturation the protein can be purified by ion exchange, hydrophobic interaction and size exclusion chromatography. Alternatively, an affinity chromatography step such as an antibody column can be used to obtain pure *B. burgdorferi* polypeptide. The purified protein is stored at 4°C or frozen at -80°C.

The following alternative method may be used to purify *B. burgdorferi* polypeptides expressed in *E. coli* when it is present in the form of inclusion bodies. Unless otherwise specified, all of the following steps are conducted at 4-10°C.

Upon completion of the production phase of the *E. coli* fermentation, the cell culture is cooled to 4-10°C and the cells are harvested by continuous centrifugation at 15,000 rpm (Heraeus Sepatech). On the basis of the expected yield of protein per unit weight of cell paste and the amount of purified protein required, an appropriate amount of cell paste, by weight, is suspended in a buffer solution containing 100 mM Tris, 50 mM EDTA, pH 7.4. The cells are dispersed to a homogeneous suspension using a high shear mixer.

The cells were then lysed by passing the solution through a microfluidizer (Microfluidics, Corp. or APV Gaulin, Inc.) twice at 4000-6000 psi. The homogenate is then mixed with NaCl solution to a final concentration of 0.5 M NaCl, followed by centrifugation at 7000 x g for 15 min. The resultant pellet is washed again using 0.5M NaCl, 100 mM Tris, 50 mM EDTA, pH 7.4.

The resulting washed inclusion bodies are solubilized with 1.5 M guanidine hydrochloride (GuHCl) for 2-4 hours. After 7000 x g centrifugation for 15 min., the pellet is discarded and the *B. burgdorferi* polypeptide-containing supernatant is incubated at 4°C overnight to allow further GuHCl extraction.

Following high speed centrifugation (30,000 x g) to remove insoluble particles, the GuHCl solubilized protein is refolded by quickly mixing the GuHCl extract with 20 volumes of buffer containing 50 mM sodium, pH 4.5, 150 mM NaCl, 2 mM EDTA by vigorous stirring. The refolded diluted protein solution is kept at 4°C without mixing for 12 hours prior to further purification steps.

To clarify the refolded *B. burgdorferi* polypeptide solution, a previously prepared tangential filtration unit equipped with 0.16 µm membrane filter with appropriate surface area (e.g., Filtron), equilibrated with 40 mM sodium acetate, pH 6.0 is employed. The filtered sample is loaded onto a cation exchange resin (e.g., Poros HS-50, Perseptive Biosystems). The column is washed with 40 mM sodium acetate, pH 6.0 and eluted with 250 mM, 500 mM, 1000 mM, and 1500 mM NaCl in the same buffer, in a stepwise manner. The absorbance at 280 nm of the effluent is continuously monitored. Fractions are collected and further analyzed by SDS-PAGE.

Fractions containing the *B. burgdorferi* polypeptide are then pooled and mixed with 4 volumes of water. The diluted sample is then loaded onto a previously prepared set of tandem columns of strong anion (Poros HQ-50, Perseptive Biosystems) and weak anion (Poros CM-20, Perseptive Biosystems) exchange resins. The columns are equilibrated with 40 mM sodium acetate, pH 6.0. Both columns are washed with 40 mM sodium acetate, pH 6.0, 200 mM NaCl. The CM-20 column is then eluted using a 10 column volume linear gradient ranging from 0.2 M NaCl, 50 mM sodium acetate, pH 6.0 to 1.0 M NaCl, 50 mM sodium acetate, pH 6.5. Fractions are collected under constant A₂₈₀ monitoring of the effluent. Fractions containing the *B. burgdorferi* polypeptide (determined, for instance, by 16% SDS-PAGE) are then pooled.

The resultant *B. burgdorferi* polypeptide exhibits greater than 95% purity after the above refolding and purification steps. No major contaminant bands are observed from Commassie blue stained 16% SDS-PAGE gel when 5 µg of purified protein is loaded. The purified protein is also tested for endotoxin/LPS contamination, and typically the LPS content is less than 0.1 ng/ml according to LAL assays.

6(d). Cloning and Expression of *B. burgdorferi* in Other Bacteria

B. burgdorferi polypeptides can also be produced in: *B. burgdorferi* using the methods of S. Skinner et al., (1988) Mol. Microbiol. 2:289-297 or J. I. Moreno (1996) Protein Expr. Purif. 8(3):332-340; *Lactobacillus* using the methods of C. Rush et al., 1997 Appl. Microbiol. Biotechnol. 47(5):537-542; or in *Bacillus subtilis* using the methods Chang et al., U.S. Patent No. 4,952,508.

7. Cloning and Expression in COS Cells

A *B. burgdorferi* expression plasmid is made by cloning a portion of the DNA encoding a

B. burgdorferi polypeptide into the expression vector pDNAI/Amp or pDNAIII (which can be obtained from Invitrogen, Inc.). The expression vector pDNAI/amp contains: (1) an *E. coli* origin of replication effective for propagation in *E. coli* and other prokaryotic cells; (2) an ampicillin resistance gene for selection of plasmid-containing prokaryotic cells; (3) an SV40 origin of replication for propagation in eukaryotic cells; (4) a CMV promoter, a polylinker, an SV40 intron; (5) several codons encoding a hemagglutinin fragment (i.e., an "HA" tag to facilitate purification) followed by a termination codon and polyadenylation signal arranged so that a DNA can be conveniently placed under expression control of the CMV promoter and operably linked to the SV40 intron and the polyadenylation signal by means of restriction sites in the polylinker. The HA tag corresponds to an epitope derived from the influenza hemagglutinin protein described by Wilson et al. 1984 Cell 37:767. The fusion of the HA tag to the target protein allows easy detection and recovery of the recombinant protein with an antibody that recognizes the HA epitope. pDNAIII contains, in addition, the selectable neomycin marker.

A DNA fragment encoding a *B. burgdorferi* polypeptide is cloned into the polylinker region of the vector so that recombinant protein expression is directed by the CMV promoter. The plasmid construction strategy is as follows. The DNA from a *B. burgdorferi* genomic DNA prep is amplified using primers that contain convenient restriction sites, much as described above for construction of vectors for expression of *B. burgdorferi* in *E. coli*. The 5' primer contains a Kozak sequence, an AUG start codon, and nucleotides of the 5' coding region of the *B. burgdorferi* polypeptide. The 3' primer, contains nucleotides complementary to the 3' coding sequence of the *B. burgdorferi* DNA, a stop codon, and a convenient restriction site.

The PCR amplified DNA fragment and the vector, pDNAI/Amp, are digested with appropriate restriction enzymes and then ligated. The ligation mixture is transformed into an appropriate *E. coli* strain such as SURE™ (Stratagene Cloning Systems, La Jolla, CA 92037), and the transformed culture is plated on ampicillin media plates which then are incubated to allow growth of ampicillin resistant colonies. Plasmid DNA is isolated from resistant colonies and examined by restriction analysis or other means for the presence of the fragment encoding the *B. burgdorferi* polypeptide.

For expression of a recombinant *B. burgdorferi* polypeptide, COS cells are transfected with an expression vector, as described above, using DEAE-dextran, as described, for instance, by Sambrook et al. (*supra*). Cells are incubated under conditions for expression of *B. burgdorferi* by the vector.

Expression of the *B. burgdorferi*-HA fusion protein is detected by radiolabeling and immunoprecipitation, using methods described in, for example Harlow et al., *supra*. To this end, two days after transfection, the cells are labeled by incubation in media containing ³⁵S-cysteine for 8 hours. The cells and the media are collected, and the cells are washed and the lysed with detergent-containing RIPA buffer: 150 mM NaCl, 1% NP-40, 0.1% SDS, 1% NP-40, 0.5% DOC, 50 mM TRIS, pH 7.5, as described by Wilson et al. (*supra*). Proteins are

precipitated from the cell lysate and from the culture media using an HA-specific monoclonal antibody. The precipitated proteins then are analyzed by SDS-PAGE and autoradiography. An expression product of the expected size is seen in the cell lysate, which is not seen in negative controls.

5

8. Cloning and Expression in CHO Cells

The vector pC4 is used for the expression of *B. burgdorferi* polypeptide in this example. Plasmid pC4 is a derivative of the plasmid pSV2-dhfr (ATCC Accession No. 37146). The plasmid contains the mouse DHFR gene under control of the SV40 early promoter. Chinese hamster ovary cells or other cells lacking dihydrofolate activity that are transfected with these plasmids can be selected by growing the cells in a selective medium (alpha minus MEM, Life Technologies) supplemented with the chemotherapeutic agent methotrexate. The amplification of the DHFR genes in cells resistant to methotrexate (MTX) has been well documented. *See, e.g.,* Alt et al., 1978, J. Biol. Chem. 253:1357-1370; Hamlin et al., 1990, Biochem. et Biophys. Acta, 1097:107-143; Page et al., 1991, Biotechnology 9:64-68. Cells grown in increasing concentrations of MTX develop resistance to the drug by overproducing the target enzyme, DHFR, as a result of amplification of the DHFR gene. If a second gene is linked to the DHFR gene, it is usually co-amplified and over-expressed. It is known in the art that this approach may be used to develop cell lines carrying more than 1,000 copies of the amplified gene(s). Subsequently, when the methotrexate is withdrawn, cell lines are obtained which contain the amplified gene integrated into one or more chromosome(s) of the host cell.

Plasmid pC4 contains the strong promoter of the long terminal repeat (LTR) of the Rouse Sarcoma Virus, for expressing a polypeptide of interest, Cullen, et al. (1985) Mol. Cell. Biol. 5:438-447; plus a fragment isolated from the enhancer of the immediate early gene of human cytomegalovirus (CMV), Boshart, et al., 1985, Cell 41:521-530. Downstream of the promoter are the following single restriction enzyme cleavage sites that allow the integration of the genes: *Bam* HI, *Xba* I, and *Asp* 718. Behind these cloning sites the plasmid contains the 3' intron and polyadenylation site of the rat preproinsulin gene. Other high efficiency promoters can also be used for the expression, e.g., the human β -actin promoter, the SV40 early or late promoters or the long terminal repeats from other retroviruses, e.g., HIV and HTLV. Clontech's Tet-Off and Tet-On gene expression systems and similar systems can be used to express the *B. burgdorferi* polypeptide in a regulated way in mammalian cells (Gossen et al., 1992, Proc. Natl. Acad. Sci. USA 89:5547-5551. For the polyadenylation of the mRNA other signals, e.g., from the human growth hormone or globin genes can be used as well. Stable cell lines carrying a gene of interest integrated into the chromosomes can also be selected upon co-transfection with a selectable marker such as gpt, G418 or hygromycin. It is advantageous to use more than one selectable marker in the beginning, e.g., G418 plus methotrexate.

The plasmid pC4 is digested with the restriction enzymes and then dephosphorylated using calf intestinal phosphates by procedures known in the art. The vector is then isolated from

a 1% agarose gel. The DNA sequence encoding the *B. burgdorferi* polypeptide is amplified using PCR oligonucleotide primers corresponding to the 5' and 3' sequences of the desired portion of the gene. A 5' primer containing a restriction site, a Kozak sequence, an AUG start codon, and nucleotides of the 5' coding region of the *B. burgdorferi* polypeptide is synthesized and used. A 3' primer, containing a restriction site, stop codon, and nucleotides complementary to the 3' coding sequence of the *B. burgdorferi* polypeptides is synthesized and used. The amplified fragment is digested with the restriction endonucleases and then purified again on a 1% agarose gel. The isolated fragment and the dephosphorylated vector are then ligated with T4 DNA ligase. *E. coli* HB101 or XL-1 Blue cells are then transformed and bacteria are identified that contain the fragment inserted into plasmid pC4 using, for instance, restriction enzyme analysis.

Chinese hamster ovary cells lacking an active DHFR gene are used for transfection. Five µg of the expression plasmid pC4 is cotransfected with 0.5 µg of the plasmid pSVneo using a lipid-mediated transfection agent such as Lipofectin™ or LipofectAMINE.™ (Life Technologies Gaithersburg, MD). The plasmid pSV2-neo contains a dominant selectable marker, the *neo* gene from Tn5 encoding an enzyme that confers resistance to a group of antibiotics including G418. The cells are seeded in alpha minus MEM supplemented with 1 mg/ml G418. After 2 days, the cells are trypsinized and seeded in hybridoma cloning plates (Greiner, Germany) in alpha minus MEM supplemented with 10, 25, or 50 ng/ml of methotrexate plus 1 mg/ml G418. After about 10-14 days single clones are trypsinized and then seeded in 6-well petri dishes or 10 ml flasks using different concentrations of methotrexate (50 nM, 100 nM, 200 nM, 400 nM, 800 nM). Clones growing at the highest concentrations of methotrexate are then transferred to new 6-well plates containing even higher concentrations of methotrexate (1 µM, 2 µM, 5 µM, 10 mM, 20 mM). The same procedure is repeated until clones are obtained which grow at a concentration of 100-200 µM. Expression of the desired gene product is analyzed, for instance, by SDS-PAGE and Western blot or by reversed phase HPLC analysis.

The disclosure of all publications (including patents, patent applications, journal articles, laboratory manuals, books, or other documents) cited herein are hereby incorporated by reference in their entireties.

The present invention is not to be limited in scope by the specific embodiments described herein, which are intended as single illustrations of individual aspects of the invention. Functionally equivalent methods and components are within the scope of the invention, in addition to those shown and described herein and will become apparant to those skilled in the art from the foregoing description and accompanying drawings. Such modifications are intended to fall within the scope of the appended claims.

TABLE 1. Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident
1	92	100363	100184	gil500722	similar to entire extracellular domain of glycine receptors [Caenorhabditis elegans]	100	66
1	537	513231	513608	gil47453	ribosomal protein S12 [Streptococcus pneumoniae]	92	85
1	283	272186	270849	gil1001376	ATP-dependent protease ATPase subunit [Synecocystis sp.]	89	75
1	847	798835	799131	gil467373	ribosomal protein S18 [Bacillus subtilis]	86	69
1	78	91504	91235	gil1573896	ribosomal protein L27 (rpl27) [Haemophilus influenzae]	85	70
1	732	687538	686753	gil1591672	phosphate transport system ATP-binding protein [Methanococcus jannaschii]	84	65
1	788	739513	739232	gil142459	initiation factor 1 [Bacillus subtilis]	84	68
1	960	901448	901780	gnl1PIDe243769	ORF YGL149w [Saccharomyces cerevisiae]	84	68
1	760	717009	715843	gil623028	orf 361; translated orf similarity to SW: RF1_SALTY peptide chain release factor 1 of Salmonella typhimurium [Coxiella burnetii]	83	60
1	115	115536	115312	gil695315	NADH dehydrogenase subunit [Digitalis grandiflora]	82	58
1	184	178954	176918	bbs157690	EF-G=elongation factor G [Thermotoga maritima, Peptide, 682 aa] [Thermotoga maritima]	82	63
1	447	425980	425453	gil143804	Ndk [Bacillus subtilis]	82	56
1	201	194702	194103	gil530438	arabinose transport protein [Mycoplasma capricolum]	81	53
1	477	446671	445589	gil882454	fructose 1,6-bisphosphate aldolase [Escherichia coli]	81	61
1	601	569453	568650	gil349227	transmembrane protein [Escherichia coli]	81	56
1	887	838084	837224	gil1237019	Srb [Bacillus subtilis]	81	52
1	889	840561	839497	gil154276	peptide chain release factor 2 [Salmonella typhimurium]	81	65
1	896	846681	845440	gil1377823	aminopeptidase [Bacillus subtilis]	81	60
1	60	71604	68890	gil1619909	DNA mismatch repair protein [Thermotoga maritima]	80	59
1	354	348744	349157	gil1765976	chemotaxis protein Che Y [Treponema pallidum]	80	42
1	423	409238	408855	gnl1PIDe211829	50S ribosomal protein L14 [Odontella sinensis]	80	61
1	426	410130	409711	gil1652420	50S ribosomal protein L16 [Synecocystis sp.]	80	59
1	507	482736	482936	gil1515924	glucosyltransferase [Saccharomyces cerevisiae]	80	40
1	534	505081	505467	pir1A02771IR	ribosomal protein L7/L12 - Micrococcus luteus	80	67

Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

					7MCM				
1	597	567506	566532	gil580899	OppF gene product [Bacillus subtilis]			80	59
1	6	11241	9994	gnlPIDle242614	arginine deiminase [Clostridium perfringens]			79	62
1	478	447926	446835	gnlPIDle288124	glucose epimerase [Bacillus thuringiensis]			79	66
1	804	758549	757704	gil455176	glucosamine-6-phosphate deaminase protein [Escherichia coli]			79	60
1	25	31595	31894	gil1017809	similar to dihydroxydipyrroline-sensitive I-type, skeletal muscle calcium channel alpha-1 subunit (SP:CIC1_RABIT, P07293) [Caenorhabditis elegans]			78	57
1	134	134667	134323	gil159199	cecropin D [Hyalophora cecropia]			78	50
1	230	215177	216028	gnlPIDle265537	DnaJ-homologue [Thermus aquaticus thermophilus]			78	59
1	531	503406	503849	gil587583	ribosomal protein L11 [Thermus aquaticus thermophilus]			78	58
1	867	817849	819579	gil912449	Na+ -ATPase alpha subunit [Enterococcus hirae]			78	60
1	127	127383	127745	gil537364	heat shock protein 60 (GroEL) like protein [Porphyromonas gingivalis]			77	60
1	190	182991	182251	gil1235082	mevalonate pyrophosphate decarboxylase [Homo sapiens]			77	51
1	225	213158	212388	gil1651340	Phosphoglycerate mutase 1 [Escherichia coli]			77	59
1	284	272770	272165	gil1001349	ATP-dependent protease ClpP [Synechocystis sp.]			77	62
1	324	318280	314789	gil1573746	DNA polymerase III, alpha chain (dnaE) [Haemophilus influenzae]			77	58
1	555	530150	531370	gil143795	transfer RNA-Tyr synthetase [Bacillus subtilis]			77	52
1	770	722470	722892	gil1653602	hypothetical protein [Synechocystis sp.]			77	54
1	833	790115	790909	gnlPIDle248886	unknown [Mycobacterium tuberculosis]			77	56
1	52	62205	61918	gnlPIDle118966	ribosomal protein S15 [Thermus aquaticus thermophilus]			76	60
1	144	141975	141736	bbs177721	KHS toxin, killer heat sensitive toxin=KHS [Saccharomyces cerevisiae, Peptide, 708 aa] [Saccharomyces cerevisiae]			76	38
1	293	280702	280529	gil1146275	VP2 protein [Bluetongue virus 9]			76	47
1	323	314795	314199	gil1651915	hypothetical protein [Synechocystis sp.]			76	48
1	362	356749	355508	gil633147	ribose-phosphate pyrophosphokinase [Bacillus caldolyticus]			76	44

Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

1	410	403332	402922	gil606232	30S ribosomal subunit protein S11 [Escherichia coli]	76	52
1	411	403754	403341	gil1652405	30S ribosomal protein S13 [Synechocystis sp.]	76	55
1	454	431743	431003	gil1016012	neural cell adhesion protein BIG-2 precursor [Rattus norvegicus]	76	61
1	710	670457	671569	gil467376	unknown [Bacillus subtilis]	76	58
1	873	824849	826675	gil1303804	YqeQ [Bacillus subtilis]	76	52
1	942	886017	886751	gil1183839	unknown [Pseudomonas aeruginosa]	76	54
1	5	9956	8943	gil1552842	OTCase [Escherichia coli]	75	62
1	51	61909	59735	gil1184680	polynucleotide phosphorylase [Bacillus subtilis]	75	54
1	55	66283	63620	gil39954	IF2 (aa 1-741) [Bacillus stearothermophilus]	75	53
1	83	93454	94410	gnlPIDle289138	similar to flagellar hook-basal body proteins [Bacillus subtilis]	75	46
1	88	97435	98283	gil687583	RpoS [Yersinia enterocolitica]	75	47
1	245	229112	230158	gil1574806	spermidine/putrescine transport ATP-binding protein (potA) [Haemophilus influenzae]	75	55
1	264	251076	250801	gil1763634	alpha LA-voltage-dependent calcium channel [Homo sapiens]	75	60
1	297	285723	284461	gil556886	serine hydroxymethyltransferase [Bacillus subtilis]	75	58
1	375	367682	366903	gil467372	3'-exo-deoxyribonuclease [Bacillus subtilis]	75	62
1	385	378055	377114	gil45986	NAD synthetase [Rhodobacter capsulatus]	75	55
1	416	406437	405925	gil1044981	ribosomal protein S5 [Bacillus subtilis]	75	56
1	418	407390	406812	gil600032	L6 ribosomal protein [Streptomyces coelicolor]	75	53
1	424	409520	409251	gil44218	ribosomal protein S17 (AA 1-85) [Mycoplasma capricolum]	75	58
1	530	502806	503366	gil396321	nusG [Escherichia coli]	75	56
1	548	523428	522904	gil1573470	H. influenzae predicted coding region HI0491 [Haemophilus influenzae]	75	55
1	575	546579	548393	pinC30010IC30010	hypothetical ORF-6 protein - Sauroleishmania tarentolae mitochondrion (SGC6)	75	50
1	906	854433	855215	gil511148	hemolysin [Serpulina hyodysenteriae]	75	56
1	68	85054	83102	gil467458	cell division protein [Bacillus subtilis]	74	57
1	162	158608	157502	gil531460	Mbl protein [Bacillus subtilis]	74	49
1	177	172327	171950	pinA45434IA45434	ribosomal protein L19 - Bacillus stearothermophilus	74	54
1	475	443773	445203	gil396501	aspartyl-tRNA synthetase [Thermus aquaticus thermophilus]	74	52

Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

1	549	524561	523374	gil1020317	S-adenosylmethionine synthetase [Staphylococcus aureus]	74	57
1	595	565672	564347	gil460259	enolase [Bacillus subtilis]	74	58
1	720	681529	680489	gil1651962	hypothetical protein [Synecocystis sp.]	74	49
1	745	702297	701173	gil289287	UDP-glucose pyrophosphorylase [Bacillus subtilis]	74	50
1	13	20409	17551	gil1652531	excinuclease ABC subunit A [Synecocystis sp.]	73	56
1	98	103790	104947	gil514330	sensor kinase [Bacillus subtilis]	73	49
1	188	182064	181102	gil887601	Erg8p [Saccharomyces cerevisiae]	73	43
1	314	303616	302786	gil473817	'ORF' [Escherichia coli]	73	53
1	366	358916	361078	gnlPIDle2457 91	ORF YLR069c [Saccharomyces cerevisiae]	73	51
1	444	424047	423181	gil1574704	hypothetical [Haemophilus influenzae]	73	51
1	556	531372	533672	gil511145	hemolysin [Serpulina hyodysenteriae]	73	52
1	576	548257	548045	gil406135	glycoprotein 120 [Simian immunodeficiency virus]	73	53
1	598	568379	567504	gil143607	sporulation protein [Bacillus subtilis]	73	55
1	604	572375	570729	bbsl161785	60 kda antigen [Borrelia coriaceae, C053, ATCC 4338, Peptide, 514 aa] [Borrelia coriaceae]	73	53
1	674	634175	633648	gil1595810	type-I signal peptidase SpsB [Staphylococcus aureus]	73	47
1	692	654267	651727	gnlPIDle2684 56	unknown [Mycobacterium tuberculosis]	73	54
1	719	679186	680499	gil500705	Similar to Seryl-tRNA synthetase [Saccharomyces cerevisiae]	73	56
1	725	682189	682899	gnlPIDle2436 81	ORF YGR248w [Saccharomyces cerevisiae]	73	63
1	895	845455	844964	gil1652288	hypothetical protein [Synecocystis sp.]	73	50
1	16	24242	26497	gil511145	hemolysin [Serpulina hyodysenteriae]	72	53
1	99	104935	106305	gil619917	NtrC/NifA-like protein regulator [Escherichia coli]	72	54
1	133	134036	135055	gil556881	Similar to Saccharomyces cerevisiae SUA5 protein [Bacillus subtilis]	72	51
1	270	256925	260308	gil467444	transcription-repair coupling factor [Bacillus subtilis]	72	49
1	280	267529	268221	gil1573812	ribosomal protein S4 (pS4) [Haemophilus influenzae]	72	51
1	282	270922	268472	gil402504	lon protease [Bacillus brevis]	72	51
1	325	319544	318363	gil48362	haemolysin releasing protein (AA 1-548) [Vibrio cholerae]	72	41
1	328	322678	321053	gil1591801	CTP synthase [Methanococcus jannaschii]	72	42

Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

1	348	341460	341182	gil145687	pisH protein [Escherichia coli]		72	55
1	405	399941	399096	gil1045937	M. genitalium predicted coding region MG246 [Mycoplasma genitalium]		72	53
1	420	408009	407779	gil580930	S14 protein (AA 1-61) [Bacillus subtilis]		72	55
1	593	563383	563850	gil1574283	ribosomal protein L13 (rplL13) [Haemophilus influenzae]		72	54
1	682	641030	643399	gil1574437	sporulation protein (spoIIIE) [Haemophilus influenzae]		72	51
1	754	710160	710750	gil460080	D-alanine:D-alanine ligase-related protein [Enterococcus faecalis]		72	47
1	767	721422	721640	gil868029	large ribosomal subunit protein L35 [Buchnera aphidicola]		72	48
1	860	811923	810511	gil1001357	asparaginyl-tRNA synthetase [Synecocystis sp.]		72	54
1	14	22434	20407	gil1737482	UvrB [Helicobacter pylori]		71	52
1	72	87471	87674	gil1016781	beta-b protein [Barley stripe mosaic virus]		71	42
1	289	278760	278239	gil534842	ORF9 [Rhizobium meliloti]		71	43
1	307	298685	296736	gil1652099	long-chain-fatty-acid CoA ligase [Synecocystis sp.]		71	48
1	321	313551	312130	gil1732243	RecG [Treponema pallidum]		71	52
1	522	494911	496383	gil459009	similar to multifunctional aminoacyl-tRNA synthetase, especially to the prolyl-tRNA synthetase region [Caenorhabditis elegans]		71	48
1	554	528795	530156	pirIS58522IS58522	glycyl-tRNA synthetase - Thermus thermophilus		71	54
1	582	553725	552271	gil285623	pyruvate kinase [Bacillus stearothermophilus]		71	52
1	684	644626	643661	gil217121	ORF1 [Synecococcus elongatus]		71	52
1	723	681731	681561	gil44228	secretion protein SecY (AA 1-482) [Mycoplasma capricolum]		71	42
1	856	806939	807700	gil216341	ORF for methionine amino peptidase [Bacillus subtilis]		71	53
1	947	890096	890665	gil147485	queA [Escherichia coli]		71	56
1	28	38112	40613	gil1439562	Cdc28p [Schizosaccharomyces pombe]		70	53
1	36	45750	44806	gil290494	o287 [Escherichia coli]		70	32
1	84	94408	95220	gil47677	flgG protein product (AA 1-260) [Salmonella typhimurium]		70	50
1	128	127889	128569	gil1574387	H. influenzae predicted coding region HI1534 [Haemophilus influenzae]		70	58
1	468	441049	441330	gil1673757	(AE000012) Mycoplasma pneumoniae, phosphocarrier protein HP+; similar to GenBank Accession Number A49683, from M. capricolum [Mycoplasma pneumoniae]		70	41
1	532	503834	504529	spiQ06797IRL1_BACSU	50S RIBOSOMAL PROTEIN L1 (BL1).		70	48

Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

1	594	563858	564280	gil606169	30S ribosomal subunit protein S9 [Escherichia coli]	70	56
1	622	591070	591606	gil153906	CheW protein [Salmonella typhimurium]	70	48
1	703	664161	662611	gnlPIDle283919	glycerol kinase [Sulfolobus solfataricus]	70	60
1	726	682886	682659	gil836815	cdc4 gene product which is essential for initiation of DNA replication in yeast [Saccharomyces cerevisiae]	70	35
1	766	720854	721417	gil436165	Dsg [Myxococcus xanthus]	70	47
1	768	721649	722008	gnlPIDle254981	ribosomal protein L20 [Bacillus subtilis]	70	48
1	965	904395	905465	gil1100074	tryptophanyl-tRNA synthetase [Clostridium longisporum]	70	47
1	87	96986	97336	gil160092	asparagine-rich protein [Plasmodium falciparum]	69	46
1	110	112658	113602	gil1001733	ABC transporter [Synechocystis sp.]	69	46
1	181	174037	173762	pirC47154C47154	ribosomal protein S16 - Bacillus subtilis	69	52
1	233	219872	218076	gil1001493	protein-export membrane protein SecD [Synechocystis sp.]	69	47
1	234	220245	219922	gil1402532	ORF1 [Enterococcus faecalis]	69	32
1	373	366148	363977	gil1574200	hypothetical [Haemophilus influenzae]	69	48
1	419	407781	407371	gil498771	ribosomal S8 protein [Thermus aquaticus thermophilus]	69	46
1	517	489315	491207	gil151932	fructose enzyme II [Rhodobacter capsulatus]	69	42
1	600	568891	568388	gil143606	sporulation protein [Bacillus subtilis]	69	44
1	733	689098	687536	gil1303856	YqgI [Bacillus subtilis]	69	46
1	874	826778	827746	pirS08183IS08183	L-lactate dehydrogenase (EC 1.1.1.27) X - Bacillus psychrosaccharolyticus	69	50
1	894	844392	844547	gil1592324	M. jannaschii predicted coding region MJ1172 [Methanococcus jannaschii]	69	53
1	934	879725	879237	gil153566	ORF (19K protein) [Enterococcus faecalis]	69	42
1	49	57779	57976	gil809583	unknown [Saccharomyces cerevisiae]	68	36
1	107	110374	111513	gnlPIDle255943	M04B2.4 [Caenorhabditis elegans]	68	48
1	132	133978	133148	gil1001663	rare lipoprotein A [Synechocystis sp.]	68	53
1	142	141239	142642	gnlPIDle233874	hypothetical protein [Bacillus subtilis]	68	45
1	148	145381	144005	gil558574	pyrophosphate--fructose-6-phosphate 1-phosphotransferase	68	48

Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

							[Entamoeba histolytica]				
1	151	147107	147295	gil193442			beta-galactoside binding protein [Mus musculus]		68	42	
1	173	170051	169296	gil1389549			ORF3 [Bacillus subtilis]		68	50	
1	182	175384	174035	gil1653392			signal recognition particle protein [Synechocystis sp.]		68	45	
1	203	195720	195439	gil146854			galactose binding protein [Escherichia coli]		68	42	
1	243	228084	227344	gil1573101			hypothetical [Haemophilus influenzae]		68	41	
1	255	237406	235943	gil1652530			glucose 6-phosphate dehydrogenase [Synechocystis sp.]		68	47	
1	263	249185	251077	gil1573422			fructose-permease IIBC component (fruA) [Haemophilus influenzae]		68	42	
1	372	364016	363333	gil976104			MHC, class IIB gene product [Poecilia reticulata]		68	50	
1	407	401421	399874	gil150209			ORF 1 [Mycoplasma mycoides]		68	40	
1	412	405181	403862	gil699588			SecY protein [Corynebacterium glutamicum]		68	44	
1	425	409759	409508	gil1591164			ribosomal protein L29 [Methanococcus jannaschii]		68	51	
1	506	482737	482087	gil1498049			adenylate kinase [Paracoccus denitrificans]		68	37	
1	550	525298	524549	gil473817			'ORF' [Escherichia coli]		68	42	
1	697	658281	657673	gnlPIDle255117			hypothetical protein [Bacillus subtilis]		68	51	
1	717	678378	675460	gil927711			D9461.18p; CAI: 0.15 [Saccharomyces cerevisiae]		68	52	
1	730	685905	686750	gil1707057			coded for by C. elegans cDNA CEES55F; coded for by C. elegans cDNA yk84a1.3; coded for by C. elegans cDNA yk78g7.3; coded for by C. elegans cDNA yk168g9.5; coded for by C. elegans cDNA yk78g7.5; coded for by C. elegans cDNA yk84a1.5; strong s		68	52	
1	747	704201	702609	gil466482			outer surface protein F [Borrelia burgdorferi]		68	44	
1	793	744799	745815	gil1652037			hypothetical protein [Synechocystis sp.]		68	50	
1	843	796077	797807	gil1072418			glcA gene product [Staphylococcus carnosus]		68	50	
1	875	829335	827776	gil147774			ORF III [Escherichia coli]		68	47	
1	900	850141	850680	gnlPIDle290282			polypeptide deformylase [Calothrix PCC7601]		68	52	
1	15	22531	24255	gnlPIDle280490			unknown [Streptococcus pneumoniae]		67	43	
1	20	26452	29640	gil498991			ILS1 protein [Saccharomyces cerevisiae]		67	49	
1	27	35545	38139	gil1652946			DNA topoisomerase I [Synechocystis sp.]		67	47	

Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

1	111	113572	114333	gil1001529	hypothetical protein [Synecocystis sp.]	67	36
1	170	166286	165876	gil567036	CapE [Staphylococcus aureus]	67	35
1	202	195499	194651	gil1674275	(AE000056) Mycoplasma pneumoniae, hypothetical ABC transporter (yjcW) homolog; similar to Swiss-Prot Accession Number P32721, from E. coli [Mycoplasma pneumoniae]	67	41
1	206	197487	197098	gil1653841	P protein [Synecocystis sp.]	67	35
1	271	260292	261551	gil349834	acetate kinase [Methanosarcina thermophila]	67	44
1	313	302731	301643	gnlPIDle249981	phosphotransacetylase [Thermoanaerobacterium thermosaccharolyticum]	67	51
1	422	408897	408535	pirA02819IR5BS24	ribosomal protein L24 - Bacillus stearothermophilus	67	49
1	480	450326	448689	gil1574032	hypothetical [Haemophilus influenzae]	67	42
1	529	502315	502509	gil1001264	50S ribosomal protein L33 [Synecocystis sp.]	67	56
1	588	559618	561111	gil1224069	amidase [Moraxella catarrhalis]	67	51
1	683	643676	643437	gil710340	ribosomal protein S21 [Myxococcus xanthus]	67	49
1	698	658454	659500	gil460955	TagE [Vibrio cholerae]	67	38
1	700	660039	660536	gil467420	unknown [Bacillus subtilis]	67	42
1	729	684089	685888	gnlPIDle267607	alanyl-tRNA synthetase [Thermus aquaticus thermophilus]	67	51
1	835	791754	792341	gnlPIDle248763	unknown [Mycobacterium tuberculosis]	67	46
1	857	807722	809191	gil1526428	GsrA protein [Yersinia enterocolitica]	67	46
1	868	819577	820905	gil1590954	ATP synthase, subunit B [Methanococcus jannaschii]	67	53
1	74	88393	88028	gil1572979	hypothetical [Haemophilus influenzae]	66	43
1	91	99152	100252	gil561690	sialoglycoprotease [Pasteurella haemolytica]	66	44
1	123	121472	120783	gil1652843	endonuclease III [Synecocystis sp.]	66	42
1	149	146362	145379	gil1216385	orf304 gene product [Treponema pallidum]	66	43
1	185	179585	179001	gil1574811	neutrophil activating protein (napA) [Haemophilus influenzae]	66	49
1	275	265075	265584	gil401785	cytidine deaminase [Mycoplasma pirum]	66	41
1	330	324514	323696	gil1574641	ribonucleotide transport ATP-binding protein (mkl) [Haemophilus influenzae]	66	41
1	335	327265	326888	gil510670	che Y gene product [Rhodobacter sphaeroides]	66	44
1	355	349142	349603	gil499382	FliS [Bacillus subtilis]	66	28

Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

1	358	351051	350827	gil1546788	tar-1 [Trichostrongylus colubriformis]	66	55
1	404	399121	398324	gil296626	hemolysin [Serpulina hyodysenteriae]	66	53
1	491	461335	460550	gil45713	P.putida genes rpmH, rnpA, 9k, 60k, 50k, gidA, gidB, uncl and uncB [Pseudomonas putida]	66	41
1	513	486046	485159	gil153903	methytransferase (cheR; EC 2.1.1.24) [Salmonella typhimurium]	66	42
1	552	526495	527316	gil340613	A 'c' was inserted after nt 369 (=nt 10459 in genomic sequence (M10126)) to correct -1 frameshift probably due to gel compression [Leishmania tarentolae]	66	40
1	611	579933	581069	gil886130	putative pectinesterase [Medicago sativa]	66	33
1	627	595395	596288	gnlPIDle263931	OrfD [Streptococcus pneumoniae]	66	47
1	772	723788	723522	gil1762342	could accelerate degradation of certain transcripts [Bacillus subtilis]	66	47
1	816	770251	770060	gil393266	glycerol ester hydrolase [Staphylococcus aureus]	66	33
1	841	795927	795208	gil662880	novel hemolytic factor [Bacillus cereus]	66	46
1	882	835002	834262	gil862629	similar to the ATP-binding transport protein family [Buchnera aphidicola]	66	40
1	73	87915	87619	gil39656	spoVG gene product [Bacillus megaterium]	65	40
1	97	103039	102803	gil532272	phosphatidylserine decarboxylase [Bacillus subtilis]	65	39
1	106	110281	109649	gil1377852	ClpP [Yersinia enterocolitica]	65	42
1	159	156186	154372	gil1572977	penicillin-binding protein 2 (pbp2) [Haemophilus influenzae]	65	41
1	172	168084	169325	gil146238	poly(A) polymerase [Bacillus subtilis]	65	38
1	268	255918	253819	gil829194	bacterial cell wall hydrolase [Enterococcus faecalis]	65	43
1	353	348568	346553	gil1574651	DNA ligase (lig) [Haemophilus influenzae]	65	45
1	696	657577	655781	gil1651216	Pz-peptidase [Bacillus licheniformis]	65	47
1	741	695297	693456	gil1575784	DNA mismatch repair protein [Aquifex pyrophilus]	65	45
1	846	798339	798827	gil1001362	single-stranded DNA-binding protein [Synechocystis sp.]	65	45
1	932	876643	878559	gil508471	gyrase A [Helicobacter pylori]	65	40
1	936	881238	882224	gil1652260	leader peptidase I [Synechocystis sp.]	65	40
1	961	902331	901519	gil1256146	YbbQ [Bacillus subtilis]	65	48
1	963	903280	904407	gil1573307	hypothetical [Haemophilus influenzae]	65	41
1	37	47101	45683	gil556014	UDP-N-acetyl muramate-alanine ligase [Bacillus subtilis]	64	46

Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

1	61	72211	71642	gill1041785	hoptry protein [Plasmodium yoelii]	64	41
1	130	131969	129336	gill1574225	valyl-tRNA synthetase (valS) [Haemophilus influenzae]	64	43
1	156	152924	151140	gill43066	threonyl-tRNA synthetase (thrS; EC 6.1.1.3) [Escherichia coli]	64	43
1	174	170326	170033	gill1652390	acyl carrier protein [Synecocystis sp.]	64	48
1	175	171105	170545	gill1573650	lipopolysaccharide core biosynthesis protein (kdtB) [Haemophilus influenzae]	64	45
1	178	173033	172293	gill1046163	tRNA (guanine-N1)-methyltransferase [Mycoplasma genitalium]	64	47
1	180	173764	173513	gnlPIDie248893	unknown [Mycobacterium tuberculosis]	64	34
1	207	197654	197436	gill1665	ORF2136 [Marchantia polymorpha]	64	47
1	217	206795	205761	gill1652866	N-acetylmuramoyl-L-alanine amidase [Synecocystis sp.]	64	30
1	244	228146	229036	gill1046160	hypothetical protein (GB:U00021_5) [Mycoplasma genitalium]	64	33
1	246	230149	230967	gill147336	transmembrane protein [Escherichia coli]	64	36
1	267	253160	253723	gill467430	unknown [Bacillus subtilis]	64	52
1	340	333349	332783	gill145520	cheW peptide [Escherichia coli]	64	42
1	384	376509	375565	gill1653737	monophosphatase [Synecocystis sp.]	64	44
1	449	428137	426437	gill467409	DNA polymerase III subunit [Bacillus subtilis]	64	41
1	510	484558	483998	pirA00547IX YEBET	protein-glutamate methyltransferase (EC 3.1.1.61) - Salmonella typhimurium	64	45
1	603	570416	569451	gill1574678	dipeptide transport system permease protein (dppB) [Haemophilus influenzae]	64	44
1	679	637996	640224	gill1001335	soluble lytic transglycosylase [Synecocystis sp.]	64	42
1	753	709637	710194	gnlPIDie283360	unknown [Mycobacterium tuberculosis]	64	42
1	817	771784	771969	gnlPIDie250307	W04B2.3 [Caenorhabditis elegans]	64	41
1	839	793892	795211	gill1573939	hypothetical [Haemophilus influenzae]	64	38
1	861	811972	812853	gill396314	glutamate synthase [Escherichia coli]	64	38
1	870	821501	823339	gill472918	v-type Na-ATPase [Enterococcus hirae]	64	42
1	901	850668	851615	gill581088	methionyl-tRNA formyltransferase [Escherichia coli]	64	38
1	904	853492	853884	gill992960	thioredoxin [Arabidopsis thaliana]	64	41
1	24	34314	31444	gill42914	SbcC (AA 1-1048) [Escherichia coli]	63	45

Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

1	77	91198	90194	gill1652022	GTP-binding protein [Synecocystis sp.]	63	45
1	209	198041	197862	gill1665	ORF2136 [Marchantia polymorpha]	63	42
1	227	214639	213956	gill1652349	oxygen independent coprophorphyrogen III oxidase [Synecocystis sp.]	63	41
1	232	218116	217193	gill1573204	protein-export membrane protein (secF) [Haemophilus influenzae]	63	36
1	247	230965	231762	sp145169 PO TC_HAEIN	SPERMIDINE/PUTRESCINE TRANSPORT SYSTEM PERMEASE PROTEIN POTC.	63	36
1	272	262171	261614	gill1780755	DJ-1 protein [Homo sapiens]	63	46
1	290	279964	278735	gill143439	DD-carboxypeptidase [Bacillus subtilis]	63	41
1	333	326012	325818	gill293954	mating type a-1 protein [Neurospora crassa]	63	42
1	508	484000	482759	gill1041116	TRAB [Plasmodium falciparum]	63	34
1	553	527314	528801	sp15189 SY E_RHIME	GLUTAMYL-TRNA SYNTHETASE (EC 6.1.1.17) (GLUTAMATE--TRNA LIGASE) (GLURS).	63	48
1	569	542317	543747	gill1652577	carboxyl-terminal protease [Synecocystis sp.]	63	49
1	620	590442	589360	gill1098641	Bts1p [Saccharomyces cerevisiae]	63	43
1	701	660784	660623	gill1339938	EC 1.1.99.5 [Mus musculus]	63	47
1	702	662231	660735	gill763191	glycerol 3 phosphate dehydrogenase [Saccharomyces cerevisiae]	63	37
1	704	664938	664159	gill142997	glycerol uptake facilitator [Bacillus subtilis]	63	45
1	746	702035	702631	gill141497	ORF 4 (AA 1-198); 20 kD [Escherichia coli]	63	36
1	748	705645	704671	gill436158	putative integral membrane protease required for high frequency lysogenization by bacteriophage lambda [Escherichia coli]	63	33
1	749	706431	705643	gill507734	HflK [Vibrio parahaemolyticus]	63	28
1	756	715040	713019	gill407881	stringent response-like protein [Streptococcus equisimilis]	63	40
1	825	780572	783289	gill746399	transcription elongation factor [Escherichia coli]	63	43
1	853	803786	804832	gill155055	basic membrane protein precursor [Treponema pallidum]	63	36
1	4	8945	7467	gill1573583	H. influenzae predicted coding region HI0594 [Haemophilus influenzae]	62	38
1	42	50587	51786	gill1573978	pantothenate metabolism flavoprotein (dfp) [Haemophilus influenzae]	62	41
1	57	67740	66271	gill49316	ORF2 gene product [Bacillus subtilis]	62	36
1	64	78979	79767	gill1001473	hypothetical protein [Synecocystis sp.]	62	48
1	80	92123	91806	gill1573583	50S ribosomal protein L21 [Odontella sinensis]	62	34

Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

1	101	107458	106793	gil1652679	hypothetical protein [Synecocystis sp.]	62	34
1	102	107464	107883	gil15893	predicted 12.5Kd protein [Mycobacteriophage L5]	62	44
1	226	213238	213969	gil1001678	ribose 5-phosphate isomerase [Synecocystis sp.]	62	39
1	266	251889	253175	gil529118	similar to APE1/LAP4, vacuolar aminopeptidase [Saccharomyces cerevisiae]	62	42
1	299	288749	287274	gil289284	cysteinyl-tRNA synthetase [Bacillus subtilis]	62	46
1	357	349982	352714	gil1633576	similar to proofreading 3'-5' exonuclease and polymerase [Treponema pallidum]	62	41
1	443	423190	422495	gil1312380	putative orfW gene product [Clostridium acetobutylicum]	62	32
1	489	458740	459582	gil40031	spoOJ93 gene product [Bacillus subtilis]	62	36
1	511	485147	484494	gil145524	cheB peptide [Escherichia coli]	62	28
1	518	491201	492322	gil146722	phosphomannose isomerase [Escherichia coli]	62	45
1	685	646727	644598	gil1574144	single-stranded-DNA-specific exonuclease (recI) [Haemophilus influenzae]	62	40
1	695	655800	655063	gil1477770	unknown [Helicobacter pylori]	62	37
1	758	715668	714979	gil1574130	protoporphyrinogen oxidase (hemK) [Haemophilus influenzae]	62	36
1	762	718374	719198	gil1652444	hypothetical protein [Synecocystis sp.]	62	40
1	837	792941	793891	gil1652668	phosphatidate cytidyltransferase [Synecocystis sp.]	62	41
1	917	862498	862737	gil440851	collagenase [Clostridium perfringens]	62	29
1	46	55889	54726	gil498141	tRNA guanine transglycosylase [Zymomonas mobilis]	61	35
1	81	92710	92174	gil726305	adenine phosphoribosyltransferase form 1 [Triticum aestivum]	61	45
1	100	106820	106557	gil460955	TagE [Vibrio cholerae]	61	45
1	109	111699	112664	gil1001126	hypothetical protein [Synecocystis sp.]	61	48
1	157	154445	153051	gil143657	endospore forming protein [Bacillus subtilis]	61	40
1	193	185315	184227	gil148409	gene not found in Erwinia uredovora crt gene cluster; ORF6 [Erwinia herbicola]	61	42
1	223	209790	210668	spIP37214IER	GTP-BINDING PROTEIN ERA HOMOLOG.	61	37
1	273	262392	264062	gil438455	possible N-terminal signal sequence; mature protein may be membrane-anchored and start at Cys-17. 17.5% identity over 354-aa overlap with Candida pelliculosa beta-glucosidase; putative [Bacillus subtilis]	61	37
1	277	265982	265581	gil1513240	ORFveg110 [Dictyostelium discoideum]	61	29

Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

1	301	291935	289686	gil1354776	MCP-1 [Treponema pallidum]	61	43
1	322	314201	313338	gil1732243	RecG [Treponema pallidum]	61	37
1	380	371430	372392	gil973332	OrfC [Bacillus subtilis]	61	38
1	408	401874	401479	gil147716	ribosomal protein L17 [Escherichia coli]	61	44
1	413	404277	404444	gil1185286	ORF [Sulfolobus shibatae]	61	47
1	415	405927	405616	pirA02827IR	ribosomal protein L30 - Bacillus stearothermophilus	61	31
			5BS3F				
1	417	406848	406435	pirB29102IR	ribosomal protein L18 - Bacillus stearothermophilus	61	44
			5BS8F				
1	441	421784	421224	gil153045	prolipoprotein signal peptidase [Staphylococcus aureus]	61	29
1	467	440722	441042	gil173128	ubiquitin-specific processing protease [Saccharomyces cerevisiae]	61	32
1	613	582695	581547	gil1303756	YqjP [Bacillus subtilis]	61	38
1	615	584397	585476	gil1551522	TpN38(b) [Treponema pallidum]	61	26
1	673	632123	633622	gil143999	dnaK homologue [Borrelia burgdorferi]	61	41
1	675	634207	635469	gil1653709	lipoprotein NlpD [Synecocystis sp.]	61	50
1	743	699438	698647	gil1303863	YqjP [Bacillus subtilis]	61	45
1	897	847575	846688	gil1573586	hydrolase (GB:Z33006_1) [Haemophilus influenzae]	61	43
1	938	882836	883282	gil1303831	YqfM [Bacillus subtilis]	61	36
1	7	10415	10627	gnlPIDle2119	T24A11.1 [Caenorhabditis elegans]	60	45
			90				
1	23	31428	30475	gil1303865	YqjR [Bacillus subtilis]	60	45
1	35	44812	44267	gil1591369	cytidylate kinase [Methanococcus jannaschii]	60	49
1	198	192994	192053	gil1045801	hypothetical protein (SP:P32720) [Mycoplasma genitalium]	60	33
1	347	341167	339440	gil602680	phosphocarrier protein (enzyme I) [Mycoplasma capricolum]	60	37
1	369	361817	362233	gil1372995	OrfH [Borrelia burgdorferi]	60	37
1	409	402924	401872	gil142463	RNA polymerase alpha-core-subunit [Bacillus subtilis]	60	40
1	438	420142	418793	gnlPIDle2768	UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus subtilis]	60	40
			30				
1	566	540696	539698	gil1573923	prolipoprotein diacylglycerol transferase (lgt) [Haemophilus influenzae]	60	57
1	587	559368	559655	gil1335805	CD45 homolog [Heterodontus francisci]	60	26
1	589	561098	562558	gil1653395	PET112 [Synecocystis sp.]	60	37

Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

1	736	690957	690076	gil1001260	hypothetical protein [Synecocystis sp.]	60	47
1	738	691078	691659	gil1399829	elongation factor P [Synecococcus PCC7942]	60	34
1	750	707879	706626	gil1573060	hypothetical [Haemophilus influenzae]	60	33
1	784	734589	735635	gil1164996	mxuC gene product [Methylobacterium extorquens]	60	26
1	829	785899	786567	gil1046033	cytidylate kinase [Mycoplasma genitalium]	60	38
1	862	812835	813773	gil1574569	hypothetical [Haemophilus influenzae]	60	36
1	863	813727	816105	gnlPIDle2550 93	hypothetical protein [Bacillus subtilis]	60	38
1	878	831250	829943	gil1742766	NifS protein. [Escherichia coli]	60	34
1	929	872578	874110	gil1002666	unknown [Schistosoma mansoni]	60	30
1	937	882211	882861	gil1595810	type-I signal peptidase SpsB [Staphylococcus aureus]	60	40
1	54	63629	63234	gil580902	ORF6 gene product [Bacillus subtilis]	59	38
1	96	102744	103802	gil467409	DNA polymerase III subunit [Bacillus subtilis]	59	40
1	120	118925	119914	gil1574678	dipeptide transport system permease protein (dppB) [Haemophilus influenzae]	59	33
1	140	139567	141174	gil42377	phosphoglucose isomerase (AA 1-549) [Escherichia coli]	59	42
1	195	186577	187659	gil1573129	hypothetical [Haemophilus influenzae]	59	41
1	259	242174	245713	gil1574781	exodeoxyribonuclease V (recB) [Haemophilus influenzae]	59	38
1	288	278281	276257	pinD64084ID 64084	rep helicase, single-stranded DNA-dependent ATPase (rep) homolog - Haemophilus influenzae (strain Rd KW20)	59	36
1	291	280005	281525	gil882504	ORF_f560 [Escherichia coli]	59	34
1	306	294923	296707	gil487937	Similar to arginyl-tRNA synthetase (E. coli) [Saccharomyces cerevisiae]	59	35
1	332	325664	324564	gil466753	alternate gene name yibD [Escherichia coli]	59	39
1	414	405646	405179	gil216338	ORF for L15 ribosomal protein [Bacillus subtilis]	59	40
1	465	439470	440759	gil39269	sigma factor (ntrA) (AA 1-502) [Azotobacter vinelandii]	59	35
1	492	462064	461411	pinA30191A 30191	hypothetical protein L - Bacillus subtilis (fragment)	59	39
1	495	462955	463752	gil467425	unknown [Bacillus subtilis]	59	38
1	503	480078	481016	gil1651878	regulatory components of sensory transduction system [Synecocystis sp.]	59	38
1	523	497621	496395	gil143002	proton glutamate symport protein [Bacillus caldotenax]	59	34

Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

1	941	885060	886019	gil1685110	tetrahydrofolate dehydrogenase/cyclohydrolase [Streptococcus thermophilus]	59	36
1	40	50348	48951	gil1574003	pantothenate permease (panF) [Haemophilus influenzae]	58	38
1	76	90160	89534	gil1303791	YqeJ [Bacillus subtilis]	58	32
1	116	115845	115654	gnlPIDle2758 92	T06E6.f [Caenorhabditis elegans]	58	37
1	179	173515	173009	gil1573163	hypothetical [Haemophilus influenzae]	58	37
1	197	191904	189634	gil1066850	putative [Rhodobacter capsulatus]	58	37
1	229	215111	214563	gil1573441	oxygen-independent coproporphyrinogen III oxidase (hemN) [Haemophilus influenzae]	58	34
1	257	238952	241873	gil1041785	rhostry protein [Plasmodium yoelii]	58	30
1	440	421010	420792	gil1674178	(AE000047) Mycoplasma pneumoniae, MG246 homolog, from M. genitalium [Mycoplasma pneumoniae]	58	37
1	557	533653	534750	gil974332	NAD(P)H-dependent dihydroxyacetone-phosphate reductase [Bacillus subtilis]	58	41
1	586	557259	559370	gil153062	helicase [Staphylococcus aureus]	58	41
1	623	591542	592435	gil1633618	hypothetical protein [Synechocystis sp.]	58	35
1	728	683208	684104	gil790935	flitG [Treponema denticola]	58	31
1	796	750629	749508	gil1574412	alanine racemase, biosynthetic (alr) [Haemophilus influenzae]	58	29
1	823	778475	778723	gil1209836	minus strand repeat motif-containing gene [Borrelia burgdorferi]	58	22
1	830	786540	788225	gil1574150	ribosomal protein S1 (rpS1) [Haemophilus influenzae]	58	34
1	842	796255	796019	gnlPIDle2434 74	ORF YGR089w [Saccharomyces cerevisiae]	58	35
1	883	834332	834520	gil1575792	low Mr GTP-binding protein Rab32 [Homo sapiens]	58	43
1	905	853953	854435	gil1303823	YqfG [Bacillus subtilis]	58	34
1	919	863594	862875	gil1256625	putative [Bacillus subtilis]	58	34
1	921	865297	864725	gil1054584	putative protein highly homologous to E. coli RNase HII [Magnetospirillum sp.]	58	42
1	196	189636	187702	gil496484	tlpC gene product [Bacillus subtilis]	57	32
1	262	249142	248192	gil46605	lacC polypeptide (AA 1-310) [Staphylococcus aureus]	57	41
1	311	300776	301660	gil467431	high level kasamycin resistance [Bacillus subtilis]	57	35
1	365	358725	358495	gil396943	early protein [Human papillomavirus type 19]	57	38
1	386	378249	378025	gil45986	NAD synthetase [Rhodobacter capsulatus]	57	32

Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

1	399	394690	394247	gil1592085	M. jannaschii predicted coding region MJ1437 [Methanococcus jannaschii]	57	31
1	402	397512	396193	gil1732241	GTP-binding protein [Treponema pallidum]	57	36
1	533	504504	505022	gil786163	Ribosomal Protein L10 [Bacillus subtilis]	57	29
1	735	689992	689096	gil1303855	YqgH [Bacillus subtilis]	57	30
1	794	745857	747644	gil11665	ORF2136 [Marchantia polymorpha]	57	33
1	814	768735	771866	gil1573914	acriflavine resistance protein (acrB) [Haemophilus influenzae]	57	31
1	821	776835	778244	gil1591660	histidyl-tRNA synthetase [Methanococcus jannaschii]	57	36
1	834	790907	791752	gil1518661	elongation factor Ts [Chlamydia trachomatis]	57	36
1	836	792328	793038	gil1573941	hypothetical [Haemophilus influenzae]	57	36
1	848	799086	799670	gil1537044	50S ribosomal subunit protein L9 [Escherichia coli]	57	39
1	849	799668	801041	gil1001271	replicative DNA helicase [Synechocystis sp.]	57	33
1	851	802510	803742	pinA640921A 64092	acetyl coenzyme A acetyltransferase (thiolase) (fadA) homolog - Haemophilus influenzae (strain Rd KW20)	57	43
1	855	805240	806952	gil1499620	M. jannaschii predicted coding region MJ0798 [Methanococcus jannaschii]	57	36
1	922	865347	867809	gil1237015	ORF4 [Bacillus subtilis]	57	38
1	12	17611	14156	pirB305651B 30565	phospholipase C (EC 3.1.4.3) precursor - Clostridium bifermentans	56	28
1	26	35530	34277	gil1657594	exonuclease SbcD [Escherichia coli]	56	39
1	59	68915	68271	gil148876	probable com101A gene [Haemophilus influenzae]	56	26
1	79	91821	91480	gil1139633	large tegument protein [Human herpesvirus 7]	56	30
1	112	113768	113571	gnlPIDie2469 33	ORF YPL216w [Saccharomyces cerevisiae]	56	35
1	147	142606	143988	gil642030	NADH oxidase [Serpulina hyodysenteriae]	56	36
1	153	148561	149100	gil1499018	M. jannaschii predicted coding region MJ0240 [Methanococcus jannaschii]	56	29
1	169	165431	164388	gil1573431	aminodeoxychorismate lyase (pabC) [Haemophilus influenzae]	56	41
1	183	176655	175432	gil143841	xylose repressor [Bacillus subtilis]	56	38
1	312	301170	300922	gnlPIDie2202 40	red algal chloroplast [Plasmodium falciparum]	56	36
1	317	308362	306992	gil1574691	UDP-N-acetylmuramoylalanine-D-glutamate ligase (murD) [Haemophilus influenzae]	56	40

Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

1	448	426477	426133	gil467410	unknown [Bacillus subtilis]	56	28
1	456	432628	434457	gil142521	deoxyribodipyrimidine photolyase [Bacillus subtilis]	56	34
1	460	438178	437312	gil882453	ORF_286; alternate name yggB; orf4 of X14436 [Escherichia coli]	56	31
1	469	441309	443438	gil148316	NaH-antiporter protein [Enterococcus hirae]	56	32
1	608	574772	574951	gil1019630	NADH dehydrogenase subunit 2 [Paramecium aurelia]	56	37
1	699	659498	660055	gil1372995	OrfH [Borrelia burgdorferi]	56	24
1	757	713509	713712	gil861327	F31D5.5 gene product [Caenorhabditis elegans]	56	40
1	791	741305	742837	gil1651873	4-alpha-glucanotransferase [Synecocystis sp.]	56	43
1	822	779478	778291	gil1500309	M. jannaschii predicted coding region MJ1428 [Methanococcus jannaschii]	56	28
1	967	907556	908932	gil1749528	similar to Saccharomyces cerevisiae probable UTP-glucose-1-phosphate uridylyltransferase, SWISS-PROT Accession Number P32861 [Schizosaccharomyces pombe]	56	37
1	39	48953	48048	gil1045895	hypothetical protein (SP:P23851) [Mycoplasma genitalium]	55	41
1	131	132989	131967	gil1574007	nitrogen fixation nifR3 protein (nifR3) (PIR:S49971) [Haemophilus influenzae]	55	39
1	152	148506	147148	gil1653100	Na+ -ATPase subunit J [Synecocystis sp.]	55	31
1	359	352690	353313	gil1213334	OrfX; hypothetical 22.5 KD protein downstream of type IV prepilin leader peptidase gene; Method: conceptual translation supplied by author [Vibrio vulnificus]	55	33
1	361	355510	354140	gil882698	L-fuculose kinase [Escherichia coli]	55	44
1	515	488398	487652	gil397486	endonuclease G [Bos taurus]	55	33
1	551	526427	525285	gil558266	orf gene product [Wolinnella succinogenes]	55	30
1	570	543745	544482	gil1303811	YqeU [Bacillus subtilis]	55	33
1	579	551201	551494	gil290487	50S ribosomal subunit protein L28 [Escherichia coli]	55	37
1	584	555359	556063	gil1592301	M. jannaschii predicted coding region MJ0687 [Methanococcus jannaschii]	55	32
1	706	665310	665936	gil403984	deoxyguanosine kinase/deoxyadenosine kinase(I) subunit [Lactobacillus acidophilus]	55	38
1	771	722876	723538	gil1736440	O-sialoglycoprotein endopeptidase (EC 3.4.24.57) (Glycoprotease). [Escherichia coli]	55	39
1	786	736537	737187	gil1589778	SPINDLY [Arabidopsis thaliana]	55	34

Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

1	810	765243	766130	gil984805	glycine betaine-binding protein precursor [Bacillus subtilis]	55	35
1	871	823341	823790	gil1590959	ATP synthase, subunit K [Methanococcus jannaschii]	55	34
1	898	847660	849462	gil1517942	aminopeptidase P [Sus scrofa]	55	46
1	924	867811	868236	gil1142660	POM1 [Plasmodium chabaudi chabaudi]	55	41
1	927	870905	870039	gil534839	CheR [Rhizobium meliloti]	55	32
1	964	904091	903900	gil312694	ARS-binding factor 1 [Kluyveromyces marxianus]	55	50
1	33	44068	43124	gil146860	delta-2-isopentenyl pyrophosphate transferase [Escherichia coli]	54	31
1	63	79094	74679	gil415736	Orf635 gene product [Euglena gracilis]	54	37
1	192	184282	182969	gil151259	HMG-CoA reductase (EC 1.1.1.88) [Pseudomonas mevalonii]	54	35
1	200	194105	192951	gil1045800	ribose transport system permease protein [Mycoplasma genitalium]	54	29
1	224	210749	212320	gil1591243	M. jannaschii predicted coding region MJ0539 [Methanococcus jannaschii]	54	45
1	256	237491	238954	gnlPIDle245024	unknown [Mycobacterium tuberculosis]	54	34
1	260	245698	247542	gil1574782	exodeoxyribonuclease V (recD) [Haemophilus influenzae]	54	36
1	320	311333	312133	gil1209528	D,D-carboxypeptidase [Enterococcus faecalis]	54	40
1	610	577096	579909	gil1499043	M. jannaschii predicted coding region MJ0263 [Methanococcus jannaschii]	54	30
1	765	720685	719999	gil290216	[bride of sevenless] gene product [Drosophila virilis]	54	25
1	789	739607	739996	gil473804	'dosage-dependent dnaK suppressor protein' [Escherichia coli]	54	35
1	845	797932	798366	gil1045767	ribosomal protein S6 [Mycoplasma genitalium]	54	35
1	951	894898	893912	gil1303842	YqfU [Bacillus subtilis]	54	28
1	86	96019	97032	gil405550	flagellar P-ring protein [Pseudomonas putida]	53	40
1	89	98331	99215	gil12478	No definition line found [Escherichia coli]	53	35
1	164	159533	158562	gil1499620	M. jannaschii predicted coding region MJ0798 [Methanococcus jannaschii]	53	39
1	250	234276	232861	gil1303989	YqkI [Bacillus subtilis]	53	28
1	278	266053	267426	gil1749686	similar to Saccharomyces cerevisiae unknown, EMBL Accession Number Z68194 [Schizosaccharomyces pombe]	53	28
1	302	292150	294309	gil1015945	methyl accepting chemotaxis homolog [Treponema denticola]	53	31
1	364	358298	357702	gil1499620	M. jannaschii predicted coding region MJ0798 [Methanococcus jannaschii]	53	41

Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

1	514	486253	486888	gil940842	orf 06111 gene product [Saccharomyces cerevisiae]	53	28
1	567	541832	540684	gil1165254	YlxH [Borrelia burgdorferi]	53	33
1	621	590418	591032	gil1592021	cell division protein J [Methanococcus jannaschii]	53	32
1	805	759748	758537	gil1732203	GlcNAc 6-P deacetylase [Vibrio furnissii]	53	35
1	854	804825	805298	gil1303915	YqhZ [Bacillus subtilis]	53	30
1	884	835705	834944	gil1574399	H. influenzae predicted coding region HI1555 [Haemophilus influenzae]	53	26
1	48	58236	56944	gil1652686	hypothetical protein [Synechocystis sp.]	52	26
1	53	63264	62383	gil42219	P35 gene product (AA 1 - 314) [Escherichia coli]	52	34
1	56	66168	65665	gil1151158	repeat organellar protein [Plasmodium chabaudi]	52	37
1	95	102255	102746	gil1574136	colicin V production protein (pur regulon) (cvpA) [Haemophilus influenzae]	52	24
1	117	115800	116879	gil288998	secA gene product [Antithamnion sp.]	52	34
1	220	208898	208446	gil1652602	hypothetical protein [Synechocystis sp.]	52	25
1	285	274152	272764	gnlPIDle2551	trigger factor [Bacillus subtilis]	52	28
1	352	344946	346532	gil160299	glutamic acid-rich protein [Plasmodium falciparum]	52	26
1	368	361087	361800	gil216861	24K membrane protein [Pseudomonas aeruginosa]	52	32
1	376	368462	367695	gil147213	phnP protein [Escherichia coli]	52	47
1	381	373209	372412	gil467459	unknown [Bacillus subtilis]	52	28
1	437	418141	416768	gil1591425	hypothetical protein (GP:X91006_2) [Methanococcus jannaschii]	52	27
1	439	420801	420166	gil1674178	(AE000047) Mycoplasma pneumoniae, MG246 homolog, from M. genitalium [Mycoplasma pneumoniae]	52	40
1	474	443436	443798	gil1573287	aspartyl-tRNA synthetase (aspS) [Haemophilus influenzae]	52	35
1	583	555235	553802	gil496254	fibronectin/fibrinogen-binding protein [Streptococcus pyogenes]	52	29
1	759	715852	715610	gil397703	dihydroorotate dehydrogenase [Plasmodium falciparum]	52	30
1	797	751384	750674	gil1063419	S2 gene product [Borrelia burgdorferi]	52	27
1	820	776768	774852	gil580936	SpoVD [Bacillus subtilis]	52	33
1	869	820887	821516	gil1592298	ATP synthase, subunit D [Methanococcus jannaschii]	52	29
1	888	839581	838106	gil1151158	repeat organellar protein [Plasmodium chabaudi]	52	30
1	916	862856	862110	gil1256625	putative [Bacillus subtilis]	52	25
1	67	83112	81610	gil587604	beta subunit RNA polymerase [Plasmodium falciparum]	51	29

Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

1	150	147190	146360	gil520844	orf4 [Bacillus subtilis]	51	26
1	194	186516	185275	gil211931	3-hydroxy-3-methylglutaryl-CoA synthase [Gallus gallus]	51	29
1	300	288759	289676	gil142833	ORF2 [Bacillus subtilis]	51	33
1	371	362209	362874	gil169880	protein antigen LmST11 [Leishmania major]	51	27
1	464	438943	439497	gil1591434	chromate resistance protein A [Methanococcus jannaschii]	51	29
1	819	772935	774842	gnlPIDle2390	AMP-binding protein [Brassica napus]	51	29
			57				
1	926	869257	869955	gil633996	a negative regulator of pho regulon [Pseudomonas aeruginosa]	51	26
1	45	54760	54062	gil505363	ORF2 [Salmonella typhimurium]	50	32
1	94	101155	102261	gil39995	phospho-N-acetyl-muramoyl-pentapeptide- transferase [Bacillus subtilis]	50	29
1	118	118397	117096	gil1762996	RING-finger protein [Helicoverpa armigera nucleopolyhedrovirus]	50	25
1	155	151159	150506	gil893358	PgsA [Bacillus subtilis]	50	35
1	239	224187	224744	gil1303843	YqfV [Bacillus subtilis]	50	29
1	274	265044	264040	gnlPIDle2767	unknown [Mycobacterium tuberculosis]	50	32
			78				
1	287	276164	274710	gil147140	peptidase D [Escherichia coli]	50	28
1	310	299525	300778	gil1652202	ComE [Synechocystis sp.]	50	33
1	349	342477	341581	gnlPIDle2202	frameshift [Plasmodium falciparum]	50	30
			45				
1	457	435120	434509	gil144839	beta-galactosidase [Thermoanaerobacterium thermosulfurigenes]	50	29
1	479	448691	447948	gil580905	B.subtilis genes rpmH, rnpA, 50kd, gidA and gidB [Bacillus subtilis]	50	32
1	680	640194	641039	gil882579	CG Site No. 29739 [Escherichia coli]	50	31
1	737	690152	690400	gil1086864	T03G11.2 gene product [Caenorhabditis elegans]	50	39
1	752	708130	709662	gil40162	murE gene product [Bacillus subtilis]	50	30
1	360	353288	354157	gil343314	involutin [Saguinus oedipus]	49	20
1	44	54046	53216	gil505363	ORF2 [Salmonella typhimurium]	48	21
1	122	119896	120774	gil405908	yejE [Escherichia coli]	48	29
1	161	157504	156653	gil143213	putative [Bacillus subtilis]	48	23
1	316	305940	306995	gil1762962	FemA [Staphylococcus simulans]	48	28
1	459	436152	437315	gil1001478	hypothetical protein [Synechocystis sp.]	48	25

Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

1	628	596267	596566	gll156218	putative [Caenorhabditis elegans]		48	32
1	694	655069	654452	gll1574476	dedA protein (dedA) [Haemophilus influenzae]		48	22
1	731	686392	686129	gll15207	gastric mucin [Sus scrofa]		48	27
1	893	844951	843476	gll152202	frameshift [Plasmodium falciparum]		48	32
			45					
1	62	74673	72196	gll1766042	outer membrane protein [Neisseria gonorrhoeae]		47	30
1	103	107896	108780	gll1256885	P24A protein (unknown function) (Swiss Prot. accession number P32802) [Saccharomyces cerevisiae]		47	27
1	187	181111	180215	gll1184118	mevalonate kinase [Methanobacterium thermoautotrophicum]		47	30
1	204	195930	196616	gll1573552	phosphoglycolate phosphatase, chromosomal (SP:P40852) [Haemophilus influenzae]		47	21
1	265	251835	251098	gll1209847	repeat motif-containing gene [Borrelia burgdorferi]		47	30
1	334	325837	326529	gll1591893	undylate kinase [Methanococcus jannaschii]		47	26
1	356	349581	349991	gll1849173	Probable essential component of the nucleoskeleton (Swiss Prot. accession number P32380) [Saccharomyces cerevisiae]		47	27
1	490	460559	459834	gll1592264	type I restriction enzyme [Methanococcus jannaschii]		47	34
1	526	499992	499264	gll1710551	ankyrin 3 [Mus musculus]		47	29
1	577	549541	548390	gll152202	frameshift [Plasmodium falciparum]		47	27
			45					
1	744	701189	699441	gll1521604	orfA gene product [Borrelia burgdorferi]		47	23
			36					
1	755	713050	710765	pir1541649IS41649	DNA polymerase - Plasmodium falciparum		47	22
1	761	717229	718392	gll1500309	M. jannaschii predicted coding region MJ1428 [Methanococcus jannaschii]		47	37
1	813	767745	768737	pir1541649IS41649	membrane fusion protein (mirC) homolog - Haemophilus influenzae (strain Rd KW20)		47	23
1	824	779587	780546	gll1687844	contains TPR domain-like repeats [Caenorhabditis elegans]		47	28
1	881	834283	833015	gll1574393	H. influenzae predicted coding region HI1548 [Haemophilus influenzae]		47	24
1	886	837236	836199	gll1887563	serine/threonine-protein kinase [Plasmodium falciparum]		47	30
1	47	57001	55880	gll1652686	hypothetical protein [Synchocystis sp.]		46	23
1	160	156659	156171	gll13261	ORF4 protein (AA 1-156) [Paramecium aurelia]		46	30

Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

1	249	231765	232829	gil1142681	Lpp38 [Pasteurella haemolytica]	46	28
1	329	323695	322838	gil562039	NADH dehydrogenase, subunit 2 [Acanthamoeba castellanii]	46	20
1	336	329090	327303	gil457146	rhoxy protein [Plasmodium yoelii]	46	18
1	442	422511	421747	gil1591598	hypothetical protein (GP:U19364_6) [Methanococcus jannaschii]	46	27
1	452	428632	429375	pirS41649IS41649	DNA polymerase - Plasmodium falciparum	46	21
1	573	545081	545596	gil1022328	Four tandem repeats of a DNA-binding domain known as the AT-hook are found at the carboxy terminus of Card. This protein has been purified and found to bind in vitro to a promoter region [Myxococcus xanthus]	46	28
1	617	586903	587865	gnlPIDie33329	ND5 protein [Ascaris suum]	46	29
1	708	668290	666710	gil1573271	apolipoprotein N-acyltransferase (cute) [Haemophilus influenzae]	46	32
1	790	741189	740008	gil458015	TpN50 precursor [Treponema pallidum]	46	29
1	892	843474	841147	gil1574537	outer membrane integrity protein (tolA) [Haemophilus influenzae]	46	19
1	903	853463	852741	gil806562	nebulin [Homo sapiens]	46	26
1	968	908917	909948	gil438455	possible N-terminal signal sequence; mature protein may be membrane-anchored and start at Cys-17. 17.5% identity over 354-aa overlap with Candida pelliculosa beta-glucosidase.; putative [Bacillus subtilis]	46	29
1	208	197467	198516	gil220578	open reading frame [Mus musculus]	45	27
1	462	438197	438949	gil687689	similar to a chromate resistance protein (ChrA) from A. eutrophus, Swiss-Prot Accession Number P17551 [Synechococcus sp.]	45	23
1	742	698657	695295	gil1499043	M. jannaschii predicted coding region MJ0263 [Methanococcus jannaschii]	45	23
1	90	99196	98756	gil303895	ORF 8: This ORF is required for the secretion of IpaB, IpaC and IpaD [Plasmid pMYSH6000]	44	26
1	253	235698	234343	gil143245	Na+/H+ antiporter [Bacillus firmus]	44	26
1	709	668406	670430	gnlPIDie236483	F54G8.4 [Caenorhabditis elegans]	44	31
1	850	802490	801045	gnlPIDie220245	frameshift [Plasmodium falciparum]	44	25
1	458	436119	435118	gil1303799	YqeN [Bacillus subtilis]	43	19

Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

1	859	810560	809967	pirS17998[S17998]	gene COX1 intron 4 protein - yeast (Kluyveromyces marxianus var. lactis) mitochondrion (SGC2)	43	30
1	935	881179	879701	gil1045905	no score generated - score shown is bogus [Mycoplasma genitalium]	43	27
1	319	311250	309877	gil1591425	hypothetical protein (GP:X91006_2) [Methanococcus jannaschii]	42	19
1	618	587863	588672	gil1045801	hypothetical protein (SP:P32720) [Mycoplasma genitalium]	42	24
1	625	593472	594572	gil343962	VAR1 protein [Candida glabrata]	42	25
1	93	100191	101021	gil413976	ipa-52r gene product [Bacillus subtilis]	41	26
1	574	545523	546581	gnlPIDle16326	MURF2 protein (AA 1-348) [Crithidia fasciculata]	41	26
1	740	693458	692403	gil1151158	repeat organellar protein [Plasmodium chabaudi]	41	20
1	3	5792	6796	gil1256888	Similar to chromosome segregation protein Smc1p of S. cerevisiae (GenBank accession number L00602), chromosome segregation protein Cut3p of S. pombe (Swiss Prot. accession number P41004), and C. elegans hypothetical proteins R13G10.1 (GenBank)	40	24
1	228	214440	214742	gil1150836	neural specific DNA binding protein [Xenopus laevis]	40	28
1	318	309735	308377	gil1591425	hypothetical protein (GP:X91006_2) [Methanococcus jannaschii]	40	19
1	453	431037	429700	gil499647	[Mus musculus (strain C3HF/RL) ORF mRNA, complete cds.], gene product [Mus musculus]	40	24
1	795	747813	749516	gil304179	wall-associated protein [Bacillus subtilis]	40	35
1	966	907336	905528	gil1151158	repeat organellar protein [Plasmodium chabaudi]	40	26

TABLE 2. Borrelia burgdorferi - Coding regions containing known proteins

Contig ID	Orf ID	Start (nt)	Stop (nt)	match accession	match gene name	percent ident	HSP nt length
1	69	86349	85018	gbIL32144	Borrelia burgdorferi peptidyl-tRNA hydrolase-like protein (pth) gene homologue, complete cds	100	220
1	70	86918	86340	gbIL32144	Borrelia burgdorferi peptidyl-tRNA hydrolase-like protein (pth) gene homologue, complete cds	100	579
1	71	87573	86911	gbIL32144	Borrelia burgdorferi peptidyl-tRNA hydrolase-like protein (pth) gene homologue, complete cds	100	129
1	124	123885	121759	gbIM60802	B.burgdorferi immunogen gene, 5' flank	99	2127
1	126	127421	125700	embX919651 BBATPBP	B.burgdorferi abp gene	97	284
1	137	136332	139151	gbIL31424	Borrelia burgdorferi (clone BbK3.11) phoA fusion protein gene, partial cds	98	248
1	138	138676	138515	gbIL31424	Borrelia burgdorferi (clone BbK3.11) phoA fusion protein gene, partial cds	96	60
1	165	160705	159932	gbIU17591	Borrelia burgdorferi primary sigma factor (rpoD) gene, complete cds	100	774
1	166	162604	160703	gbIU17591	Borrelia burgdorferi primary sigma factor (rpoD) gene, complete cds	100	1902
1	167	162835	162602	gbIU17591	Borrelia burgdorferi primary sigma factor (rpoD) gene, complete cds	99	232
1	168	164397	162811	gbIU17591	Borrelia burgdorferi primary sigma factor (rpoD) gene, complete cds	99	1216
1	210	198495	199028	gbIU61498	Borrelia burgdorferi CheA (cheA) gene, partial cds, CheW (cheW), CheX (cheX) and CheY (cheY) genes, complete cds	98	127
1	211	199527	199069	gbIU61498	Borrelia burgdorferi CheA (cheA) gene, partial cds, CheW (cheW), CheX (cheX) and CheY (cheY) genes, complete cds	99	459
1	212	200067	199549	gbIU61498	Borrelia burgdorferi CheA (cheA) gene, partial cds, CheW (cheW), CheX (cheX) and CheY (cheY) genes, complete cds	99	519
1	213	201455	200046	gbIU61498	Borrelia burgdorferi CheA (cheA) gene, partial	99	1410

TABLE 2. *Borrelia burgdorferi* - Coding regions containing known proteins

1	214	204053	201453	gblU28962l	cds, CheW (cheW), CheX (cheX) and CheY (cheY) genes, complete cds	99	2601
1	215	205173	204115	gblU62900l	<i>Borrelia burgdorferi</i> histidine kinase (cheA) gene, complete cds	98	1059
1	216	205780	205220	gblU62900l	<i>Borrelia burgdorferi</i> flagellar filament outsheath protein (flaA) gene, complete cds, and chemotaxis histidine kinase (cheA) gene, partial cds	98	277
1	235	220591	220232	embX65139l BBHSP60	<i>B. burgdorferi</i> hsp60 gene for 60kDa heat shock protein	98	139
1	236	222288	220594	embX65139l BBHSP60	<i>B. burgdorferi</i> hsp60 gene for 60kDa heat shock protein	99	1695
1	237	222396	224114	embX54059l BBGROEL	<i>Borrelia burgdorferi</i> groEL gene for a common antigen	94	416
1	241	227310	225754	gblL31417l	<i>Borrelia burgdorferi</i> (clone BbK1.4) phoA fusion protein gene, partial cds	99	231
1	295	281749	283629	embX87725l BBDNA66K D	<i>B. burgdorferi</i> p66 gene for 66kDa protein	100	1881
1	296	284438	283683	gblM58431l	<i>Borrelia burgdorferi</i> PCR target sequence	93	356
1	315	303735	305942	gblL32146l	<i>Borrelia burgdorferi</i> methionyl tRNA synthetase (metG) gene, partial cds	99	345
1	337	330246	329077	gblU60236l	<i>Borrelia burgdorferi</i> response regulator gene, partial cds	100	191
1	338	332455	330299	gblL39965l	<i>Borrelia burgdorferi</i> histidine kinase (cheA) gene, complete cds	99	1361
1	344	336894	335473	gblU51878l	<i>Borrelia burgdorferi</i> phosphotransferase enzyme II (crr) gene, hsp90 (hptg) gene, complete cds	100	95
1	345	336851	338830	gblU51878l	<i>Borrelia burgdorferi</i> phosphotransferase enzyme	99	1980

TABLE 2. *Borrelia burgdorferi* - Coding regions containing known proteins

							II (crr) gene, hsp90 (hptg) gene, complete cds		
1	346	339458	338868	gblU51878l			<i>Borrelia burgdorferi</i> phosphotransferase enzyme II (crr) gene, hsp90 (hptg) gene, complete cds	100	591
1	388	378955	379590	gblM96847l			<i>Borrelia burgdorferi</i> GrpE protein homologue gene, DnaK protein homologue gene, and DnaJ protein homologue gene, complete cds's	100	636
1	389	379566	381521	emblX67646l BBHSPRO			<i>B. burgdorferi</i> dnaK gene for heat-shock protein	100	1956
1	390	381512	381943	gblM97914l			<i>Borrelia burgdorferi</i> DnaJ gene, complete cds	97	424
1	391	381907	382617	gblM96847l			<i>Borrelia burgdorferi</i> GrpE protein homologue gene, DnaK protein homologue gene, and DnaJ protein homologue gene, complete cds's	100	687
1	392	382656	383360	gblM96847l			<i>Borrelia burgdorferi</i> GrpE protein homologue gene, DnaK protein homologue gene, and DnaJ protein homologue gene, complete cds's	95	144
1	393	383005	382688	gblM96847l			<i>Borrelia burgdorferi</i> GrpE protein homologue gene, DnaK protein homologue gene, and DnaJ protein homologue gene, complete cds's	95	144
1	394	384408	383416	gblU82978l			<i>Borrelia burgdorferi</i> phenylalanyl-tRNA synthetase alpha subunit (pheS), phenylalanyl-tRNA synthetase beta subunit (pheT) and thioredoxin reductase (trxB) genes, complete cds	99	956
1	395	384799	384467	gblU82978l			<i>Borrelia burgdorferi</i> phenylalanyl-tRNA synthetase alpha subunit (pheS), phenylalanyl-tRNA synthetase beta subunit (pheT) and thioredoxin reductase (trxB) genes, complete cds	99	292
1	396	386169	384733	gblU82978l			<i>Borrelia burgdorferi</i> phenylalanyl-tRNA synthetase alpha subunit (pheS), phenylalanyl-tRNA synthetase beta subunit (pheT) and thioredoxin reductase (trxB) genes, complete cds	99	1416
1	397	387733	386144	gblU82978l			<i>Borrelia burgdorferi</i> phenylalanyl-tRNA synthetase alpha subunit (pheS), phenylalanyl-tRNA synthetase beta subunit (pheT) and thioredoxin reductase (trxB) genes, complete cds	99	1220

TABLE 2. *Borrelia burgdorferi* - Coding regions containing known proteins

1	398	394257	387727	gblU829781	<i>Borrelia burgdorferi</i> phenylalanyl-tRNA synthetase alpha subunit (pheS), phenylalanyl-tRNA synthetase beta subunit (pheT) and thioredoxin reductase (trxB) genes, complete cds	99	230
1	421	408559	407981	gblM286811	<i>B. burgdorferi</i> promoter region DNA	98	152
1	427	411019	410132	gblU781931	<i>Borrelia burgdorferi</i> tuf-s10 operon: elongation factor (tuf), ribosomal proteins S10 (rpsJ), L3 (rplC), L4 (rplD), L23 (rplW), L2 (rplB), S19 (rpsS), and L22 (rplV) genes, complete cds, and S3 (rpsC) gene, partial cds	99	287
1	428	411388	411017	gblU781931	<i>Borrelia burgdorferi</i> tuf-s10 operon: elongation factor (tuf), ribosomal proteins S10 (rpsJ), L3 (rplC), L4 (rplD), L23 (rplW), L2 (rplB), S19 (rpsS), and L22 (rplV) genes, complete cds, and S3 (rpsC) gene, partial cds	96	357
1	429	411676	411386	gblU781931	<i>Borrelia burgdorferi</i> tuf-s10 operon: elongation factor (tuf), ribosomal proteins S10 (rpsJ), L3 (rplC), L4 (rplD), L23 (rplW), L2 (rplB), S19 (rpsS), and L22 (rplV) genes, complete cds, and S3 (rpsC) gene, partial cds	99	291
1	430	412531	411674	gblU781931	<i>Borrelia burgdorferi</i> tuf-s10 operon: elongation factor (tuf), ribosomal proteins S10 (rpsJ), L3 (rplC), L4 (rplD), L23 (rplW), L2 (rplB), S19 (rpsS), and L22 (rplV) genes, complete cds, and S3 (rpsC) gene, partial cds	98	858
1	431	412852	412529	gblU781931	<i>Borrelia burgdorferi</i> tuf-s10 operon: elongation factor (tuf), ribosomal proteins S10 (rpsJ), L3 (rplC), L4 (rplD), L23 (rplW), L2 (rplB), S19 (rpsS), and L22 (rplV) genes, complete cds, and S3 (rpsC) gene, partial cds	99	324
1	432	413487	412846	gblU781931	<i>Borrelia burgdorferi</i> tuf-s10 operon: elongation factor (tuf), ribosomal proteins S10 (rpsJ), L3 (rplC), L4 (rplD), L23 (rplW), L2 (rplB), S19 (rpsS), and L22 (rplV) genes, complete cds, and S3 (rpsC) gene, partial cds	99	642

TABLE 2. *Borrelia burgdorferi* - Coding regions containing known proteins

							S3 (rpsC) gene, partial cds		
1	433	414117	413485	gbIU781931			<i>Borrelia burgdorferi</i> tuf-s10 operon: elongation factor (tuf), ribosomal proteins S10 (rpsJ), L3 (rplC), L4 (rplD), L23 (rplW), L2 (rplB), S19 (rpsS), and L22 (rplV) genes, complete cds, and S3 (rpsC) gene, partial cds	99	633
1	434	414464	414141	gbIU781931			<i>Borrelia burgdorferi</i> tuf-s10 operon: elongation factor (tuf), ribosomal proteins S10 (rpsJ), L3 (rplC), L4 (rplD), L23 (rplW), L2 (rplB), S19 (rpsS), and L22 (rplV) genes, complete cds, and S3 (rpsC) gene, partial cds	100	324
1	435	415714	414503	gbL231251			<i>Borrelia burgdorferi</i> elongation factor EF-Tu (tuf) gene, complete cds	100	1212
1	481	450681	450310	gbIU045271			<i>Borrelia burgdorferi</i> 212 DNA gyrase b subunit (gyrB) and ribonuclease P protein component (rnpA) genes, partial cds, DnaA protein (dnaA), DNA polymerase III beta subunit (dnaN), and ribosomal protein L34 (rpmH) genes, complete cds	100	148
1	482	450820	450650	gbIU045271			<i>Borrelia burgdorferi</i> 212 DNA gyrase b subunit (gyrB) and ribonuclease P protein component (rnpA) genes, partial cds, DnaA protein (dnaA), DNA polymerase III beta subunit (dnaN), and ribosomal protein L34 (rpmH) genes, complete cds	100	171
1	483	451208	450897	gbIU045271			<i>Borrelia burgdorferi</i> 212 DNA gyrase b subunit (gyrB) and ribonuclease P protein component (rnpA) genes, partial cds, DnaA protein (dnaA), DNA polymerase III beta subunit (dnaN), and ribosomal protein L34 (rpmH) genes, complete cds	100	312
1	484	451288	451467	gbIU045271			<i>Borrelia burgdorferi</i> 212 DNA gyrase b subunit (gyrB) and ribonuclease P protein component (rnpA) genes, partial cds, DnaA protein (dnaA),	100	180

TABLE 2. *Borrelia burgdorferi* - Coding regions containing known proteins

1	485	452456	451287	gbIU045271	DNA polymerase III beta subunit (dnaN), and ribosomal protein L34 (rpmH) genes, complete cds	99	1170
1	486	454181	452685	gbIU045271	<i>Borrelia burgdorferi</i> 212 DNA gyrase b subunit (gyrB) and ribonuclease P protein component (rnpA) genes, partial cds, DnaA protein (dnaA), DNA polymerase III beta subunit (dnaN), and ribosomal protein L34 (rpmH) genes, complete cds	100	1497
1	487	454315	456237	gbIU045271	<i>Borrelia burgdorferi</i> 212 DNA gyrase b subunit (gyrB) and ribonuclease P protein component (rnpA) genes, partial cds, DnaA protein (dnaA), DNA polymerase III beta subunit (dnaN), and ribosomal protein L34 (rpmH) genes, complete cds	98	904
1	488	456228	458681	embIZ12165[B. burgdorferi gyrA gene encoding DNA gyrase subunit A (partial)		96	289
1	496	463825	464394	gbIU033961	<i>Borrelia burgdorferi</i> B31 Ala-tRNA (alaT), Ile-tRNA (ileT), 16S rRNA, 23S rRNA (rrlA and rrlB), and 5S rRNA (rrfA and rrfB) genes, complete sequence	100	570
1	497	466650	466958	gbIU033961	<i>Borrelia burgdorferi</i> B31 Ala-tRNA (alaT), Ile-tRNA (ileT), 16S rRNA, 23S rRNA (rrlA and rrlB), and 5S rRNA (rrfA and rrfB) genes, complete sequence	96	210
1	498	467437	468033	gbIU033961	<i>Borrelia burgdorferi</i> B31 Ala-tRNA (alaT), Ile-tRNA (ileT), 16S rRNA, 23S rRNA (rrlA and rrlB), and 5S rRNA (rrfA and rrfB) genes,	99	209

TABLE 2.
Borrelia burgdorferi - Coding regions containing known proteins

1	499	468167	468433	gblU033961	complete sequence	98	267
					Borrelia burgdorferi B31 Ala-tRNA (alaT), Ile-tRNA (ileT), 16S rRNA, 23S rRNA (rrlA and rrlB), and 5S rRNA (rrfA and rrfB) genes, complete sequence		
1	500	468391	468999	gblU033961	Borrelia burgdorferi B31 Ala-tRNA (alaT), Ile-tRNA (ileT), 16S rRNA, 23S rRNA (rrlA and rrlB), and 5S rRNA (rrfA and rrfB) genes, complete sequence	95	386
1	501	470714	470445	gblM883301	Borrelia burgdorferi 23S ribosomal RNA gene	100	270
1	502	475597	480090	gblU033961	Borrelia burgdorferi B31 Ala-tRNA (alaT), Ile-tRNA (ileT), 16S rRNA, 23S rRNA (rrlA and rrlB), and 5S rRNA (rrfA and rrfB) genes, complete sequence	97	131
1	535	505532	509017	gblL484881	Borrelia burgdorferi RNA polymerase beta subunit (rpoB) gene, complete cds, RNA polymerase beta' subunit (rpoC) gene, 5' end of cds	98	2490
1	536	509015	513166	gblL484881	Borrelia burgdorferi RNA polymerase beta subunit (rpoB) gene, complete cds, RNA polymerase beta' subunit (rpoC) gene, 5' end of cds	97	76
1	538	513606	514106	gblU354501	Borrelia burgdorferi membrane protein D (bmpD) gene, complete cds	100	82
1	539	514120	515229	gblU354501	Borrelia burgdorferi membrane protein D (bmpD) gene, complete cds	99	1110
1	540	515472	516605	gblU499381	Borrelia burgdorferi potential virulence gene cluster membrane proteins BmpC (bmpC) and BmpA (bmpA), BmpB protein (bmpB), putative protein 4, Mg ion transporter MgtE (mgtE), protein kinase C1 inhibitor PKCI (pkci) genes, complete cds	99	1134
1	541	516641	517666	gblL241941	Borrelia burgdorferi immunodominant antigen P39 gene, complete cds	99	1026

TABLE 2. Borrelia burgdorferi - Coding regions containing known proteins

1	542	517732	518256	gblL35050	Borrelia burgdorferi (clone pB46) membrane lipoprotein A (bmpA) gene, 3' end, membrane lipoprotein (bmpB) gene, 5' end	98	457
1	543	518168	518779	gblL24194	Borrelia burgdorferi immunodominant antigen P39 gene, complete cds	99	606
1	544	518856	520316	gblU49938	Borrelia burgdorferi potential virulence gene cluster membrane proteins BmpC (bmpC) and BmpA (bmpA), BmpB protein (bmpB), putative protein 4, Mg ion transporter MgtE (mgtE), protein kinase C1 inhibitor PKCI (pkci) genes, complete cds	99	1461
1	545	520349	521734	gblU49938	Borrelia burgdorferi potential virulence gene cluster membrane proteins BmpC (bmpC) and BmpA (bmpA), BmpB protein (bmpB), putative protein 4, Mg ion transporter MgtE (mgtE), protein kinase C1 inhibitor PKCI (pkci) genes, complete cds	99	1386
1	546	521752	522204	gblU49938	Borrelia burgdorferi potential virulence gene cluster membrane proteins BmpC (bmpC) and BmpA (bmpA), BmpB protein (bmpB), putative protein 4, Mg ion transporter MgtE (mgtE), protein kinase C1 inhibitor PKCI (pkci) genes, complete cds	100	453
1	547	522168	522893	gblU49938	Borrelia burgdorferi potential virulence gene cluster membrane proteins BmpC (bmpC) and BmpA (bmpA), BmpB protein (bmpB), putative protein 4, Mg ion transporter MgtE (mgtE), protein kinase C1 inhibitor PKCI (pkci) genes, complete cds	98	130
1	559	535086	534772	embIX78708 BBYSCI	B. burgdorferi (ZS7) YSCI-like gene	99	314
1	560	536461	535058	embIX78708 BBYSCI	B. burgdorferi (ZS7) YSCI-like gene	100	1404
1	561	536545	537144	embIX70826	B. burgdorferi gene for lipoprotein	100	600

TABLE 2. *Borrelia burgdorferi* - Coding regions containing known proteins

1	562	537652	537191	BBLA7 embIX708261 BBLA7	B. burgdorferi gene for lipoprotein	100	57
1	563	539695	537665	gblM900841	Borrelia burgdorferi 22 kD antigen	100	786
1	564	537705	537968	gblM900841	Borrelia burgdorferi 22 kD antigen	100	264
1	565	538395	538757	gblM900841	Borrelia burgdorferi 22 kD antigen	100	56
1	606	574092	572497	gblU291431	Borrelia burgdorferi periplasmic substrate-binding protein homolog (p30) gene, complete cds	92	805
1	607	575817	574204	gblU291431	Borrelia burgdorferi periplasmic substrate-binding protein homolog (p30) gene, complete cds	100	84
1	616	585458	586936	gblL314221	Borrelia burgdorferi (clone Bb2.13) phoA fusion protein gene, partial cds	100	354
1	629	596586	597983	gblU437391	Borrelia burgdorferi fesmid clone 31, complete sequence	100	1185
1	630	597967	599052	embIX966851 BBCDG	B. burgdorferi cell division genes	99	912
1	631	599050	600153	embIX966851 BBCDG	B. burgdorferi cell division genes	99	1104
1	632	600183	600932	embIX964331 BBFTSWQA	B. burgdorferi ftsW, ftsQ & ftsA genes	99	750
1	633	600905	602173	gblU437391	Borrelia burgdorferi fesmid clone 31, complete sequence	100	1269
1	634	602171	603394	gblU437391	Borrelia burgdorferi fesmid clone 31, complete sequence	100	1224
1	635	603392	604087	gblU437391	Borrelia burgdorferi fesmid clone 31, complete sequence	100	696
1	636	604085	605041	gblL763031	Borrelia burgdorferi ftsA gene, 3' end of cds, ftsZ, orf230, smf, hslVU, flgBCE, flhFGHI, flhABC genes, complete cds	98	712
1	637	605039	605599	gblU437391	Borrelia burgdorferi fesmid clone 31, complete sequence	100	561

TABLE 2. *Borrelia burgdorferi* - Coding regions containing known proteins

1	638	605535	606938	embIX966851 BBCDG	B. burgdorferi cell division genes	97	1404
1	639	606936	607379	gbIU43739I	Borrelia burgdorferi fesmid clone 31, complete sequence	100	444
1	640	607382	607861	gbIU43739I	Borrelia burgdorferi fesmid clone 31, complete sequence	100	480
1	641	607831	608208	gbL76303I	Borrelia burgdorferi ftsA gene, 3' end of cds, ftsZ, orf230, smf, hslVU, flgBCE, flieFGHI, flbABC genes, complete cds	100	378
1	642	608163	609932	gbL76303I	Borrelia burgdorferi ftsA gene, 3' end of cds, ftsZ, orf230, smf, hslVU, flgBCE, flieFGHI, flbABC genes, complete cds	100	1770
1	643	609930	610982	gbIU43739I	Borrelia burgdorferi fesmid clone 31, complete sequence	100	1053
1	644	610961	611917	gbIU43739I	Borrelia burgdorferi fesmid clone 31, complete sequence	100	957
1	645	611915	613246	gbL76303I	Borrelia burgdorferi ftsA gene, 3' end of cds, ftsZ, orf230, smf, hslVU, flgBCE, flieFGHI, flbABC genes, complete cds	99	1332
1	646	613222	613674	gbL76303I	Borrelia burgdorferi ftsA gene, 3' end of cds, ftsZ, orf230, smf, hslVU, flgBCE, flieFGHI, flbABC genes, complete cds	99	453
1	647	613655	614284	gbIU43739I	Borrelia burgdorferi fesmid clone 31, complete sequence	100	630
1	648	614250	615470	gbL76303I	Borrelia burgdorferi ftsA gene, 3' end of cds, ftsZ, orf230, smf, hslVU, flgBCE, flieFGHI, flbABC genes, complete cds	99	1221
1	649	615481	615927	gbL76303I	Borrelia burgdorferi ftsA gene, 3' end of cds, ftsZ, orf230, smf, hslVU, flgBCE, flieFGHI, flbABC genes, complete cds	100	447
1	650	615911	617260	gbIU43739I	Borrelia burgdorferi fesmid clone 31, complete sequence	100	1350
1	651	617277	617507	gbIU43739I	Borrelia burgdorferi fesmid clone 31, complete sequence	100	231

1	652	617498	618286	gblU43739I	Borrelia burgdorferi f31, complete sequence	100	789
1	653	618280	619068	gblU43739I	Borrelia burgdorferi f31, complete sequence	100	789
1	654	619066	619653	gblU43739I	Borrelia burgdorferi f31, complete sequence	100	588
1	655	619688	620749	gblU43739I	Borrelia burgdorferi f31, complete sequence	100	1062
1	656	620789	621136	gblU43739I	Borrelia burgdorferi f31, complete sequence	100	348
1	657	621114	621755	gblU43739I	Borrelia burgdorferi f31, complete sequence	100	642
1	658	621742	622530	gblL75945I	Borrelia burgdorferi flagellar hook protein (flgE), flbD, flagellar motor apparatus (motAB), flil, flhB, flhF, flbE genes	99	789
1	659	622028	621822	gblL75945I	Borrelia burgdorferi flagellar hook protein (flgE), flbD, flagellar motor apparatus (motAB), flil, flhB, flhF, flbE genes	100	207
1	660	622515	622802	gblL75945I	Borrelia burgdorferi flagellar hook protein (flgE), flbD, flagellar motor apparatus (motAB), flil, flhB, flhF, flbE genes	100	288
1	661	622811	623623	gblL75945I	Borrelia burgdorferi flagellar hook protein (flgE), flbD, flagellar motor apparatus (motAB), flil, flhB, flhF, flbE genes	99	813
1	662	623007	622819	gblL75945I	Borrelia burgdorferi flagellar hook protein (flgE), flbD, flagellar motor apparatus (motAB), flil, flhB, flhF, flbE genes	100	189
1	663	623706	623458	gblL75945I	Borrelia burgdorferi flagellar hook protein (flgE), flbD, flagellar motor apparatus (motAB), flil, flhB, flhF, flbE genes	100	249

TABLE 2.
Borrelia burgdorferi - Coding regions containing known proteins

							fliM, fliZ, flagellar export apparatus (fliPQR, fliH), fliF, fliE genes		
1	664	623608	624741	gblL75945			Borrelia burgdorferi flagellar hook protein (fliE), fliD, flagellar motor apparatus (motAB), fliL, fliM, fliZ, flagellar export apparatus (fliPQR, fliH), fliF, fliE genes	99	1134
1	665	624735	626843	gblL75945			Borrelia burgdorferi flagellar hook protein (fliE), fliD, flagellar motor apparatus (motAB), fliL, fliM, fliZ, flagellar export apparatus (fliPQR, fliH), fliF, fliE genes	100	2109
1	666	626841	628013	gblU43739			Borrelia burgdorferi fliM clone 31, complete sequence	100	1173
1	667	627998	628912	gblU43739			Borrelia burgdorferi fliM clone 31, complete sequence	99	816
1	668	629151	628807	gblU43739			Borrelia burgdorferi fliM clone 31, complete sequence	100	345
1	669	628910	629398	gblU43739			Borrelia burgdorferi fliM clone 31, complete sequence	100	489
1	670	629371	631305	gblU43739			Borrelia burgdorferi fliM clone 31, complete sequence	100	1935
1	671	631314	631634	gblU43739			Borrelia burgdorferi fliM clone 31, complete sequence	100	286
1	676	636891	635476	gblM28682			B.burgdorferi promoter element DNA	100	78
1	687	646982	649420	gblL77216			Borrelia burgdorferi (strain B31) protease (lon) gene, complete cds	99	2439
1	688	651760	649409	gblL77216			Borrelia burgdorferi (strain B31) protease (lon) gene, complete cds	100	274
1	711	671567	672412	gblU35673			Borrelia burgdorferi OrfR gene, partial cds, and S20, Hbb, OrfH and Rho genes, complete cds	99	542
1	712	672418	672744	gblU35673			Borrelia burgdorferi OrfR gene, partial cds, and S20, Hbb, OrfH and Rho genes, complete cds	100	327
1	713	672751	673083	gblU48651			Borrelia burgdorferi PIG histone-like protein HBbu (hbb) gene, complete cds	100	327

TABLE 2.
Borrelia burgdorferi - Coding regions containing known proteins

1	714	673081	673491	gbIU356731	Borrelia burgdorferi OrfR gene, partial cds, and S20, Hbb, OrfH and Rho genes, complete cds	99	411
1	715	673553	675118	gbIU356731	Borrelia burgdorferi OrfR gene, partial cds, and S20, Hbb, OrfH and Rho genes, complete cds	99	1566
1	716	675164	675424	gbIU356731	Borrelia burgdorferi OrfR gene, partial cds, and S20, Hbb, OrfH and Rho genes, complete cds	100	106
1	773	724171	723770	gbIU629011	Borrelia burgdorferi thdF gene, partial cds, putative motility protein (flbF), flagellar hook associated proteins FlgK (flgK) and FlgL (flgL) genes, complete cds	97	67
1	774	723891	724181	gbIU629011	Borrelia burgdorferi thdF gene, partial cds, putative motility protein (flbF), flagellar hook associated proteins FlgK (flgK) and FlgL (flgL) genes, complete cds	97	77
1	775	725456	724164	gbIU629011	Borrelia burgdorferi thdF gene, partial cds, putative motility protein (flbF), flagellar hook associated proteins FlgK (flgK) and FlgL (flgL) genes, complete cds	99	780
1	776	727348	725441	gbIU629011	Borrelia burgdorferi thdF gene, partial cds, putative motility protein (flbF), flagellar hook associated proteins FlgK (flgK) and FlgL (flgL) genes, complete cds	99	1841
1	777	727854	727336	gbIU629011	Borrelia burgdorferi thdF gene, partial cds, putative motility protein (flbF), flagellar hook associated proteins FlgK (flgK) and FlgL (flgL) genes, complete cds	99	519
1	778	727908	729308	embIX956691 BBTHDFGID	B.burgdorferi thdF and gidA genes	98	1185
1	779	729284	731176	embIZ121601B BGIDAG	B.burgdorferi thdF, gidA and gidB genes	99	1893
1	780	731149	731799	embIX956681 BBGIDMOX R	B.burgdorferi gidA, gidB and moxR genes	98	381
1	781	731772	732848	embIX964341	B.burgdorferi gidB moxR genes and ORF	99	789

TABLE 2.

						BBGIDBMO X				
1	782	732815	733738			embIX96434 BBGIDBMO X	B.burgdorferi gidB	maxR genes and ORF	100	84
1	798	752154	751372			gblU51878	Borrelia burgdorferi phosphotransferase enzyme II (crr) gene, hsp90 (hptg) gene, complete cds	100	57	
1	800	754266	753118			gblAF003354	Borrelia burgdorferi SecA (secA) gene, complete cds	97	67	
1	801	753992	754243			gblAF003354	Borrelia burgdorferi SecA (secA) gene, complete cds	96	50	
1	802	754283	757015			gblAF003354	Borrelia burgdorferi SecA (secA) gene, complete cds	99	2041	
1	803	756991	757641			gblAF003354	Borrelia burgdorferi SecA (secA) gene, complete cds	100	158	
1	806	759909	761930			gblU66699	Borrelia burgdorferi flagellar filament cap (flfD) gene, complete cds and flagellin protein (flaB) gene, partial cds	98	1149	
1	807	762051	763067			embIX16833 BBFAA	Borrelia burgdorferi gene for flagellum- associated 41kD antigen (flagellin)	99	1017	
1	808	763194	764339			embIX63898 BBHYPP	B.burgdorferi DNA for hypothetical protein	99	1146	
1	809	764337	765245			embIX63898 BBHYPP	B.burgdorferi DNA for hypothetical protein	92	253	
1	826	783276	784400			gblU23457	Borrelia burgdorferi RecA (recA) gene, complete cds	99	1122	
1	827	784412	785182			gblU23457	Borrelia burgdorferi RecA (recA) gene, complete cds	82	476	
1	828	785142	785918			gblU23457	Borrelia burgdorferi RecA (recA) gene, complete cds	99	139	
1	907	855179	857182			gblU28760	Borrelia burgdorferi glyceraldehyde-3-phosphate dehydrogenase (GAPDH), phosphoglycerate kinase (PGK), triosephosphate isomerase (TPI)	94	75	

TABLE 2.
Borrelia burgdorferi - Coding regions containing known proteins

1	908	857228	858262	gblU28760l	genes, complete cds	99	1035
					Borrelia burgdorferi glyceraldehyde-3-phosphate dehydrogenase (GAPDH), phosphoglycerate kinase (PGK), triosephosphate isomerase (TPI) genes, complete cds		
1	909	858270	859463	gblU28760l	Borrelia burgdorferi glyceraldehyde-3-phosphate dehydrogenase (GAPDH), phosphoglycerate kinase (PGK), triosephosphate isomerase (TPI) genes, complete cds	99	1194
1	910	859315	860226	gblU28760l	Borrelia burgdorferi glyceraldehyde-3-phosphate dehydrogenase (GAPDH), phosphoglycerate kinase (PGK), triosephosphate isomerase (TPI) genes, complete cds	99	912
1	911	860224	860604	gblU57683l	Borrelia burgdorferi sequence 3' to the triosephosphate isomerase (TPI) gene	97	183
1	912	860645	860316	gblU57683l	Borrelia burgdorferi sequence 3' to the triosephosphate isomerase (TPI) gene	95	94
1	913	861447	860704	gblU57684l	Borrelia burgdorferi uracil DNA glycosylase (UDG) gene, partial cds	92	294
1	914	861020	861397	gblU57684l	Borrelia burgdorferi uracil DNA glycosylase (UDG) gene, partial cds	93	244
1	915	861439	862113	gblU57684l	Borrelia burgdorferi uracil DNA glycosylase (UDG) gene, partial cds	96	128
1	930	874089	874859	gblL32861l	Borrelia burgdorferi 1-acyl-sn-glycerol-3-phosphate acetyltransferase (plsC) gene, 3' end; topoisomerase IV beta-subunit (parE) gene, 5' end	99	408
1	931	874877	876679	gblL32861l	Borrelia burgdorferi 1-acyl-sn-glycerol-3-phosphate acetyltransferase (plsC) gene, 3' end; topoisomerase IV beta-subunit (parE) gene, 5' end	100	252
1	943	887900	886758	embLY08885l BBRUVA BH L	B. burgdorferi ruvA, ruvB and queA genes	98	293

TABLE 2. Borrelia burgdorferi - Coding regions containing known proteins

1	944	887965	888570	emb Y08885 BBRUVABH L	B.burgdorferi ruvA, ruvB and queA genes	99	606
1	945	888603	889658	emb Y08885 BBRUVABH L	B.burgdorferi ruvA, ruvB and queA genes	99	1056
1	946	889615	890271	emb Y08885 BBRUVABH L	B.burgdorferi ruvA, ruvB and queA genes	97	342
1	948	890719	892404	emb Y09140 BBPFPB	B.burgdorferi pfpB gene	99	1320
1	950	892893	893909	emb Y09142 BBYFII	B.burgdorferi yfiI gene	97	919
1	952	894973	895371	emb X97449 BBPRIAUDK	B.burgdorferi priA and udk genes	88	324
1	953	895308	895991	emb X97449 BBPRIAUDK	B.burgdorferi priA and udk genes	99	684
1	954	897976	895988	emb X97449 BBPRIAUDK	B.burgdorferi priA and udk genes	99	1989
1	955	898577	897963	emb X97449 BBPRIAUDK	B.burgdorferi priA and udk genes	100	152
1	956	899298	898555	emb Y09141 BBTRUA	B.burgdorferi truA gene	99	741

TABLE 3.
Borrelia burgdorferi - Putative coding regions of novel proteins not similar to know proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
1	1	2330	1134
1	2	3317	2934
1	8	11375	13021
1	9	11673	11386
1	10	12925	13629
1	11	13538	14146
1	17	25212	24700
1	18	25782	25357
1	19	26115	25870
1	21	27308	27051
1	22	29628	30458
1	29	40696	41217
1	30	41201	41992
1	31	42542	41985
1	32	42593	42982
1	34	44234	44031
1	38	48041	47079
1	41	49318	49617
1	43	53234	51810
1	50	59737	58208
1	58	68227	67733
1	65	79757	80404
1	66	81516	80401
1	75	89552	88353
1	82	93338	92766
1	85	95207	95854
1	104	108788	108621
1	105	109764	108943
1	108	112003	111599
1	113	114317	115846
1	114	114522	114316
1	119	118439	118927
1	121	119802	119599
1	125	125688	123967
1	129	128594	129235
1	135	136116	135259
1	136	136558	136298
1	139	139149	139559
1	141	140573	140121
1	143	141738	141412
1	145	142218	142060
1	146	142686	142342
1	154	150528	149074
1	158	153832	153981
1	163	158277	158474

Borrelia burgdorferi - Putative coding regions of novel proteins not similar to know proteins

1	171	168052	166205
1	176	171592	171038
1	186	179607	180089
1	189	182345	182046
1	191	182567	182773
1	199	192561	192716
1	205	196592	197476
1	218	207717	206752
1	219	207733	208437
1	221	209337	208915
1	222	209712	209335
1	231	217179	216025
1	238	223660	223418
1	240	224720	225724
1	242	227006	227275
1	248	231761	231501
1	251	232973	233308
1	252	233669	234004
1	254	235115	235456
1	258	241824	242198
1	261	248009	247773
1	269	256846	255872
1	276	265430	265158
1	279	266582	266298
1	281	268474	268280
1	286	274157	274384
1	292	280495	280274
1	294	281344	281042
1	298	287276	285714
1	303	292943	292644
1	304	293273	293037
1	305	294965	294648
1	308	299427	298699
1	309	299051	299212
1	326	320375	319785
1	327	320425	321036
1	331	324198	324413
1	339	332785	332459
1	341	333503	334138
1	342	334116	334739
1	343	334880	335446
1	350	342916	342443
1	351	344789	342897
1	363	357596	356931
1	367	361065	360859
1	370	362519	362196

Borrelia burgdorferi - Putative coding regions of novel proteins not similar to know proteins

1	374	366905	366114
1	377	368632	369537
1	378	369928	370560
1	379	370532	371353
1	382	375028	373193
1	383	375102	375542
1	387	378677	378198
1	400	394952	394722
1	401	396247	394937
1	403	397569	398327
1	406	399103	399294
1	436	416160	416570
1	445	424660	423950
1	446	425181	424642
1	450	428559	428200
1	451	428933	428619
1	455	432590	431628
1	461	437823	438092
1	463	438690	438313
1	466	440749	440222
1	470	441568	441350
1	471	442039	441614
1	472	442216	442037
1	473	442666	442262
1	476	445202	445017
1	493	462106	462519
1	494	462893	462549
1	504	482111	481035
1	505	481552	481800
1	509	483249	483668
1	512	484864	485157
1	516	489171	488527
1	519	492989	492375
1	520	493626	492997
1	521	494169	494864
1	524	497185	497385
1	525	497674	499254
1	527	500251	501294
1	528	501281	502156
1	558	533912	533667
1	568	541267	541491
1	571	544436	544257
1	572	544565	545068
1	578	549603	551198
1	580	551508	551657
1	581	552337	551513

Borrelia burgdorferi - Putative coding regions of novel proteins not similar to known proteins

1	585	556051	557271
1	590	561342	561139
1	591	561825	561520
1	592	562536	563360
1	596	565758	566519
1	599	568389	568682
1	602	568680	568856
1	605	570829	571167
1	609	576170	577093
1	612	581549	581091
1	614	582910	584013
1	619	589384	588674
1	624	592665	593465
1	626	594542	595405
1	672	631642	632175
1	677	636650	636892
1	678	637059	638078
1	681	640861	640412
1	686	644887	645207
1	689	649716	649961
1	690	650436	650735
1	691	650733	651056
1	693	653303	653689
1	705	664733	664918
1	707	665979	666770
1	718	679155	678391
1	721	680664	681047
1	722	681523	681849
1	724	681809	682171
1	727	682853	683272
1	734	687648	688067
1	739	691613	692290
1	751	707290	707718
1	763	719197	718904
1	764	720030	719257
1	769	722198	722482
1	783	733736	734647
1	785	735554	736618
1	787	737124	739184
1	792	742924	744801
1	799	753128	752655
1	811	766129	765980
1	812	766438	767772
1	815	770062	769790
1	818	771890	772282
1	831	788219	788836

Borrelia burgdorferi - Putative coding regions of novel proteins not similar to know proteins

1	832	788824	789615
1	838	793566	793414
1	840	794295	794119
1	844	796774	796586
1	852	803096	802908
1	858	809371	809970
1	864	816108	816497
1	865	816672	817283
1	866	817281	817838
1	872	823841	824836
1	876	828191	828739
1	877	828749	829147
1	879	831328	831714
1	880	831698	833005
1	885	836201	835677
1	890	841171	840590
1	891	840594	840860
1	899	849453	850148
1	902	851608	852687
1	918	862867	863109
1	920	864292	864705
1	923	865660	865346
1	925	868212	869273
1	928	871012	872580
1	933	878576	879166
1	939	884338	883268
1	940	884999	884325
1	949	892388	892924
1	957	900141	899296
1	958	900534	900139
1	959	901526	900510
1	962	902383	903258

TABLE 4.
Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% Ident
69	1	291	4	gil146582	beta-lactamase [Escherichia coli]	100	98
69	2	692	240	gil344797	galactosidase fusion protein [unidentified]	100	99
26	3	1575	2093	gil458219	ORF 4 [Borrelia burgdorferi]	94	76
2	48	41836	41459	gil47453	ribosomal protein S12 [Streptococcus pneumoniae]	92	85
6	20	14234	12951	bbs161785	60 kda antigen [Borrelia coriaceae, C053, ATCC 4338, Peptide, 514 aa] [Borrelia coriaceae]	88	67
52	5	1080	1652	gnlPIDle201250	ORF-D gene product [Borrelia burgdorferi]	88	74
152	1	337	26	gnlPIDle158979	orfA gene product [Borrelia burgdorferi]	86	75
71	2	1421	1128	gnlPIDle160437	orfD gene product [Borrelia burgdorferi]	85	46
131	1	381	674	gil458220	ORF 5 [Borrelia burgdorferi]	85	76
3	113	98152	97367	gil1591672	phosphate transport system ATP-binding protein [Methanococcus jannaschii]	84	65
2	107	108403	109485	gil882454	fructose 1,6-bisphosphate aldolase [Escherichia coli]	81	61
19	4	4059	4754	pirA34520A34520	29K calcium-binding protein, brain-specific - guinea pig (fragments)	81	56
20	9	6084	5791	gnlPIDle201249	ORF-C gene product [Borrelia burgdorferi]	81	72
2	52	49986	49600	pirA02771IR7MCML	ribosomal protein L7/L12 - Micrococcus luteus	80	67
14	1	3071	3	gil1522636	M. jannaschii predicted coding region MJEC502 [Methanococcus jannaschii]	80	60
29	2	218	409	gil1752736	gene required for phosphorylation of oligosaccharides/ has high homology with YJR061w [Saccharomyces cerevisiae]	80	37
32	2	719	925	gil433720	CDC25 [Homo sapiens]	80	73
100	1	2	946	gil1522636	M. jannaschii predicted coding region MJEC502 [Methanococcus jannaschii]	80	60

Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

2	106	107148	108239	gnlPIDle2881 24	glucose epimerase [Bacillus thuringiensis]	79	66
8	4	4878	4735	gil1543076	outer membrane porin protein Oms28 precursor [Borrelia burgdorferi]	79	69
2	55	51661	51218	gil587583	ribosomal protein L11 [Thermus aquaticus thermophilus]	78	58
4	54	39290	38742	gnlPIDle1604 37	orfD gene product [Borrelia burgdorferi]	78	57
5	46	27416	27177	gnlPIDle2532 11	ORF YDL065c [Saccharomyces cerevisiae]	78	57
7	4	2382	2966	gnlPIDle2012 48	ORF-B gene product [Borrelia burgdorferi]	78	60
19	5	5107	4943	gil882579	CG Site No. 29739 [Escherichia coli]	78	42
78	1	1	171	gnlPIDle2012 49	ORF-C gene product [Borrelia burgdorferi]	78	60
105	2	503	742	gnlPIDle2532 11	ORF YDL065c [Saccharomyces cerevisiae]	78	57
2	30	24917	23697	gil143795	transfer RNA-Tyr synthetase [Bacillus subtilis]	77	52
6	34	22722	24080	gil466474	cellobiose phosphotransferase enzyme II" [Bacillus stearothermophilus]	77	50
8	1	688	536	gil1017809	similar to dihydropyridine-sensitive I-type, skeletal muscle calcium channel alpha-1 subunit (SP:CIC1_RABIT, P07293) [Caenorhabditis elegans]	77	55
3	91	81071	82183	gil467376	unknown [Bacillus subtilis]	76	58
11	1	208	2	gil1065989	(pos:5995..5997,aa:Met) [Bacillus subtilis]	76	56
68	1	605	3	gnlPIDle1589 80	orfC gene product [Borrelia burgdorferi]	76	56
2	9	8488	6674	pirC300101C3 0010	hypothetical ORF-6 protein - Sauroleishmania tarentolae mitochondrion (SGC6)	75	50
2	37	31639	32163	gil1573470	H. influenzae predicted coding region HI0491 [Haemophilus influenzae]	75	55
2	56	52261	51701	gil396321	nusG [Escherichia coli]	75	56

Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

20	1	653	414	gil520778	protein p23 [Borrelia burgdorferi]	75	62
20	3	2437	1652	gnlPIDle201249	ORF-C gene product [Borrelia burgdorferi]	75	60
58	1	856	62	gnlPIDle201249	ORF-C gene product [Borrelia burgdorferi]	75	37
68	3	1153	578	gil458217	ORF 2 [Borrelia burgdorferi]	75	55
117	1	744	388	gil520783	unknown [Borrelia burgdorferi]	75	42
130	1	1	684	gnlPIDle160436	orfA gene product [Borrelia burgdorferi]	75	58
2	36	30506	31693	gil1020317	S-adenosylmethionine synthetase [Staphylococcus aureus]	74	57
2	109	111301	109871	gil396501	aspartyl-tRNA synthetase [Thermus aquaticus thermophilus]	74	52
3	101	92143	91103	gil1651962	hypothetical protein [Synechocystis sp.]	74	49
20	5	4080	2974	gnlPIDle158979	orfA gene product [Borrelia burgdorferi]	74	56
36	2	468	1253	gnlPIDle158984	orfC gene product [Borrelia burgdorferi]	74	59
42	1	396	719	gil1655798	CdsK [Borrelia burgdorferi]	74	58
2	10	6810	7022	gil406135	glycoprotein 120 [Simian immunodeficiency virus]	73	53
2	29	23695	21395	gil511145	hemolysin [Serpulina hyodysenteriae]	73	52
3	56	44789	44262	gil1595810	type-I signal peptidase SpsB [Staphylococcus aureus]	73	47
3	73	64881	62341	gnlPIDle268456	unknown [Mycobacterium tuberculosis]	73	54
3	100	89800	91113	gil500705	Similar to Seryl-tRNA synthetase [Saccharomyces cerevisiae]	73	56
3	106	92803	93513	gnlPIDle243681	ORF YGR248w [Saccharomyces cerevisiae]	73	63
4	4	3697	3512	gil562035	NADH dehydrogenase, subunit 5 [Acanthamoeba castellanii]	73	53
7	9	8519	8079	gil694092	emml gene product [Streptococcus pyogenes]	73	40

Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

8	16	17562	17756	gll1500401	reverse gyrase [Methanococcus jannaschii]	73	40
14	3	4280	4438	gll520778	protein p23 [Borrelia burgdorferi]	73	55
19	9	7074	6742	gll177311	NADH dehydrogenase [Ceanothus cuneatus]	73	36
25	3	2369	2587	gll1655790	CdsC [Borrelia burgdorferi]	73	64
78	2	176	619	gllPID1e2012 50	ORF-D gene product [Borrelia burgdorferi]	73	50
108	1	2	382	gll1573074	adhesin B precursor (fimA) [Haemophilus influenzae]	73	41
120	1	97	342	gll1978	heat shock protein 70 [Sus scrofa]	73	46
3	64	51644	54013	gll1574437	sporulation protein (spoIIIE) [Haemophilus influenzae]	72	51
5	6	2899	2654	gll212383	myosin heavy chain [Gallus gallus]	72	41
6	31	22140	21799	gll895748	putative cellobiose phosphotransferase enzyme II' [Bacillus subtilis]	72	46
8	8	8812	9600	gll1655859	Orf1 [Borrelia hermsii]	72	55
10	12	8579	8376	gll536681	ORF YBR257w [Saccharomyces cerevisiae]	72	36
45	2	1440	394	gll1699017	ErpB2 [Borrelia burgdorferi]	72	42
2	2	1342	2796	gll285623	pyruvate kinase [Bacillus stearothermophilus]	71	52
2	31	26272	24911	pirS58522IS5 8522	glycyl-tRNA synthetase - Thermus thermophilus	71	54
2	64	60156	58684	gll459009	similar to multifunctional aminoacyl-tRNA synthetase, especially to the prolyl-tRNA synthetase region [Caenorhabditis elegans]	71	48
3	66	55240	54275	gll217121	ORF1 [Synechococcus elongatus]	71	52
3	104	92345	92175	gll44228	secretion protein Sec Y (AA 1-482) [Mycoplasma capricolum]	71	42
5	43	25567	25734	gll213778	sodium-hydrogen exchange protein-beta [Onchocerca mykiss]	71	50
7	3	1179	2384	gll458216	ORF 1 [Borrelia burgdorferi]	71	60
20	4	2964	2392	gll458217	ORF 2 [Borrelia burgdorferi]	71	47
51	2	984	2066	gll1373144	ErpD [Borrelia burgdorferi]	71	41
54	1	251	883	gll145280	ORF1 [Escherichia coli]	71	40

Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

2	54	51233	50538	spQ06797/RL L_BACSU	50S RIBOSOMAL PROTEIN L1 (BL1).	70	48
2	116	114025	113744	gil1673757	(AE000012) Mycoplasma pneumoniae, phosphocarrier protein HPR; similar to GenBank Accession Number A49683, from M. capricolum [Mycoplasma pneumoniae]	70	41
3	4	1684	2220	gil153906	CheW protein [Salmonella typhimurium]	70	48
3	84	74775	73225	gnlPIDle2839 19	glycerol kinase [Sulfolobus solfataricus]	70	60
3	107	93500	93273	gil836815	cdc4 gene product which is essential for initiation of DNA replication in yeast [Saccharomyces cerevisiae]	70	35
4	1	926	123	gil167913	Thy1 protein [Dictyostelium discoideum]	70	51
4	47	35616	35807	gil48808	dcIAE gene product [Bacillus subtilis]	70	58
4	65	48320	47976	gil1421734	ORF 5 [Borrelia burgdorferi]	70	48
6	23	16458	15904	gil1655860	Orf2 [Borrelia hermsii]	70	54
17	4	2940	3173	gil1255880	F01G12.6 gene product [Caenorhabditis elegans]	70	40
20	8	5470	5237	gil1236921	Var1p [Saccharomyces douglasii]	70	47
23	5	4173	3970	pirS16447/IS1 6447	NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - wheat mitochondrion	70	47
36	3	1270	1653	gnlPIDle1604 37	orfD gene product [Borrelia burgdorferi]	70	50
2	69	65752	63860	gil151932	fructose enzyme II [Rhodobacter capsulatus]	69	42
3	114	99712	98150	gil1303856	YqgI [Bacillus subtilis]	69	46
4	36	25614	24694	gil1663561	orf1; product unknown [Borrelia burgdorferi]	69	46
6	21	14584	14204	gil1616644	P30 [Borrelia burgdorferi]	69	47
12	12	7025	7258	gil150176	protein 69 [Mycoplasma hyorhinis]	69	38
12	14	8414	8587	gil13233	ND6 (AA 1 - 296) [Podospora anserina]	69	26
54	2	1332	2402	gnlPIDle1589 79	orfA gene product [Borrelia burgdorferi]	69	46
2	35	29769	30518	gil473817	'ORF' [Escherichia coli]	68	42
2	79	72330	72980	gil1498049	adenylate kinase [Paracoccus denitrificans]	68	37

Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

2	104	104748	106385	gil1574032	hypothetical [Haemophilus influenzae]	68	42
3	78	68895	68287	gnlPIDle255117	hypothetical protein [Bacillus subtilis]	68	51
3	98	88992	86074	gil927711	D9461.18p; CAI: 0.15 [Saccharomyces cerevisiae]	68	52
3	111	96519	97364	gil1707057	coded for by C. elegans cDNA CEES55F; coded for by C. elegans cDNA yk84a1.3; coded for by C. elegans cDNA yk78g7.3; coded for by C. elegans cDNA yk168g9.5; coded for by C. elegans cDNA yk78g7.5; coded for by C. elegans cDNA yk84a1.5; strong s	68	52
4	56	40648	40046	gil458217	ORF 2 [Borrelia burgdorferi]	68	54
4	57	41916	40678	gil458216	ORF 1 [Borrelia burgdorferi]	68	57
6	24	17296	16520	gil1655859	Orf1 [Borrelia hermsii]	68	43
7	5	2894	3694	gil1655859	Orf1 [Borrelia hermsii]	68	48
29	6	3832	3254	gil458217	ORF 2 [Borrelia burgdorferi]	68	46
72	2	927	1133	gil577175	L8479.4 gene product [Saccharomyces cerevisiae]	68	44
2	57	52752	52558	gil1001264	50S ribosomal protein L33 [Synecocystis sp.]	67	56
3	65	54290	54051	gil710340	ribosomal protein S21 [Myxococcus xanthus]	67	49
3	79	69068	70114	gil460955	TagE [Vibrio cholerae]	67	38
3	81	70653	71150	gil467420	unknown [Bacillus subtilis]	67	42
3	110	94703	96502	gnlPIDle267607	alanyl-tRNA synthetase [Thermus aquaticus thermophilus]	67	51
4	42	30304	31941	bbs1161785	60 kDa antigen [Borrelia coriaceae, C053, ATCC 4338, Peptide, 514 aa] [Borrelia coriaceae]	67	49
12	6	3590	2967	gnlPIDle160437	orfD gene product [Borrelia burgdorferi]	67	41
12	9	5524	6276	gil1655859	Orf1 [Borrelia hermsii]	67	51
12	10	6611	6889	gnlPIDle8903	SERA protein [Plasmodium falciparum]	67	48
17	6	4995	5906	gil1752736	gene required for phosphorylation of oligosaccharides/ has high homology with YJR061w [Saccharomyces cerevisiae]	67	37
34	2	1221	1817	gnlPIDle1589	orfB gene product [Borrelia burgdorferi]	67	47

Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

58	2	1347	796	83	ORF 2 [Borrelia burgdorferi]	67	52
2	33	28572	27751	gil340613	A 'c' was inserted after nt 369 (=nt 10459 in genomic sequence (M10126)) to correct -1 frameshift probably due to gel compression [Leishmania tarentolae]	66	40
2	73	69021	69908	gil153903	methyltransferase (cheR; EC 2.1.1.24) [Salmonella typhimurium]	66	42
2	93	93739	94524	gil45713	P. putida genes rpmH, rnpA, 9k, 60k, 50k, gidA, gidB, uncl and uncB [Pseudomonas putida]	66	41
3	9	6009	6902	gnlPIDle2639	OrfD [Streptococcus pneumoniae]	66	47
4	28	20922	20665	gil471731	vacuolating cytotoxin homolog [Helicobacter pylori]	66	50
4	64	47985	47107	gil1421735	ORF 6 [Borrelia burgdorferi]	66	43
6	13	7227	8591	gil1591045	hypothetical protein (SP:P31466) [Methanococcus jannaschii]	66	48
34	4	2556	3161	gil458218	ORF 3 [Borrelia burgdorferi]	66	42
37	1	982	689	gil974334	non-receptor tyrosine kinase [Dictyostelium discoideum]	66	55
3	77	68191	66395	gil1651216	Pz-peptidase [Bacillus licheniformis]	65	47
3	123	105911	104070	gil1575784	DNA mismatch repair protein [Aquifex pyrophilus]	65	45
6	9	5726	7126	gil1591045	hypothetical protein (SP:P31466) [Methanococcus jannaschii]	65	49
8	9	9684	10325	gnlPIDle2012	ORF-D gene product [Borrelia burgdorferi]	65	48
10	1	3	971	gil1373144	ErpD [Borrelia burgdorferi]	65	47
13	5	3956	3411	gil1209872	REV [Borrelia burgdorferi]	65	47
2	76	70509	71069	pirA005471X	protein-glutamate methyltransferase (EC 3.1.1.61) - Salmonella typhimurium	64	45
3	61	48610	50838	gil1001335	soluble lytic transglycosylase [Synecocystis sp.]	64	42
4	5	3519	3773	gil1263021	M protein [Streptococcus pyogenes]	64	32
4	53	38288	37824	gil1373141	ORF-10 [Borrelia burgdorferi]	64	50

Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

6	10	5985	5824	gil40271	delta-endotoxin CryIG protoxin [Bacillus thuringiensis]	64	30
7	7	7798	4499	gil1041785	rhostry protein [Plasmodium yoelii]	64	35
7	30	19738	19289	gil1209840	2.9-3 ORF-D [Borrelia burgdorferi]	64	46
11	3	1608	2339	gil1652934	hypothetical protein [Synechocystis sp.]	64	30
16	1	537	839	gnlPIDle276380	AARP1 protein [Plasmodium falciparum]	64	44
19	1	308	1177	gil1553115	P35 antigen protein [Borrelia burgdorferi]	64	35
42	3	1928	1788	gil1752736	gene required for phosphorylation of oligosaccharides/ has high homology with YJR061w [Saccharomyces cerevisiae]	64	41
142	1	589	2	gil162142	kinetoplast-associated protein [Trypanosoma cruzi]	64	52
2	3	2837	2592	gnlPIDle236274	ZK287.2 [Caenorhabditis elegans]	63	27
2	15	12750	11320	gil1652577	carboxyl-terminal protease [Synechocystis sp.]	63	49
2	32	27753	26266	spP151891SY E_RHIME	GLUTAMYL-TRNA SYNTHETASE (EC 6.1.1.17) (GLUTAMATE--TRNA LIGASE) (GLURS).	63	48
2	77	71067	72308	gil1041116	TRAB [Plasmodium pPD1]	63	34
3	2	1056	58	gil1098641	Bts1p [Saccharomyces cerevisiae]	63	43
3	82	71398	71237	gil1339938	EC 1.1.99.5 [Mus musculus]	63	47
3	83	72845	71349	gil763191	glycerol 3 phosphate dehydrogenase [Saccharomyces cerevisiae]	63	37
3	85	75552	74773	gil142997	glycerol uptake facilitator [Bacillus subtilis]	63	45
7	6	3747	4304	gnlPIDle201250	ORF-D gene product [Borrelia burgdorferi]	63	40
7	38	24123	24956	gil467330	replicative DNA helicase [Bacillus subtilis]	63	40
11	5	4161	3853	gil1592217	bifunctional protein [Methanococcus jannaschii]	63	38
12	13	9558	7906	gil633167	adenine deaminase [Bacillus subtilis]	63	48
32	1	753	268	gil520783	unknown [Borrelia burgdorferi]	63	42
2	68	63866	62745	gil146722	phosphomannose isomerase [Escherichia coli]	62	45
2	75	69920	70573	gil145524	cheB peptide [Escherichia coli]	62	28

Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

2	95	96334	95492	gil140031	spoJ93 gene product [Bacillus subtilis]	62	36
3	67	57341	55212	gil1574144	single-stranded-DNA-specific exonuclease (recJ) [Haemophilus influenzae]	62	40
3	76	66414	65677	gil1477770	unknown [Helicobacter pylori]	62	37
6	1	1762	104	gil1072419	glcB gene product [Staphylococcus carnosus]	62	43
18	4	4431	5144	gil1591493	glutamine transport ATP-binding protein Q [Methanococcus jannaschii]	62	36
19	8	6743	6976	gil1513302	CigB [Dictyostelium discoideum]	62	56
20	6	4563	4378	bbs144872	Fu=putative serine/threonine kinase [Drosophila melanogaster, Peptide Partial Mutant, 152 aa] [Drosophila melanogaster]	62	37
81	1	56	538	gnlPIDle1539	ORF-A gene product [Borrelia burgdorferi]	62	36
106	2	586	356	gil1151158	repeat organellar protein [Plasmodium chabaudi]	62	43
114	1	138	629	gnlPIDle1539	ORF-A gene product [Borrelia burgdorferi]	62	36
2	117	114352	114032	gil173128	ubiquitin-specific processing protease [Saccharomyces cerevisiae]	61	32
3	55	42737	44236	gil143999	dnaK homologue [Borrelia burgdorferi]	61	41
3	57	44821	46083	gil1653709	lipoprotein NlpD [Synecocystis sp.]	61	50
3	125	110052	109261	gil1303863	YcgP [Bacillus subtilis]	61	45
4	63	47119	46478	gil1421736	ORF 7 [Borrelia burgdorferi]	61	34
7	35	21496	22971	gil1655797	CdsJ [Borrelia burgdorferi]	61	44
8	7	8300	8872	gil458217	ORF 2 [Borrelia burgdorferi]	61	48
12	8	5006	5551	gil458217	ORF 2 [Borrelia burgdorferi]	61	50
14	10	9398	8652	gnlPIDle2012	ORF-D gene product [Borrelia burgdorferi]	61	44
15	12	6206	4377	gil836624	methyltransferase [Bacillus aneurinolyticus]	61	38
16	4	2449	2240	gil1066497	Similar to S. cerevisiae hypothetical protein Ykl012p (Swiss Prot. accession number P33203) and C. elegans hypothetical protein ZK1098.1 (Swiss Prot. accession number P34600) [Saccharomyces	61	38

Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

						cerevisiae]		
29	4	2323	1853	gnlPIDle1604 37	orfD gene product [Borrelia burgdorferi]		61	45
50	2	1374	1156	gnlPIDle2763 80	AARP1 protein [Plasmodium falciparum]		61	52
2	18	14371	15369	gil1573923	prolipoprotein diacylglycerol transferase (lgt) [Haemophilus influenzae]		60	57
3	118	101571	100690	gil1001260	hypothetical protein [Synechocystis sp.]		60	47
3	120	101692	102273	gil1399829	elongation factor P [Synechococcus PCC7942]		60	34
6	32	21869	22162	gil192960	L-type calcium channel alpha-1 [Mus musculus]		60	50
7	37	23373	24101	gil458217	ORF 2 [Borrelia burgdorferi]		60	40
8	11	13570	13851	gil1065989	(pos:5995..5997,aa:Met) [Bacillus subtilis]		60	47
14	5	5327	5091	gil147158	pfs [Escherichia coli]		60	51
15	7	3316	2984	gil153727	M protein [group G streptococcus]		60	36
27	3	2744	3772	pirS40422IS4 0422	hypothetical protein - Staphylococcus aureus		60	31
2	62	57446	58672	gil143002	proton glutamate symport protein [Bacillus caldotenax]		59	34
2	82	74989	74051	gil1651878	regulatory components of sensory transduction system [Synechocystis sp.]		59	38
2	89	92119	91322	gil467425	unknown [Bacillus subtilis]		59	38
2	92	93010	93663	pirA30191IA3 0191	hypothetical protein L - Bacillus subtilis (fragment)		59	39
2	118	115604	114315	gil39269	sigma factor (ntrA) (AA 1-502) [Azotobacter vinelandii]		59	35
4	41	29875	29210	gil1209831	lipoprotein [Borrelia burgdorferi]		59	34
6	4	3323	2058	gil624056	contains 4 ankyrin repeats; similar to D. melanogaster notch protein, Swiss-Prot Accession Number P07027 [Paramecium bursaria Chlorella virus 1]		59	37
6	25	17793	17257	gnlPIDle2012 48	ORF-B gene product [Borrelia burgdorferi]		59	43

Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

6	33	22493	22125	gil153677	enzyme III [Streptococcus mutans]	59	36
10	9	6241	6026	gil1339977	skeletal myosin heavy chain [Thunnus thynnus]	59	40
19	6	5383	5970	gil160299	glutamic acid-rich protein [Plasmodium falciparum]	59	30
25	7	4008	3742	gil1055144	similar to galactoside 3(4)-l-fucosyltransferase [Caenorhabditis elegans]	59	37
59	1	835	8	gil1359436	Mag44 [Dermatophagoides farinae]	59	24
2	27	21414	20317	gil974332	NAD(P)H-dependent dihydroxyacetone-phosphate reductase [Bacillus subtilis]	58	41
3	5	2156	3049	gil1653618	hypothetical protein [Synecocystis sp.]	58	35
3	109	93822	94718	gil790935	fliG [Treponema denticola]	58	31
4	3	2423	3340	gil1553115	P35 antigen protein [Borrelia burgdorferi]	58	39
4	35	24696	24238	gil1663562	orf11: product unknown [Borrelia burgdorferi]	58	32
4	46	35509	34904	gnlPIDle264708	myosin heavy chain [Sus scrofa]	58	31
15	8	3683	3468	gil457336	Pv200 [Plasmodium vivax]	58	32
50	3	1941	1498	gnlPIDle220350	brca2 gene product [Homo sapiens]	58	41
55	1	2322	247	gil1522636	M. jannaschii predicted coding region MJCS02 [Methanococcus jannaschii]	58	32
2	53	50563	50045	gil786163	Ribosomal Protein L10 [Bacillus subtilis]	57	29
3	117	100606	99710	gil1303855	YqgH [Bacillus subtilis]	57	30
6	38	26564	26232	gil1499632	M. jannaschii predicted coding region MJ0809 [Methanococcus jannaschii]	57	40
8	10	12350	13117	gil1553115	P35 antigen protein [Borrelia burgdorferi]	57	33
11	4	3183	2470	pirA45605A45605	mature-parasite-infected erythrocyte surface antigen MESA - Plasmodium falciparum	57	35
14	8	7117	7899	gil1553115	P35 antigen protein [Borrelia burgdorferi]	57	36
15	6	3027	2818	gnlPIDle261409	nuclear/mitotic apparatus protein [Xenopus laevis]	57	30
17	1	336	1178	gil473817	'ORF' [Escherichia coli]	57	31
20	2	1654	1064	gnlPIDle201250	ORF-D gene product [Borrelia burgdorferi]	57	34

Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

2	111	113765	111636	gil148316	NaH-antiporter protein [Enterococcus hirae]	56	32
3	80	70112	70669	gil1372995	OrfH [Borrelia burgdorferi]	56	24
3	116	98976	99212	pirE22845IE2 2845	hypothetical protein 4 - Trypanosoma brucei mitochondrion (SGC6)	56	36
6	26	18732	17791	gil1655797	CdsJ [Borrelia burgdorferi]	56	41
7	21	14706	13510	gil1574247	H. influenzae predicted coding region HI1410 [Haemophilus influenzae]	56	32
11	8	6722	7087	gnlPIDle2428 97	aBIM [Lactococcus lactis]	56	28
53	7	2446	2018	gil1421737	ORF 8 [Borrelia burgdorferi]	56	38
61	2	712	1410	gil583161	albumin binding protein [unidentified]	56	35
2	6	3866	3573	gil290487	50S ribosomal subunit protein L28 [Escherichia coli]	55	37
2	14	11322	10585	gil1303811	YqeU [Bacillus subtilis]	55	33
2	34	28640	29782	gil558266	orf gene product [Wolinnella succinogenes]	55	30
2	71	66669	67415	gil397486	endonuclease G [Bos taurus]	55	33
3	87	75924	76550	gil403984	deoxyguanosine kinase/deoxyadenosine kinase(I) subunit [Lactobacillus acidophilus]	55	38
4	66	48434	48958	gil1100900	70 kDa heat shock protein [Theileria parva]	55	32
140	1	322	68	gil15611	gene 17, tail fiber protein [Bacteriophage T7]	55	38
4	34	24244	23867	gil1663563	orfIII; product unknown [Borrelia burgdorferi]	54	31
5	9	5510	4179	gil1513238	ORFveg132; similar to Caenorhabditis elegans ORF F59B10.1 encoded by EMBL Accession Number Z49132 [Dictyostelium discoideum]	54	25
5	45	27187	25895	gnlPIDle2614 09	nuclear/mitotic apparatus protein [Xenopus laevis]	54	30
7	28	17905	18162	gil36501	C protein [Homo sapiens]	54	41
11	6	4415	5215	gil1707287	putative outer membrane protein [Borrelia burgdorferi]	54	25
19	2	1674	2501	gil392799	G5/D6 ORF [Dictyostelium discoideum]	54	25
29	5	3284	2532	gnlPIDle1589 80	orfC gene product [Borrelia burgdorferi]	54	33
31	3	3328	4137	pirS41649IS4	DNA polymerase - Plasmodium falciparum	54	28

Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

				1649			
32	5	2560	2865	gil499695	bud-emergence protein [Saccharomyces cerevisiae]	54	36
95	1	95	997	gil763227	Rpilp [Saccharomyces cerevisiae]	54	37
2	16	13235	14383	gil1165254	YlxH [Borrelia burgdorferi]	53	33
2	72	68814	68179	gil940842	orf 06111 gene product [Saccharomyces cerevisiae]	53	28
3	3	1032	1646	gil1592021	cell division protein J [Methanococcus jannaschii]	53	32
4	18	14627	14427	gil1039462	vacuolar aspartic proteinase precursor [Candida albicans]	53	35
5	63	34850	34152	gil1699017	ErpB2 [Borrelia burgdorferi]	53	25
10	5	3672	3893	gil398581	XLR related protein [Mus musculus]	53	27
15	17	8485	8925	gnlPIDle2483 24	T07C12.4 [Caenorhabditis elegans]	53	28
25	5	3497	3679	gil1055100	coded for by C. elegans cDNA yk54h9.5; coded for by C. elegans cDNA yk54h9.3; similar to matrin F/G (DNA binding protein, SP:MAFG_RAT, Q00910) [Caenorhabditis elegans]	53	25
29	1	70	291	gil398581	XLR related protein [Mus musculus]	53	27
34	3	1787	2527	gil1655859	Orf1 [Borrelia hermsii]	53	42
2	1	3	1265	gil496254	fibronectin/fibrinogen-binding protein [Streptococcus pyogenes]	52	29
2	110	111638	111276	gil1573287	aspartyl-tRNA synthetase (aspS) [Haemophilus influenzae]	52	35
4	8	5323	6150	gil457146	rhopty protein [Plasmodium yoelii]	52	24
4	44	32562	31999	gil1151158	repeat organellar protein [Plasmodium chabaudi]	52	26
7	29	18485	18808	gnlPIDle2439 27	ORF YGR023w [Saccharomyces cerevisiae]	52	26
25	4	3287	3499	gil500655	YHR146w gene product [Saccharomyces cerevisiae]	52	35
92	2	38	241	gil1236411	NADH dehydrogenase, subunit 5 [Allomyces macrogynus]	52	52
148	2	119	322	gil1236411	NADH dehydrogenase, subunit 5 [Allomyces macrogynus]	52	52
2	120	116131	115577	gil1591434	chromate resistance protein A [Methanococcus	51	29

Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

4	9	6362	7153	gil1553115	[jannaschii]			
10	10	6603	7196	gnlPIDle256393	P35 antigen protein [Borrelia burgdorferi]		51	26
11	12	10333	9422	pirA42771A42771	anti-P.falci-parum antigenic polypeptide [Saimiri sciureus]		51	34
19	7	5919	6179	gil173241	reticulocyte-binding protein I - Plasmodium vivax		51	31
23	1	3	287	gil1498320	ZIP1 protein [Saccharomyces cerevisiae]		51	38
2	105	106383	107126	gil580905	cell wall-associated protease precursor [Bacillus subtilis]		51	25
3	1	1	195	gnlPIDle220201	B. subtilis genes rpmH, rnpA, 50kd, gidA and gidB [Bacillus subtilis]		50	32
3	62	50808	51653	gil882579	rps5 gene product [Plasmodium falciparum]		50	38
3	119	100766	101014	gil1086864	CG Site No. 29739 [Escherichia coli]		50	31
4	32	23555	22992	gil1663565	T03G1.2 gene product [Caenorhabditis elegans]		50	39
5	8	4168	3470	gil49402	orfV, product unknown [Borrelia burgdorferi]		50	36
10	7	5190	4612	gnlPIDle158981	M1.1 protein [Streptococcus pyogenes]		50	27
11	2	1277	504	gil1553115	orfE gene product [Borrelia burgdorferi]		50	28
13	3	1948	1634	gnlPIDle268243	P35 antigen protein [Borrelia burgdorferi]		50	26
92	3	582	941	gnlPIDle201250	p21 [Borrelia afzelii]		50	32
148	1	339	4	gnlPIDle236901	ORF-D gene product [Borrelia burgdorferi]		50	40
28	3	2001	2630	gil499325	unknown [Saccharomyces cerevisiae]		50	34
3	10	6881	7180	gil156218	STARP antigen [Plasmodium falciparum]		49	22
3	75	65683	65066	gil1574476	putative [Caenorhabditis elegans]		48	32
3	112	97006	96743	gil915207	dedA protein (dedA) [Haemophilus influenzae]		48	22
7	23	14743	14970	gil172294	gastric mucin [Sus scrofa]		48	27
					protein-tyrosine phosphatase [Saccharomyces cerevisiae]		48	33

Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

11	11	7980	9293	gil1046137	M. genitalium predicted coding region MG422 [Mycoplasma genitalium]	48	28
28	4	2628	2825	gil1591322	chorismate mutase subunit B [Methanococcus jannaschii]	48	30
2	8	5526	6677	gnlPIDle220245	frameshift [Plasmodium falciparum]	47	27
2	60	55075	55803	gil710551	ankyrin 3 [Mus musculus]	47	29
2	94	94515	95240	gil1592264	type I restriction enzyme [Methanococcus jannaschii]	47	34
4	11	9057	9941	gil1553115	P35 antigen protein [Borrelia burgdorferi]	47	32
2	12	9986	9471	gil1022328	Four tandem repeats of a DNA-binding domain known as the AT-hook are found at the carboxy terminus of CarD. This protein has been purified and found to bind in vitro to a promoter region [Myxococcus xanthus]	46	28
3	89	78904	77324	gil1573271	apolipoprotein N-acyltransferase (cute) [Haemophilus influenzae]	46	32
6	36	24361	25719	gil1592272	ribosomal protein S19 [Methanococcus jannaschii]	46	23
10	13	9895	8816	gil160299	glutamic acid-rich protein [Plasmodium falciparum]	46	21
13	4	3412	3648	gnlPIDle275506	C41G6.i [Caenorhabditis elegans]	46	37
138	1	632	15	gil157006	bicaudalD protein [Drosophila melanogaster]	46	23
3	124	109271	105909	gil1499043	M. jannaschii predicted coding region MJ0263 [Methanococcus jannaschii]	45	23
4	17	14212	15465	pirS30782IS30782	integrin homolog - yeast (Saccharomyces cerevisiae)	45	23
23	4	3950	4852	gnlPIDle236901	unknown [Saccharomyces cerevisiae]	45	27
92	1	258	4	gnlPIDle236901	unknown [Saccharomyces cerevisiae]	45	27
3	90	79020	81044	gnlPIDle236483	F54G8.4 [Caenorhabditis elegans]	44	31
12	7	4075	5019	gil1151158	repeat organellar protein [Plasmodium chabaudi]	44	26

Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

17	3	1735	2142	pirA42771IA4 2771	reticulocyte-binding protein I - Plasmodium vivax	44	26
22	7	4179	2827	gil563812	XCAP-C [Xenopus laevis]	44	20
31	2	1682	2761	gil1438951	cutinase negative acting protein [Fusarium solani f. sp. pisi]	43	23
3	7	4086	5186	gil343962	VAR1 protein [Candida glabrata]	42	25
28	1	110	496	gil157804	laminin B2 chain [Drosophila melanogaster]	42	23
28	5	2889	3833	pirS30782IS3 0782	integrin homolog - yeast (Saccharomyces cerevisiae)	42	18
34	1	209	1234	gil1655797	CdsJ [Borrelia burgdorferi]	42	27
65	3	1035	1415	gil1654220	variable major protein 16 [Borrelia hermsii]	42	34
2	11	9544	8486	gnlPIDle1632 6	MURF2 protein (AA 1-348) [Crithidia fasciculata]	41	26
3	122	104072	103017	gil1151158	repeat organellar protein [Plasmodium chabaudi]	41	20
18	6	5122	6366	gil1591494	M. jannaschii predicted coding region MJ0797 [Methanococcus jannaschii]	40	20
6	6	4662	3964	gil600448	var1 protein (aa 1-339) [Candida utilis]	39	24
4	10	7637	8914	gil1293695	microfilarial sheath protein SHP3 [Litomosoides sigmodontis]	37	19

TABLE 5. *Borrelia burgdorferi* - Coding regions containing to know proteins

Contig ID	Orf ID	Start (nt)	Stop (nt)	match accession	match gene name	percent ident	HSP nt length
2	20	15372	17402	gbIM90084I	<i>Borrelia burgdorferi</i> 22 kD antigen	100	786
2	21	16672	16310	gbIM90084I	<i>Borrelia burgdorferi</i> 22 kD antigen	100	56
2	22	17362	17099	gbIM90084I	<i>Borrelia burgdorferi</i> 22 kD antigen	100	264
2	23	17415	17876	embIX70826IB BLA7	<i>B. burgdorferi</i> gene for lipoprotein	100	57
2	24	18522	17923	embIX70826IB BLA7	<i>B. burgdorferi</i> gene for lipoprotein	100	600
2	25	18606	20009	embIX78708IB BYSC1	<i>B. burgdorferi</i> (ZS7) YSC1-like gene	100	1404
2	26	19981	20295	embIX78708IB BYSC1	<i>B. burgdorferi</i> (ZS7) YSC1-like gene	99	314
2	38	32899	32174	gbIU49938I	<i>Borrelia burgdorferi</i> potential virulence gene cluster membrane proteins BmpC (bmpC) and BmpA (bmpA), BmpB protein (bmpB), putative protein 4, Mg ion transporter MgtE (mgtE), protein kinase C1 inhibitor PKCI (pkci) genes, complete cds	98	130
2	39	33315	32863	gbIU49938I	<i>Borrelia burgdorferi</i> potential virulence gene cluster membrane proteins BmpC (bmpC) and BmpA (bmpA), BmpB protein (bmpB), putative protein 4, Mg ion transporter MgtE (mgtE), protein kinase C1 inhibitor PKCI (pkci) genes, complete cds	100	453
2	40	34718	33333	gbIU49938I	<i>Borrelia burgdorferi</i> potential virulence gene cluster membrane proteins BmpC (bmpC) and BmpA (bmpA), BmpB protein (bmpB), putative protein 4, Mg ion transporter MgtE (mgtE), protein kinase C1 inhibitor PKCI (pkci) genes, complete cds	99	1386
2	41	36211	34751	gbIU49938I	<i>Borrelia burgdorferi</i> potential virulence gene cluster membrane proteins BmpC (bmpC) and BmpA (bmpA), BmpB protein (bmpB), putative protein 4, Mg ion transporter MgtE (mgtE), protein kinase C1 inhibitor PKCI (pkci) genes, complete cds	99	1461
2	42	36899	36288	gbIL24194I	<i>Borrelia burgdorferi</i> immunodominant antigen P39	99	606

Borrelia burgdorferi - Coding regions containing to know proteins

2	43	37335	36811	gblL35050	gene, complete cds	98	457
2	44	38426	37401	gblL24194	Borrelia burgdorferi (clone pB46) membrane lipoprotein A (bmpA) gene, 3' end, membrane lipoprotein (bmpB) gene, 5' end	99	1026
2	45	39595	38462	gblU49938	Borrelia burgdorferi potential virulence gene cluster membrane proteins BmpC (bmpC) and BmpA (bmpA), BmpB protein (bmpB), putative protein 4, Mg ion transporter MgtE (mgtE), protein kinase C1 inhibitor PKCI (pkci) genes, complete cds	99	1134
2	46	40947	39838	gblU35450	Borrelia burgdorferi membrane protein D (bmpD) gene, complete cds	99	1110
2	47	41461	40961	gblU35450	Borrelia burgdorferi membrane protein D (bmpD) gene, complete cds	100	82
2	49	46052	41901	gblL48488	Borrelia burgdorferi RNA polymerase beta subunit (rpoB) gene, complete cds, RNA polymerase beta' subunit (rpoC) gene, 5' end of cds	97	76
2	51	49535	46050	gblL48488	Borrelia burgdorferi RNA polymerase beta subunit (rpoB) gene, complete cds, RNA polymerase beta' subunit (rpoC) gene, 5' end of cds	98	2490
2	83	79470	74977	gblU03396	Borrelia burgdorferi B31 Ala-tRNA (alaT), Ile-tRNA (ileT), 16S rRNA, 23S rRNA (rrlA and rrlB), and 5S rRNA (rrfA and rrfB) genes, complete sequence	97	131
2	84	84351	84620	gblM88330	Borrelia burgdorferi 23S ribosomal RNA gene	100	270
2	85	86923	86066	gblU03396	Borrelia burgdorferi B31 Ala-tRNA (alaT), Ile-tRNA (ileT), 16S rRNA, 23S rRNA (rrlA and rrlB), and 5S rRNA (rrfA and rrfB) genes, complete sequence	95	386
2	86	87637	87041	gblU03396	Borrelia burgdorferi B31 Ala-tRNA (alaT), Ile-tRNA (ileT), 16S rRNA, 23S rRNA (rrlA and rrlB), and 5S rRNA (rrfA and rrfB) genes, complete sequence	99	209

Borrelia burgdorferi - Coding regions containing to know proteins

2	87	88424	88116	gblU03396l	Borrelia burgdorferi B31 Ala-tRNA (alaT), Ile-tRNA (ileT), 16S rRNA, 23S rRNA (rrlA and rrlB), and 5S rRNA (rrfA and rrfB) genes, complete sequence	96	210
2	88	91249	90680	gblU03396l	Borrelia burgdorferi B31 Ala-tRNA (alaT), Ile-tRNA (ileT), 16S rRNA, 23S rRNA (rrlA and rrlB), and 5S rRNA (rrfA and rrfB) genes, complete sequence	100	570
2	96	98846	96393	embZ12165IB BGYRAG	B.burgdorferi gyrA gene encoding DNA gyrase subunit A (partial)	96	289
2	97	100759	98837	gblU04527l	Borrelia burgdorferi 212 DNA gyrase b subunit (gyrB) and ribonuclease P protein component (rnpA) genes, partial cds, DnaA protein (dnaA), DNA polymerase III beta subunit (dnaN), and ribosomal protein L34 (rpmH) genes, complete cds	98	904
2	98	100893	102389	gblU04527l	Borrelia burgdorferi 212 DNA gyrase b subunit (gyrB) and ribonuclease P protein component (rnpA) genes, partial cds, DnaA protein (dnaA), DNA polymerase III beta subunit (dnaN), and ribosomal protein L34 (rpmH) genes, complete cds	100	1497
2	99	102618	103787	gblU04527l	Borrelia burgdorferi 212 DNA gyrase b subunit (gyrB) and ribonuclease P protein component (rnpA) genes, partial cds, DnaA protein (dnaA), DNA polymerase III beta subunit (dnaN), and ribosomal protein L34 (rpmH) genes, complete cds	99	1170
2	100	103786	103607	gblU04527l	Borrelia burgdorferi 212 DNA gyrase b subunit (gyrB) and ribonuclease P protein component (rnpA) genes, partial cds, DnaA protein (dnaA), DNA polymerase III beta subunit (dnaN), and ribosomal protein L34 (rpmH) genes, complete cds	100	180
2	101	103866	104177	gblU04527l	Borrelia burgdorferi 212 DNA gyrase b subunit (gyrB) and ribonuclease P protein component (rnpA) genes, partial cds, DnaA protein (dnaA), DNA polymerase III beta subunit (dnaN), and ribosomal protein L34 (rpmH) genes, complete cds	100	312

Borrelia burgdorferi - Coding regions containing to know proteins

2	102	104254	104424	gblU04527I	ribosomal protein L34 (rpmH) genes, complete cds	100	171
					Borrelia burgdorferi 212 DNA gyrase b subunit (gyrB) and ribonuclease P protein component (rnpA) genes, partial cds, DnaA protein (dnaA), DNA polymerase III beta subunit (dnaN), and ribosomal protein L34 (rpmH) genes, complete cds		
2	103	104393	104764	gblU04527I	Borrelia burgdorferi 212 DNA gyrase b subunit (gyrB) and ribonuclease P protein component (rnpA) genes, partial cds, DnaA protein (dnaA), DNA polymerase III beta subunit (dnaN), and ribosomal protein L34 (rpmH) genes, complete cds	100	148
3	11	7200	8597	gblU43739I	Borrelia burgdorferi fmsmid clone 31, complete sequence	100	1185
3	12	8581	9666	embIX96685IB BCDG	B.burgdorferi cell division genes	99	912
3	13	9664	10767	embIX96685IB BCDG	B.burgdorferi cell division genes	99	1104
3	14	10826	10614	embIX96433IB BFTSWQA	B.burgdorferi ftsW, ftsQ & ftsA genes	100	213
3	15	10797	11546	embIX96433IB BFTSWQA	B.burgdorferi ftsW, ftsQ & ftsA genes	99	750
3	16	11519	12787	gblU43739I	Borrelia burgdorferi fmsmid clone 31, complete sequence	100	1269
3	17	12785	14008	gblU43739I	Borrelia burgdorferi fmsmid clone 31, complete sequence	100	1224
3	18	14006	14701	gblU43739I	Borrelia burgdorferi fmsmid clone 31, complete sequence	100	696
3	19	14699	15655	gblL76303I	Borrelia burgdorferi ftsA gene, 3' end of cds, ftsZ, orf230, smf, hslVU, flgBCE, flIEFGHI, flbABC genes, complete cds	98	712
3	20	15653	16213	gblU43739I	Borrelia burgdorferi fmsmid clone 31, complete sequence	100	561
3	21	16149	17552	embIX96685IB BCDG	B.burgdorferi cell division genes	97	1404

Borrelia burgdorferi - Coding regions containing to know proteins

3	22	17550	17993	gblU43739I	Borrelia burgdorferi fesmid clone 31, complete sequence	100	444
3	23	17996	18475	gblU43739I	Borrelia burgdorferi fesmid clone 31, complete sequence	100	480
3	24	18445	18822	gblL76303I	Borrelia burgdorferi ftsA gene, 3' end of cds, ftsZ, orf230, smf, hslVU, flgBCE, flieFGHI, flbABC genes, complete cds	100	378
3	25	18777	20546	gblL76303I	Borrelia burgdorferi ftsA gene, 3' end of cds, ftsZ, orf230, smf, hslVU, flgBCE, flieFGHI, flbABC genes, complete cds	100	1770
3	26	20544	21596	gblU43739I	Borrelia burgdorferi fesmid clone 31, complete sequence	100	1053
3	27	21575	22531	gblU43739I	Borrelia burgdorferi fesmid clone 31, complete sequence	100	957
3	28	22529	23860	gblL76303I	Borrelia burgdorferi ftsA gene, 3' end of cds, ftsZ, orf230, smf, hslVU, flgBCE, flieFGHI, flbABC genes, complete cds	99	1332
3	29	23836	24288	gblL76303I	Borrelia burgdorferi ftsA gene, 3' end of cds, ftsZ, orf230, smf, hslVU, flgBCE, flieFGHI, flbABC genes, complete cds	99	453
3	30	24269	24898	gblU43739I	Borrelia burgdorferi fesmid clone 31, complete sequence	100	630
3	31	24864	26084	gblL76303I	Borrelia burgdorferi ftsA gene, 3' end of cds, ftsZ, orf230, smf, hslVU, flgBCE, flieFGHI, flbABC genes, complete cds	99	1221
3	32	26095	26541	gblL76303I	Borrelia burgdorferi ftsA gene, 3' end of cds, ftsZ, orf230, smf, hslVU, flgBCE, flieFGHI, flbABC genes, complete cds	100	447
3	33	26525	27874	gblU43739I	Borrelia burgdorferi fesmid clone 31, complete sequence	100	1350
3	34	27891	28121	gblU43739I	Borrelia burgdorferi fesmid clone 31, complete sequence	100	231
3	35	28112	28900	gblU43739I	Borrelia burgdorferi fesmid clone 31, complete sequence	100	789

Borrelia burgdorferi - Coding regions containing to know proteins

3	36	28894	29682	gblU43739I	Borrelia burgdorferi fesmid clone 31, complete sequence	100	789
3	37	29680	30267	gblU43739I	Borrelia burgdorferi fesmid clone 31, complete sequence	100	588
3	38	30302	31363	gblU43739I	Borrelia burgdorferi fesmid clone 31, complete sequence	100	1062
3	39	31403	31750	gblU43739I	Borrelia burgdorferi fesmid clone 31, complete sequence	100	348
3	40	31728	32369	gblU43739I	Borrelia burgdorferi fesmid clone 31, complete sequence	100	642
3	41	32356	33144	gblL75945I	Borrelia burgdorferi flagellar hook protein (figE), flbD, flagellar motor apparatus (motAB), flil, flilM, fliz, flagellar export apparatus (flpQR, flhB), flhF, flbE genes	99	789
3	42	32642	32436	gblL75945I	Borrelia burgdorferi flagellar hook protein (figE), flbD, flagellar motor apparatus (motAB), flil, flilM, fliz, flagellar export apparatus (flpQR, flhB), flhF, flbE genes	100	207
3	43	33129	33416	gblL75945I	Borrelia burgdorferi flagellar hook protein (figE), flbD, flagellar motor apparatus (motAB), flil, flilM, fliz, flagellar export apparatus (flpQR, flhB), flhF, flbE genes	100	288
3	44	33425	34237	gblL75945I	Borrelia burgdorferi flagellar hook protein (figE), flbD, flagellar motor apparatus (motAB), flil, flilM, fliz, flagellar export apparatus (flpQR, flhB), flhF, flbE genes	100	813
3	45	34320	34072	gblL75945I	Borrelia burgdorferi flagellar hook protein (figE), flbD, flagellar motor apparatus (motAB), flil, flilM, fliz, flagellar export apparatus (flpQR, flhB), flhF, flbE genes	100	249
3	46	34222	35355	gblL75945I	Borrelia burgdorferi flagellar hook protein (figE), flbD, flagellar motor apparatus (motAB), flil, flilM, fliz, flagellar export apparatus (flpQR, flhB), flhF, flbE genes	99	1134

Borrelia burgdorferi - Coding regions containing to know proteins

3	47	35349	37457	gblL75945l	Borrelia burgdorferi flagellar hook protein (figE), flbD, flagellar motor apparatus (motAB), flilL, flilM, flilZ, flagellar export apparatus (flpQR, flhB), flhF, flhE genes	100	2109
3	48	37455	38627	gblU43739l	Borrelia burgdorferi fesmid clone 31, complete sequence	100	1173
3	49	38612	39526	gblU43739l	Borrelia burgdorferi fesmid clone 31, complete sequence	99	816
3	50	39765	39421	gblU43739l	Borrelia burgdorferi fesmid clone 31, complete sequence	100	345
3	51	39524	40012	gblU43739l	Borrelia burgdorferi fesmid clone 31, complete sequence	100	489
3	52	39985	41919	gblU43739l	Borrelia burgdorferi fesmid clone 31, complete sequence	100	1935
3	53	41928	42248	gblU43739l	Borrelia burgdorferi fesmid clone 31, complete sequence	100	286
3	58	47505	46090	gblM28682l	B.burgdorferi promoter element DNA	100	78
3	68	57596	60034	gblL77216l	Borrelia burgdorferi (strain B31) protease (lon) gene, complete cds	99	2439
3	69	62374	60023	gblL77216l	Borrelia burgdorferi (strain B31) protease (lon) gene, complete cds	100	274
3	92	82181	83026	gblU35673l	Borrelia burgdorferi OrfR gene, partial cds, and S20, Hbb, OrfH and Rho genes, complete cds	99	542
3	93	83032	83358	gblU35673l	Borrelia burgdorferi OrfR gene, partial cds, and S20, Hbb, OrfH and Rho genes, complete cds	100	327
3	94	83365	83697	gblU48651l	Borrelia burgdorferi P1G histone-like protein HBbu (hbb) gene, complete cds	100	327
3	95	83695	84105	gblU35673l	Borrelia burgdorferi OrfR gene, partial cds, and S20, Hbb, OrfH and Rho genes, complete cds	99	411
3	96	84167	85732	gblU35673l	Borrelia burgdorferi OrfR gene, partial cds, and S20, Hbb, OrfH and Rho genes, complete cds	99	1566
3	97	85778	86038	gblU35673l	Borrelia burgdorferi OrfR gene, partial cds, and S20, Hbb, OrfH and Rho genes, complete cds	100	106

Borrelia burgdorferi - Coding regions containing to know proteins

4	2	1935	1147	gbU611421	Borrelia burgdorferi outer membrane porin protein Oms28 precursor (oms28) gene, complete cds	99	789
4	12	10037	11002	gbU594871	Borrelia burgdorferi P35 antigen protein gene, and 7.5 kDa lipoprotein gene, complete cds	100	966
4	13	11365	11153	gbU598591	Borrelia burgdorferi strain B31 6.6 kDa lipoprotein gene, complete cds	100	213
4	14	11577	12230	gbU594871	Borrelia burgdorferi P35 antigen protein gene, and 7.5 kDa lipoprotein gene, complete cds	100	373
4	15	12578	13414	gbM852161	Borrelia burgdorferi 27kD protein antigen gene (p27), complete cds	78	370
4	16	13511	13753	gbU224511	Borrelia burgdorferi 49kb linear plasmid small 12kDa lipoprotein gene, complete cds	99	243
4	23	18668	17793	gbL314271	Borrelia burgdorferi (clone BbK2.1) phoA fusion protein gene, partial cds	100	169
4	49	36694	36347	gbU758671	Borrelia burgdorferi decorin binding protein B (DbpB) gene, complete cds	99	329
4	50	36351	36929	gbU758671	Borrelia burgdorferi decorin binding protein B (DbpB) gene, complete cds	99	564
4	51	36838	36692	gbU758671	Borrelia burgdorferi decorin binding protein B (DbpB) gene, complete cds	100	147
4	52	37001	37624	gbU758661	Borrelia burgdorferi decorin binding protein A (DbpA) gene, complete cds	93	533
4	55	40073	39318	gbU425991	Borrelia burgdorferi plasmid cp18, OspE (ospE) gene, partial cds	69	731
4	58	43349	42447	gbL231371	Borrelia burgdorferi (27985CT2) OspA gene, 3' end and OspB gene, complete cds	99	903
4	59	44228	43347	embIA040091A04009	B.burgdorferi OspA gene and 5'flanking region	100	882
4	60	44792	44403	gbL197021	Borrelia burgdorferi outer surface protein A (ospA) and outer surface protein B (ospB) genes, complete cds	88	370
4	61	45198	44758	gbL197021	Borrelia burgdorferi outer surface protein A (ospA) and outer surface protein B (ospB) genes, complete	89	375

Borrelia burgdorferi - Coding regions containing to know proteins

4	62	46440	45382	gbL197021	cds	Borrelia burgdorferi outer surface protein A (ospA) and outer surface protein B (ospB) genes, complete cds	85	622
4	67	49363	50622	gbL340161	cds	Borrelia burgdorferi (clone 8) S1 gene, complete cds	99	1260
4	68	50708	51580	gbL340171	cds	Borrelia burgdorferi (clone 8) S2 gene, complete cds	99	837
4	69	52203	51655	gbL314231	cds	Borrelia burgdorferi (clone BbK2.14) phoA fusion protein gene, partial cds	99	292
4	70	53018	52488	gbL411511	cds	Borrelia burgdorferi (clone 8) s3 gene, complete cds	99	297
5	1	535	71	gbU606421	cds	Borrelia burgdorferi plasmid cp32-4, sequence at position 4-6kb	91	465
5	2	1526	546	gbU606421	cds	Borrelia burgdorferi plasmid cp32-4, sequence at position 4-6kb	89	374
5	4	2395	2129	gbL314251	cds	Borrelia burgdorferi (clone BbK3.168) phoA fusion protein gene, partial cds	98	135
5	11	6832	6542	gbS667081	cds	{target sequence for detection of Lyme disease agent} [Borrelia burgdorferi, B31, 30-kb circular plasmid pIP87, Plasmid, 416 nt]	97	290
5	12	7422	6817	gbU449141	cds	Borrelia burgdorferi plasmid cp32-2, erpC and erpD genes, complete cds	87	595
5	13	8167	7565	gbU449141	cds	Borrelia burgdorferi plasmid cp32-2, erpC and erpD genes, complete cds	84	147
5	14	9408	8284	gbU449141	cds	Borrelia burgdorferi plasmid cp32-2, erpC and erpD genes, complete cds	72	568
5	15	10122	9427	gbU306171	cds	Borrelia burgdorferi BbK2.11 (bbk2.10), complete cds	93	560
5	16	10533	11324	gbU449121	cds	Borrelia burgdorferi plasmid cp32-1, erpA and erpB genes, complete cds	93	790
5	17	11590	11330	gbU449131	cds	Borrelia burgdorferi plasmid cp32-4, erpH gene, complete cds	95	261

Borrelia burgdorferi - Coding regions containing to know proteins

5	18	11761	11588	gbU42599I	Borrelia burgdorferi plasmid cp18, OspE (ospE) gene, partial cds	96	173
5	19	13256	11808	gbU42599I	Borrelia burgdorferi plasmid cp18, OspE (ospE) gene, partial cds	95	1431
5	20	14187	13636	embIX87201IB BBRGABCD	B. burgdorferi plasmid, orfA, B, C, D, E, & F genes, clone pOMB14 and pOMB17	100	552
5	21	14727	14185	embIX87201IB BBRGABCD	B. burgdorferi plasmid, orfA, B, C, D, E, & F genes, clone pOMB14 and pOMB17	100	511
5	22	15588	14788	embIX87201IB BBRGABCD	B. burgdorferi plasmid, orfA, B, C, D, E, & F genes, clone pOMB14 and pOMB17	99	801
5	23	16097	15519	embIX87201IB BBRGABCD	B. burgdorferi plasmid, orfA, B, C, D, E, & F genes, clone pOMB14 and pOMB17	98	579
5	24	17276	16158	embIX87201IB BBRGABCD	B. burgdorferi plasmid, orfA, B, C, D, E, & F genes, clone pOMB14 and pOMB17	94	1075
5	25	17558	18526	gbU45425I	Borrelia burgdorferi 2.9-5 locus, ORF-A-D, REP+, REP-, and lipoprotein (LP) genes, complete cds	86	927
5	26	19040	18564	gbU45422I	Borrelia burgdorferi 2.9-2 locus, ORF-C gene, partial cds, ORF-D, REP+, REP-, and lipoprotein (LP) genes, complete cds	89	379
5	27	19712	19116	gbU45421I	Borrelia burgdorferi 2.9-1 locus, ORF 5-8, ORF-A-D, REP+, REP-, and lipoprotein (LP) genes, complete cds	85	596
5	28	20164	19775	gbU45421I	Borrelia burgdorferi 2.9-1 locus, ORF 5-8, ORF-A-D, REP+, REP-, and lipoprotein (LP) genes, complete cds	97	390
5	29	20504	20121	gbU45426I	Borrelia burgdorferi 2.9-6 locus, ORF-A-D genes, complete cds and REP+ gene, partial cds	99	384
5	30	20799	20446	gbU96714I	Borrelia burgdorferi B31 BlyA (blyA) and BlyB (blyB) genes, complete cds	99	354
5	31	21006	20797	gbU45426I	Borrelia burgdorferi 2.9-6 locus, ORF-A-D genes, complete cds and REP+ gene, partial cds	97	210
5	32	21903	21076	gbU96714I	Borrelia burgdorferi B31 BlyA (blyA) and BlyB	95	440

Borrelia burgdorferi - Coding regions containing to know proteins

5	33	21470	21625	gbU96714I	(blyB) genes, complete cds			
					Borrelia burgdorferi B31 BlyA (blyA) and BlyB (blyB) genes, complete cds	94	151	
5	34	22518	22051	gbU45421I	Borrelia burgdorferi 2.9-1 locus, ORF 5-8, ORF-A-D, REP+, REP-, and lipoprotein (LP) genes, complete cds	90	467	
5	35	22806	22516	gbU45421I	Borrelia burgdorferi 2.9-1 locus, ORF 5-8, ORF-A-D, REP+, REP-, and lipoprotein (LP) genes, complete cds	93	286	
5	36	23082	22840	gbU45421I	Borrelia burgdorferi 2.9-1 locus, ORF 5-8, ORF-A-D, REP+, REP-, and lipoprotein (LP) genes, complete cds	95	242	
5	37	23397	23080	gbU45421I	Borrelia burgdorferi 2.9-1 locus, ORF 5-8, ORF-A-D, REP+, REP-, and lipoprotein (LP) genes, complete cds	96	317	
5	38	23768	23388	gbU45421I	Borrelia burgdorferi 2.9-1 locus, ORF 5-8, ORF-A-D, REP+, REP-, and lipoprotein (LP) genes, complete cds	95	381	
5	39	24331	23750	gbU45421I	Borrelia burgdorferi 2.9-1 locus, ORF 5-8, ORF-A-D, REP+, REP-, and lipoprotein (LP) genes, complete cds	90	495	
5	51	29986	29417	gbU60642I	Borrelia burgdorferi plasmid cp32-4, sequence at position 4-6kb	97	300	
5	52	30414	29980	gbU60642I	Borrelia burgdorferi plasmid cp32-4, sequence at position 4-6kb	99	435	
5	53	30803	30357	gbU60642I	Borrelia burgdorferi plasmid cp32-4, sequence at position 4-6kb	97	447	
5	54	31204	30740	gbU60642I	Borrelia burgdorferi plasmid cp32-4, sequence at position 4-6kb	96	465	
5	55	31775	31215	gbU60642I	Borrelia burgdorferi plasmid cp32-4, sequence at position 4-6kb	98	374	
5	59	33577	32804	gbL31425I	Borrelia burgdorferi (clone BbK3.168) phoA fusion protein gene, partial cds	87	135	

Borrelia burgdorferi - Coding regions containing to know proteins

6	16	9678	9022	gbU018941	Borrelia burgdorferi B31 outer surface protein C (ospC) gene, complete cds	100	657
6	17	9836	11425	gbL258831	Borrelia burgdorferi 26 kb plasmid GMP synthetase (guaA) gene, complete cds	98	1590
6	18	11435	12664	gbU133721	Borrelia burgdorferi 26 kb plasmid IMP dehydrogenase (guaB) gene, partial cds	100	1212
6	19	12195	11686	gbU133721	Borrelia burgdorferi 26 kb plasmid IMP dehydrogenase (guaB) gene, partial cds	100	510
7	1	695	3	gbU855881	Borrelia burgdorferi transposase-like protein (tra) gene, partial cds	99	693
7	2	1081	677	gbU855881	Borrelia burgdorferi transposase-like protein (tra) gene, partial cds	98	375
7	39	25041	25847	gbU454231	Borrelia burgdorferi 2.9-3 locus, ORF-C gene, partial cds, ORF-D, REP+, and lipoprotein (LP) genes, complete cds	77	437
8	2	1420	746	gbU454241	Borrelia burgdorferi 2.9-4 locus, ORF-C gene, partial cds, ORF-D, REP+, and lipoprotein (LP) genes, complete cds	80	193
8	12	14287	14087	gbU843961	Borrelia burgdorferi 16 kb plasmid DNA fragment	95	140
8	17	18352	17876	gbU855881	Borrelia burgdorferi transposase-like protein (tra) gene, partial cds	96	362
9	1	2815	2507	gbU434141	Borrelia burgdorferi linear plasmid lp16 DNA, complete sequence	100	309
9	2	3522	2767	gbU434141	Borrelia burgdorferi linear plasmid lp16 DNA, complete sequence	99	756
9	3	5188	5862	gbU434141	Borrelia burgdorferi linear plasmid lp16 DNA, complete sequence	100	675
9	4	6809	7255	gbU434141	Borrelia burgdorferi linear plasmid lp16 DNA, complete sequence	100	447
9	5	8621	7467	gbU434141	Borrelia burgdorferi linear plasmid lp16 DNA, complete sequence	100	1155
9	6	9079	8735	gbU434141	Borrelia burgdorferi linear plasmid lp16 DNA, complete sequence	100	345

Borrelia burgdorferi - Coding regions containing to know proteins

9	7	10224	9214	gbU43414I	Borrelia burgdorferi linear plasmid Ip16 DNA, complete sequence	100	911
9	8	10370	10972	gbU43414I	Borrelia burgdorferi linear plasmid Ip16 DNA, complete sequence	100	603
9	9	11844	11107	gbU43414I	Borrelia burgdorferi linear plasmid Ip16 DNA, complete sequence	100	738
9	10	13299	13027	gbU43414I	Borrelia burgdorferi linear plasmid Ip16 DNA, complete sequence	99	273
9	11	13612	13241	gbU43414I	Borrelia burgdorferi linear plasmid Ip16 DNA, complete sequence	99	372
10	2	2164	1604	gbU45422I	Borrelia burgdorferi 2.9-2 locus, ORF-C gene, partial cds, ORF-D, REP+, REP-, and lipoprotein (LP) genes, complete cds	78	278
10	3	2686	2886	gbU12332I	Borrelia burgdorferi 16 kb plasmid hypothetical protein gene, complete cds	97	143
13	1	3	842	gbU03641I	Borrelia burgdorferi Ip21 circular plasmid, complete sequence	91	290
13	2	1525	983	gbL16625I	Borrelia burgdorferi exported neurotoxin-like protein gene, complete cds	99	531
13	6	4098	4901	gbU03641I	Borrelia burgdorferi Ip21 circular plasmid, complete sequence	86	713
13	7	4691	4467	gbU03641I	Borrelia burgdorferi Ip21 circular plasmid, complete sequence	88	224
13	8	6348	5041	gbU42599I	Borrelia burgdorferi plasmid cp18, OspE (ospE) gene, partial cds	82	1202
13	9	6673	7788	embX87127IB BPBRGEA	B burgdorferi repeated DNA element, 30.5 kb circular plasmid copy	81	519
13	10	7786	8355	gbU03641I	Borrelia burgdorferi Ip21 circular plasmid, complete sequence	78	414
13	11	8393	8968	gbU03641I	Borrelia burgdorferi Ip21 circular plasmid, complete sequence	84	576
13	12	9290	9544	gbU03641I	Borrelia burgdorferi Ip21 circular plasmid, complete sequence	91	210

Borrelia burgdorferi - Coding regions containing to know proteins

14	6	5768	6217	gblL316161	Borrelia burgdorferi protein p23 gene, complete cds	89	396
14	7	6126	6671	gblL316161	Borrelia burgdorferi protein p23 gene, complete cds	85	242
16	5	3660	2854	gblM974521	Borrelia burgdorferi outer surface protein D (ospD) gene, complete cds	100	807
19	3	3136	3657	gblL411511	Borrelia burgdorferi (clone 8) s3 gene, complete cds	77	267
21	1	849	4	gblU609631	Borrelia burgdorferi plasmid cp32-1 PCR target site, partial sequence	95	296
21	2	1427	834	gblU449141	Borrelia burgdorferi plasmid cp32-2, erpC and erpD genes, complete cds	93	594
21	3	2168	1581	gblU449141	Borrelia burgdorferi plasmid cp32-2, erpC and erpD genes, complete cds	83	130
21	4	2946	2257	gblU809561	Borrelia burgdorferi strain 297CH putative outer membrane protein (ospF) gene, complete cds	91	350
21	5	3794	2964	gblU449131	Borrelia burgdorferi plasmid cp32-4, erpH gene, complete cds	100	401
21	6	4334	5143	gblU449131	Borrelia burgdorferi plasmid cp32-4, erpH gene, complete cds	99	413
21	7	5362	5183	gblU449131	Borrelia burgdorferi plasmid cp32-4, erpH gene, complete cds	91	180
21	8	5581	5360	gblU425991	Borrelia burgdorferi plasmid cp18, OspE (ospE) gene, partial cds	97	221
22	1	306	4	gblU454211	Borrelia burgdorferi 2.9-1 locus, ORF 5-8, ORF-A-D, REP+, REP-, and lipoprotein (LP) genes, complete cds	95	303
22	2	664	317	gblU454211	Borrelia burgdorferi 2.9-1 locus, ORF 5-8, ORF-A-D, REP+, REP-, and lipoprotein (LP) genes, complete cds	97	336
22	3	1230	658	gblU454211	Borrelia burgdorferi 2.9-1 locus, ORF 5-8, ORF-A-D, REP+, REP-, and lipoprotein (LP) genes, complete cds	89	406
24	1	69	4058	gblU764061	Borrelia burgdorferi putative vls recombination cassettes Vls2-Vls16b (vls) gene, complete	97	2305

Borrelia burgdorferi - Coding regions containing to know proteins .

						sequence		
24	2	4056	5108	gblU76406l		Borrelia burgdorferi putative vls recombination cassettes Vls2-Vls16b (vls) gene, complete sequence	94	750
25	1	383	760	gblU43414l		Borrelia burgdorferi linear plasmid lp16 DNA, complete sequence	100	378
25	2	1333	1536	gblU43414l		Borrelia burgdorferi linear plasmid lp16 DNA, complete sequence	100	204
26	1	684	82	embIX87127lB BPBRGEA		B. burgdorferi repeated DNA element, 30.5 kb circular plasmid copy	96	603
26	2	903	682	embIX87127lB BPBRGEA		B. burgdorferi repeated DNA element, 30.5 kb circular plasmid copy	96	221
26	4	2181	2573	gblAF000270l		Borrelia burgdorferi strain B31 2.9-like locus, OrfC, OrfD, Rev (rev), lipoprotein (LP), and 36 kDa-like orf2 genes, complete cds, and 36 kDa-like orf1 gene, partial cds	94	362
26	5	3073	2621	gblU45427l		Borrelia burgdorferi 2.9-7 locus, ORF-A-D, REV, and lipoprotein (LPA and LPB) genes, complete cds	80	220
26	6	3745	3149	gblU45423l		Borrelia burgdorferi 2.9-3 locus, ORF-C gene, partial cds, ORF-D, REP+, REP-, and lipoprotein (LP) genes, complete cds	87	478
26	8	4663	4355	gblU45424l		Borrelia burgdorferi 2.9-4 locus, ORF-C gene, partial cds, ORF-D, REP+, REP-, and lipoprotein (LP) genes, complete cds	98	309
27	1	997	434	gblL31615l		Borrelia burgdorferi (clone BbK2.5-6) unknown protein gene, complete cds	96	219
27	2	1395	2258	gblL31616l		Borrelia burgdorferi protein p23 gene, complete cds	98	610
30	1	252	686	embIX87127lB BPBRGEA		B. burgdorferi repeated DNA element, 30.5 kb circular plasmid copy	97	419
30	2	760	1545	embIX87127lB BPBRGEA		B. burgdorferi repeated DNA element, 30.5 kb circular plasmid copy	100	786
30	3	1543	2157	embIX87127lB		B. burgdorferi repeated DNA element, 30.5 kb	100	615

Borrelia burgdorferi - Coding regions containing to know proteins

30	4	2158	BPBRGEA	circular plasmid copy			
		2802	embIX87127IB	B.burgdorferi repeated DNA element, 30.5 kb	100	645	
30	5	3247	BPBRGEA	circular plasmid copy			
		4230	gblU42599I	Borrelia burgdorferi plasmid cp18, OspE (ospE) gene, partial cds	95	976	
33	1	450	gblU72996I	Borrelia burgdorferi plasmid cp32-5, erpI gene, complete cds	100	546	
33	2	1008	gblU78764I	Borrelia burgdorferi plasmid cp32-1, erpA and erpB2 genes, complete cds	100	1152	
33	3	2253	gblU44914I	Borrelia burgdorferi plasmid cp32-2, erpC and erpD genes, complete cds	98	379	
33	4	3050	gblU44914I	Borrelia burgdorferi plasmid cp32-2, erpC and erpD genes, complete cds	93	577	
35	1	3	gblU03396I	Borrelia burgdorferi B31 Ala-tRNA (alaT), Ile-tRNA (ileT), 16S rRNA, 23S rRNA (rrlA and rrlB), and 5S rRNA (rrfA and rrfB) genes, complete sequence	91	174	
35	2	976	gblM88330I	Borrelia burgdorferi 23S ribosomal RNA gene	100	240	
36	1	1	embIX87201IB	B.burgdorferi plasmid, orfA, B, C, D, E, & F genes, clone pOMB14 and pOMB17	77	159	
38	1	672	BBRGABCD				
		28	gblU44914I	Borrelia burgdorferi plasmid cp32-2, erpC and erpD genes, complete cds	92	571	
38	2	850	gblU42598I	Borrelia burgdorferi plasmid cp32-3, ErpG (erpG) and BapA (bapA) genes, complete cds	100	133	
38	3	1516	embIX82409IB	B.burgdorferi ospG and bapA genes	100	534	
			BOSPG				
38	4	2200	embIX82409IB	B.burgdorferi ospG and bapA genes	100	597	
			BOSPG				
38	5	2602	gblU42598I	Borrelia burgdorferi plasmid cp32-3, ErpG (erpG) and BapA (bapA) genes, complete cds	99	529	
39	1	967	embIX87202IB	B.burgdorferi plasmid, orfA, B, C, D, E, & G genes, clone pOMB10	97	170	
			BBRGBCDE				
39	2	1505	embIX87202IB	B.burgdorferi plasmid, orfA, B, C, D, E, & G	89	176	

Borrelia burgdorferi - Coding regions containing to know proteins

39	3	2353	BBRGBCDE	genes, clone pOMB10			
39	4	2574	embIX87201IB BBRGABCD	Borrelia burgdorferi plasmid cp18, OspE (ospE) gene, partial cds	91		137
39	5	2874	embIX87127IB BPBRGEA	B.burgdorferi plasmid, orfA, B, C, D, E, & F genes, clone pOMB14 and pOMB17	94		291
39	6	3028	embIX87127IB BPBRGEA	B.burgdorferi repeated DNA element, 30.5 kb circular plasmid copy	91		284
40	1	596	embIX87127IB BPBRGEA	B.burgdorferi repeated DNA element, 30.5 kb circular plasmid copy	93		168
40	2	1753	575 gblU76406l	Borrelia burgdorferi putative vls recombination cassettes Vls2-Vls16b (vls) gene, complete sequence	100		465
40	3	3000	1732 gblU76406l	Borrelia burgdorferi putative vls recombination cassettes Vls2-Vls16b (vls) gene, complete sequence	99		1269
41	1	1	411 embIX87201IB BBRGABCD	B.burgdorferi plasmid, orfA, B, C, D, E, & F genes, clone pOMB14 and pOMB17	99		411
41	2	342	1127 embIX87201IB BBRGABCD	B.burgdorferi plasmid, orfA, B, C, D, E, & F genes, clone pOMB14 and pOMB17	80		785
41	3	1172	1747 embIX87201IB BBRGABCD	B.burgdorferi plasmid, orfA, B, C, D, E, & F genes, clone pOMB14 and pOMB17	80		572
41	4	1745	2338 gblU42599l	Borrelia burgdorferi plasmid cp18, OspE (ospE) gene, partial cds	65		571
42	2	1133	1384 gblU85588l	Borrelia burgdorferi transposase-like protein (tra) gene, partial cds	93		236
43	1	360	4 embIX87127IB BPBRGEA	B.burgdorferi repeated DNA element, 30.5 kb circular plasmid copy	96		356
43	2	635	1741 gblAF000270l	Borrelia burgdorferi strain B31 2.9-like locus, OrfC, OrfD, Rev (rev), lipoprotein (LP), and 36 kDa-like orf2 genes, complete cds, and 36 kDa-like	90		392

Borrelia burgdorferi - Coding regions containing to know proteins

43	3	2242	1784	gblU45423l	orfI gene, partial cds		
43	4	2860	2318	gblU45421l	Borrelia burgdorferi 2.9-3 locus, ORF-C gene, partial cds, ORF-D, REP+, REP-, and lipoprotein (LP) genes, complete cds	85	421
44	1	1158	178	gblU60642l	Borrelia burgdorferi 2.9-1 locus, ORF 5-8, ORF-A-D, REP+, REP-, and lipoprotein (LP) genes, complete cds	95	259
44	3	2531	1761	gblL31425l	Borrelia burgdorferi plasmid cp32-4, sequence at position 4-6kb	89	374
45	1	287	3	gblU78764l	Borrelia burgdorferi (clone BbK3.168) phoA fusion protein gene, partial cds	99	135
45	3	2037	1453	gblL13924l	Borrelia burgdorferi plasmid cp32-1, erpA and erpB2 genes, complete cds	84	153
45	4	2663	2893	gblU44912l	Borrelia burgdorferi outer surface protein E (OspE) gene, complete cds	90	386
46	1	174	338	gblU42599l	Borrelia burgdorferi plasmid cp32-1, erpA and erpB genes, complete cds	90	230
46	2	259	966	gblU42599l	Borrelia burgdorferi plasmid cp18, OspE (ospE) gene, partial cds	96	91
46	3	964	1527	gblU42599l	Borrelia burgdorferi plasmid cp18, OspE (ospE) gene, partial cds	100	692
46	4	1509	2111	gblU42599l	Borrelia burgdorferi plasmid cp18, OspE (ospE) gene, partial cds	100	564
46	5	2537	2851	embIX87201lB BBRGABCD	Borrelia burgdorferi plasmid, orfA, B, C, D, E, & F genes, clone pOMB14 and pOMB17	99	603
47	1	2	526	gblU45425l	Borrelia burgdorferi 2.9-5 locus, ORF-A-D, REP+, REP-, and lipoprotein (LP) genes, complete cds	98	315
47	2	1245	724	gblU45424l	Borrelia burgdorferi 2.9-4 locus, ORF-C gene, partial cds, ORF-D, REP+, REP-, and lipoprotein (LP) genes, complete cds	95	525
47						94	483

Borrelia burgdorferi - Coding regions containing to know proteins

47	3	1971	1321	gb U45424	Borrelia burgdorferi 2.9-4 locus, ORF-C gene, partial cds, ORF-D, REP+, REP-, and lipoprotein (LP) genes, complete cds	89	651
48	1	363	25	gb U44914	Borrelia burgdorferi plasmid cp32-2, erpC and erpD genes, complete cds	87	327
48	2	412	1182	gb U72997	Borrelia burgdorferi plasmid cp32-6, erpK gene, complete cds	100	91
48	3	2047	1244	gb U72997	Borrelia burgdorferi plasmid cp32-6, erpK gene, complete cds	99	804
49	1	713	18	gb U76406	Borrelia burgdorferi putative vls recombination cassettes Vls2-Vls16b (vls) gene, complete sequence	99	606
49	2	2308	704	gb U76406	Borrelia burgdorferi putative vls recombination cassettes Vls2-Vls16b (vls) gene, complete sequence	98	1596
51	1	613	2	gb U42599	Borrelia burgdorferi plasmid cp18, OspE (ospE) gene, partial cds	99	612
51	3	2203	2487	gb U44914	Borrelia burgdorferi plasmid cp32-2, erpC and erpD genes, complete cds	86	269
52	1	3	236	emb X87202 B BBRGBCDE	B. burgdorferi plasmid, orfA, B, C, D, E, & G genes, clone pOMB10	94	146
52	2	179	319	emb X87201 B BBRGABCD	B. burgdorferi plasmid, orfA, B, C, D, E, & F genes, clone pOMB14 and pOMB17	94	140
52	3	250	1050	gb U42599	Borrelia burgdorferi plasmid cp18, OspE (ospE) gene, partial cds	86	146
52	6	1650	2201	gb U42599	Borrelia burgdorferi plasmid cp18, OspE (ospE) gene, partial cds	81	422
53	1	93	581	gb AF000270	Borrelia burgdorferi strain B31 2.9-like locus, OrfC, OrfD, Rev (rev), lipoprotein (LP), and 36 kDa-like orf2 genes, complete cds, and 36 kDa-like orf1 gene, partial cds	99	489
53	2	883	719	gb AF000270	Borrelia burgdorferi strain B31 2.9-like locus, OrfC, OrfD, Rev (rev), lipoprotein (LP), and 36 kDa-like orf2 genes, complete cds, and 36 kDa-like	100	101

Borrelia burgdorferi - Coding regions containing to know proteins

53	3	1107	811	gblAF000270	orf1 gene, partial cds	orf1 gene, partial cds	100	289
53	4	1447	1064	gblAF000270	Borrelia burgdorferi strain B31 2.9-like locus, OrfC, OrfD, Rev (rev), lipoprotein (LP), and 36 kDa-like orf2 genes, complete cds, and 36 kDa-like orf1 gene, partial cds	Borrelia burgdorferi strain B31 2.9-like locus, OrfC, OrfD, Rev (rev), lipoprotein (LP), and 36 kDa-like orf2 genes, complete cds, and 36 kDa-like orf1 gene, partial cds	96	381
53	5	1742	1380	gblU45427	Borrelia burgdorferi 2.9-7 locus, ORF-A-D, REV, and lipoprotein (LPA and LPB) genes, complete cds	Borrelia burgdorferi 2.9-7 locus, ORF-A-D, REV, and lipoprotein (LPA and LPB) genes, complete cds	93	362
53	6	1949	1740	gblU45426	Borrelia burgdorferi 2.9-6 locus, ORF-A-D genes, complete cds and REP+ gene, partial cds	Borrelia burgdorferi 2.9-6 locus, ORF-A-D genes, complete cds and REP+ gene, partial cds	98	210
57	1	3	434	gblU45422	Borrelia burgdorferi 2.9-2 locus, ORF-C gene, partial cds, ORF-D, REP+, REP-, and lipoprotein (LP) genes, complete cds	Borrelia burgdorferi 2.9-2 locus, ORF-C gene, partial cds, ORF-D, REP+, REP-, and lipoprotein (LP) genes, complete cds	92	326
57	2	1580	471	gblAF000270	Borrelia burgdorferi strain B31 2.9-like locus, OrfC, OrfD, Rev (rev), lipoprotein (LP), and 36 kDa-like orf2 genes, complete cds, and 36 kDa-like orf1 gene, partial cds	Borrelia burgdorferi strain B31 2.9-like locus, OrfC, OrfD, Rev (rev), lipoprotein (LP), and 36 kDa-like orf2 genes, complete cds, and 36 kDa-like orf1 gene, partial cds	98	362
57	3	1837	2109	embIX87127/B BPBRGEA	B. burgdorferi repeated DNA element, 30.5 kb circular plasmid copy	B. burgdorferi repeated DNA element, 30.5 kb circular plasmid copy	84	246
58	4	1573	1800	gblL31425	Borrelia burgdorferi (clone BbK3.168) phoA fusion protein gene, partial cds	Borrelia burgdorferi (clone BbK3.168) phoA fusion protein gene, partial cds	90	118
60	1	668	111	embIX87201/B BBRGABCD	B. burgdorferi plasmid, orfA, B, C, D, E, & F genes, clone pOMB14 and pOMB17	B. burgdorferi plasmid, orfA, B, C, D, E, & F genes, clone pOMB14 and pOMB17	75	519
60	2	1479	694	embIX87127/B BPBRGEA	B. burgdorferi repeated DNA element, 30.5 kb circular plasmid copy	B. burgdorferi repeated DNA element, 30.5 kb circular plasmid copy	72	786
60	3	1907	1410	embIX87201/B BBRGABCD	B. burgdorferi plasmid, orfA, B, C, D, E, & F genes, clone pOMB14 and pOMB17	B. burgdorferi plasmid, orfA, B, C, D, E, & F genes, clone pOMB14 and pOMB17	95	498
62	1	284	3	embIX87201/B BBRGABCD	B. burgdorferi plasmid, orfA, B, C, D, E, & F genes, clone pOMB14 and pOMB17	B. burgdorferi plasmid, orfA, B, C, D, E, & F genes, clone pOMB14 and pOMB17	79	260
62	2	878	282	embIX87202/B	B. burgdorferi plasmid, orfA, B, C, D, E, & G	B. burgdorferi plasmid, orfA, B, C, D, E, & G	74	501

Borrelia burgdorferi - Coding regions containing to know proteins

				BBRGBCDE	genes, clone pOMB10		
62	3	1704	910	gblU42599	Borrelia burgdorferi plasmid cp18, OspE (ospE) gene, partial cds	78	351
64	1	563	54	gblU43414	Borrelia burgdorferi linear plasmid lp16 DNA, complete sequence	100	510
64	2	1320	1117	gblU43414	Borrelia burgdorferi linear plasmid lp16 DNA, complete sequence	100	204
66	1	647	75	gblU60642	Borrelia burgdorferi plasmid cp32-4, sequence at position 4-6kb	93	300
66	2	1075	641	gblU60642	Borrelia burgdorferi plasmid cp32-4, sequence at position 4-6kb	96	435
66	3	1530	1018	gblU60642	Borrelia burgdorferi plasmid cp32-4, sequence at position 4-6kb	94	440
70	1	3	275	gblU96714	Borrelia burgdorferi B31 BlyA (blyA) and BlyB (blyB) genes, complete cds	98	207
70	2	217	600	gblU45426	Borrelia burgdorferi 2.9-6 locus, ORF-A-D genes, complete cds and REP+ gene, partial cds	99	384
70	3	357	946	gblU45423	Borrelia burgdorferi 2.9-3 locus, ORF-C gene, partial cds, ORF-D, REP+, REP-, and lipoprotein (LP) genes, complete cds	98	390
70	4	1424	1083	gblAF000270	Borrelia burgdorferi strain B31 2.9-like locus, OrfC, OrfD, Rev (rev), lipoprotein (LP), and 36 kDa-like orf2 genes, complete cds, and 36 kDa-like orf1 gene, partial cds	99	342
75	1	2	925	gblU60642	Borrelia burgdorferi plasmid cp32-4, sequence at position 4-6kb	98	374
75	2	936	1328	gblU60642	Borrelia burgdorferi plasmid cp32-4, sequence at position 4-6kb	96	393
76	1	464	12	gblU45422	Borrelia burgdorferi 2.9-2 locus, ORF-C gene, partial cds, ORF-D, REP+, REP-, and lipoprotein (LP) genes, complete cds	85	281
76	2	1256	540	gblU45425	Borrelia burgdorferi 2.9-5 locus, ORF-A-D, REP+, REP-, and lipoprotein (LP) genes, complete	91	552

Borrelia burgdorferi - Coding regions containing to know proteins

						cds			
77	1	433	2	gblU45422l		Borrelia burgdorferi 2.9-2 locus, ORF-C gene, partial cds, ORF-D, REP+, REP-, and lipoprotein (LP) genes, complete cds	90	379	
77	2	1159	509	gblU45424l		Borrelia burgdorferi 2.9-4 locus, ORF-C gene, partial cds, ORF-D, REP+, REP-, and lipoprotein (LP) genes, complete cds	97	651	
81	2	657	1034	gblU43414l		Borrelia burgdorferi linear plasmid lp16 DNA, complete sequence	80	255	
83	1	3	1202	gblU76406l		Borrelia burgdorferi putative vls recombination cassettes Vls2-Vls16b (vls) gene, complete sequence	99	1198	
85	1	1	360	gblU45421l		Borrelia burgdorferi 2.9-1 locus, ORF 5-8, ORF-A-D, REP+, REP-, and lipoprotein (LP) genes, complete cds	91	347	
85	2	358	1008	gblU96714l		Borrelia burgdorferi B31 BlyA (blyA) and BlyB (blyB) genes, complete cds	84	440	
85	3	791	636	gblU96714l		Borrelia burgdorferi B31 BlyA (blyA) and BlyB (blyB) genes, complete cds	80	151	
86	1	891	289	gblU45422l		Borrelia burgdorferi 2.9-2 locus, ORF-C gene, partial cds, ORF-D, REP+, REP-, and lipoprotein (LP) genes, complete cds	86	486	
86	2	1151	954	gblU45427l		Borrelia burgdorferi 2.9-7 locus, ORF-A-D, REV, and lipoprotein (LPA and LPB) genes, complete cds	97	148	
88	1	137	3	gblU60642l		Borrelia burgdorferi plasmid cp32-4, sequence at position 4-6kb	97	135	
88	2	325	131	gblU60642l		Borrelia burgdorferi plasmid cp32-4, sequence at position 4-6kb	98	195	
88	3	565	323	gblU60642l		Borrelia burgdorferi plasmid cp32-4, sequence at position 4-6kb	98	243	
88	4	954	508	gblU60642l		Borrelia burgdorferi plasmid cp32-4, sequence at position 4-6kb	98	447	

Borrelia burgdorferi - Coding regions containing to know proteins

88	5	1091	891	gblU60640	Borrelia burgdorferi plasmid cp32-2, sequence at position 5kb	98	201
91	1	927	34	gblU45422	Borrelia burgdorferi 2.9-2 locus, ORF-C gene, partial cds, ORF-D, REP+, REP-, and lipoprotein (LP) genes, complete cds	97	313
93	1	162	578	gblU45421	Borrelia burgdorferi 2.9-1 locus, ORF 5-8, ORF-A-D, REP+, REP-, and lipoprotein (LP) genes, complete cds	89	331
93	2	572	940	gblU45421	Borrelia burgdorferi 2.9-1 locus, ORF 5-8, ORF-A-D, REP+, REP-, and lipoprotein (LP) genes, complete cds	96	368
94	1	3	245	gblU45425	Borrelia burgdorferi 2.9-5 locus, ORF-A-D, REP+, REP-, and lipoprotein (LP) genes, complete cds	97	243
94	2	749	282	gblAF000270	Borrelia burgdorferi strain B31 2.9-like locus, OrfC, OrfD, Rev (rev), lipoprotein (LP), and 36 kDa-like orf2 genes, complete cds, and 36 kDa-like orf1 gene, partial cds	90	458
97	1	506	3	gblU44914	Borrelia burgdorferi plasmid cp32-2, erpC and erpD genes, complete cds	94	472
98	1	827	264	gblU42599	Borrelia burgdorferi plasmid cp18, OspE (ospE) gene, partial cds	70	380
99	1	175	408	gblU43414	Borrelia burgdorferi linear plasmid lp16 DNA, complete sequence	100	234
99	2	329	757	gblU43414	Borrelia burgdorferi linear plasmid lp16 DNA, complete sequence	98	220
101	1	207	440	gblU43414	Borrelia burgdorferi linear plasmid lp16 DNA, complete sequence	100	234
101	2	361	837	gblU43414	Borrelia burgdorferi linear plasmid lp16 DNA, complete sequence	99	477
102	1	3	911	gblU76406	Borrelia burgdorferi putative vls recombination cassettes Vls2-Vls16b (vls) gene, complete sequence	99	889
104	1	388	242	gblU45426	Borrelia burgdorferi 2.9-6 locus, ORF-A-D genes,	100	146

Borrelia burgdorferi - Coding regions containing to know proteins

104	2	595	386	gblU96714	complete cds and REP+ gene, partial cds Borrelia burgdorferi B31 BlyA (blyA) and BlyB (blyB) genes, complete cds	100	210
107	1	2	811	gblU45425	Borrelia burgdorferi 2.9-5 locus, ORF-A-D, REP+, REP-, and lipoprotein (LP) genes, complete cds	95	789
109	1	264	4	gblL31616	Borrelia burgdorferi protein p23 gene, complete cds	86	201
109	2	598	173	gblL31616	Borrelia burgdorferi protein p23 gene, complete cds	93	396
109	3	807	580	gblL31615	Borrelia burgdorferi (clone BbK2.5-6) unknown protein gene, complete cds	99	228
110	1	1	456	gblU45421	Borrelia burgdorferi 2.9-1 locus, ORF 5-8, ORF-A-D, REP+, REP-, and lipoprotein (LP) genes, complete cds	95	456
110	2	450	761	gblU45421	Borrelia burgdorferi 2.9-1 locus, ORF 5-8, ORF-A-D, REP+, REP-, and lipoprotein (LP) genes, complete cds	93	310
111	1	787	215	gblU45421	Borrelia burgdorferi 2.9-1 locus, ORF 5-8, ORF-A-D, REP+, REP-, and lipoprotein (LP) genes, complete cds	89	405
119	1	653	84	gblU60642	Borrelia burgdorferi plasmid cp32-4, sequence at position 4-6kb	98	300
121	1	719	123	gblU60642	Borrelia burgdorferi plasmid cp32-4, sequence at position 4-6kb	98	374
122	1	403	2	gblU44914	Borrelia burgdorferi plasmid cp32-2, erpC and erpD genes, complete cds	85	391
128	1	175	408	gblU43414	Borrelia burgdorferi linear plasmid lp16 DNA, complete sequence	100	234
128	2	329	700	gblU43414	Borrelia burgdorferi linear plasmid lp16 DNA, complete sequence	99	356
129	1	458	697	embIX87201B BBRGABCD	B. burgdorferi plasmid, orfA, B, C, D, E, & F genes, clone pOMB14 and pOMB17	100	238
132	1	234	467	gblU43414	Borrelia burgdorferi linear plasmid lp16 DNA, complete sequence	100	234

Borrelia burgdorferi - Coding regions containing to know proteins

132	2	388	660	gblU43414	Borrelia burgdorferi linear plasmid lp16 DNA, complete sequence	99	171
133	1	3	560	embIX87127/IB BPBRGEA	B.burgdorferi repeated DNA element, 30.5 kb circular plasmid copy	80	243
134	1	339	4	embIX87202/IB BBRGBCDE	B.burgdorferi plasmid, orfA, B, C, D, E, & G genes, clone pOMB10	78	331
141	1	554	33	gblU96714	Borrelia burgdorferi B31 BlyA (blyA) and BlyB (blyB) genes, complete cds	100	513
141	2	124	276	gblU96714	Borrelia burgdorferi B31 BlyA (blyA) and BlyB (blyB) genes, complete cds	100	153
143	1	67	498	gblU42598	Borrelia burgdorferi plasmid cp32-3, ErpG (erpG) and BapA (bapA) genes, complete cds	98	432
144	1	497	3	embIX87127/IB BPBRGEA	B.burgdorferi repeated DNA element, 30.5 kb circular plasmid copy	94	495
146	1	193	2	gblU03641	Borrelia burgdorferi lp21 circular plasmid, complete sequence	86	144
147	1	3	542	gblU60642	Borrelia burgdorferi plasmid cp32-4, sequence at position 4-6kb	88	296
153	1	352	2	gblM96847	Borrelia burgdorferi GrpE protein homologue gene, DnaK protein homologue gene, and DnaJ protein homologue gene, complete cds's	97	351

TABLE 6.

Borrelia burgdorferi - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
2	4	2730	3554
2	5	3559	3410
2	7	5464	3869
2	13	10502	9999
2	17	13800	13576
2	19	15368	15204
2	28	21155	21400
2	50	41944	42186
2	58	53786	52911
2	59	54816	53773
2	61	57393	55813
2	63	57882	57682
2	65	60898	60203
2	66	61441	62070
2	67	62078	62692
2	70	65896	66540
2	74	70203	69910
2	78	71818	71399
2	80	72956	74032
2	81	73515	73267
2	90	92181	92525
2	91	92968	92555
2	108	109872	110057
2	112	112408	112812
2	113	112858	113037
2	114	113035	113460
2	115	113506	113724
2	119	114325	114852
3	6	3279	4079
3	8	5156	6019
3	54	42256	42789
3	59	47264	47506
3	60	47673	48692
3	63	51475	51026
3	70	60330	60575
3	71	61050	61349
3	72	61347	61670
3	74	63917	64303
3	86	75347	75532
3	88	76593	77384
3	99	89769	89005
3	102	91278	91661
3	103	92137	92463
3	105	92423	92785
3	108	93467	93886
3	115	98262	98681

Borrelia burgdorferi - Putative coding regions of novel proteins not similar to know proteins

3	121	102227	102904
3	126	111308	110055
4	6	3751	4179
4	7	4218	5042
4	19	16115	15516
4	20	17028	16075
4	21	17379	17092
4	22	17735	17397
4	24	19243	18785
4	25	18942	19196
4	26	20677	19259
4	27	19431	19751
4	29	21376	20876
4	30	21899	21423
4	31	22918	21845
4	33	23951	23553
4	37	26253	25627
4	38	26991	26332
4	39	28181	26931
4	40	29175	28522
4	43	30605	30342
4	45	34906	33548
4	48	35750	35932
5	3	2102	1527
5	5	2656	2393
5	7	3460	2900
5	10	6544	5645
5	40	25278	24322
5	41	25235	25600
5	42	25665	25276
5	44	25881	25663
5	47	27883	27410
5	48	28351	27881
5	49	29028	28324
5	50	29454	29026
5	56	32199	31666
5	57	32571	32200
5	58	32826	32569
5	60	32913	33245
5	61	33766	33575
5	62	34173	33742
5	64	35514	34861
6	2	954	1181
6	3	1590	1763
6	5	3400	3954
6	7	4691	5218
6	8	5187	5699

Borrelia burgdorferi - Putative coding regions of novel proteins not similar to know proteins

6	11	6498	5983
6	12	6975	6727
6	14	7978	7448
6	15	8479	7976
6	22	15106	15636
6	27	19999	18842
6	28	20036	20668
6	29	21814	20690
6	30	20949	21269
6	35	24136	23630
6	37	25697	26248
7	8	8100	7792
7	10	8145	8288
7	11	9374	8517
7	12	9771	9325
7	13	9652	10185
7	14	10163	9765
7	15	10517	10173
7	16	11363	10524
7	17	11904	11392
7	18	12495	11902
7	19	13516	12473
7	20	12807	13154
7	22	15149	14697
7	24	15855	15046
7	25	15503	15826
7	26	16638	15853
7	27	19344	16636
7	31	19473	19727
7	32	20067	19675
7	33	20762	20049
7	34	21136	20738
7	36	22975	23406
7	40	26667	25870
8	3	2907	4118
8	5	5898	6059
8	6	7399	8313
8	13	15645	15899
8	14	17281	16331
8	15	16905	17111
10	4	3211	3684
10	6	3857	4456
10	8	5982	5599
10	11	8038	7802
10	14	10255	10100
11	7	5688	5828
11	9	7248	7685

Borrelia burgdorferi - Putative coding regions of novel proteins not similar to know proteins

11	10	7672	8028
11	13	9642	10154
12	1	101	370
12	2	982	680
12	3	1390	1115
12	4	1528	1388
12	5	1913	1431
12	11	7308	6616
14	2	3588	3328
14	4	4657	4815
14	9	7981	8511
15	1	1	327
15	2	325	1077
15	3	1478	657
15	4	2360	1758
15	5	2839	2507
15	9	3922	3743
15	10	4145	3900
15	11	4112	4270
15	13	7677	6127
15	14	7852	7709
15	15	8052	7825
15	16	8222	7857
16	2	1733	1936
16	3	1905	2063
16	6	5212	4220
16	7	8903	8505
17	2	1500	1709
17	5	4097	4660
17	7	6344	6189
18	1	1635	2465
18	2	2509	3306
18	3	3332	4390
18	5	4933	4727
18	7	6353	7084
18	8	7098	7625
20	7	4700	4557
22	4	2175	1228
22	5	2132	2314
22	6	2829	2173
22	8	3254	3601
22	9	4408	4169
22	10	4875	4402
22	11	5343	4873
23	2	2283	1537
23	3	3564	2617
25	6	3677	4147

Borrelia burgdorferi - Putative coding regions of novel proteins not similar to know proteins

26	7	4251	3889
28	2	732	1739
29	3	310	885
31	1	28	195
32	3	935	1603
32	4	1637	2332
37	2	1379	1059
42	4	2708	2388
44	2	1734	1159
44	4	2942	2532
47	4	2336	2115
50	1	908	120
52	4	674	501
56	1	152	1465
56	2	611	459
56	3	1479	2150
58	3	1691	1329
58	5	1867	2046
59	2	2018	1044
61	1	1	657
61	3	1389	1907
62	4	1115	1345
63	1	663	325
63	2	769	446
63	3	1759	1013
65	1	472	903
65	2	901	1236
67	1	387	4
67	2	979	401
67	3	1482	961
68	2	451	612
69	3	840	574
71	1	363	4
72	1	586	933
73	1	300	4
73	2	824	279
73	3	1396	1145
79	1	22	1119
82	1	701	303
82	2	1188	775
84	1	331	134
84	2	983	348
87	1	277	2
87	2	1136	267
96	1	434	57
96	2	748	557
97	2	976	659

Borrelia burgdorferi - Putative coding regions of novel proteins not similar to know proteins

103	1	301	2
103	2	886	299
105	1	36	509
106	1	425	3
106	3	761	600
112	1	416	799
113	1	685	59
118	1	1	489
118	2	487	753
120	2	299	691
124	1	1	630
127	1	702	322
135	1	287	3
135	2	649	407
136	1	1	645
140	2	619	332
145	1	1	480

(1) GENERAL INFORMATION:

(i) APPLICANT: Human Genome Sciences, Inc. et al.

(ii) TITLE OF INVENTION: *Borrelia burgdorferi* Polynucleotides and Sequences

(iii) NUMBER OF SEQUENCES: 155

(iv) CORRESPONDENCE ADDRESS:

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(C) CITY: Rockville

(D) STATE: Maryland

(E) COUNTRY: USA

(F) ZIP: 20850

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

(B) COMPUTER: HP Vectra 486/33

(C) OPERATING SYSTEM: MSDOS version 6.2

(D) SOFTWARE: ASCII Text

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE: Herewith

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

157

- (A) NAME: Brookes, A. Anders
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(C) REFERENCE/DOCKET NUMBER: PB370PCT

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- (A) TELEPHONE: (301) 309-8504
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(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 910715 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ATATAATTTT TAATTAGTAT AGAATATGTT AAACCTTACC CTTGAATTTT TCTACTCTAT	60
TTGTATATTC TATAGAAAAA ACGATTAGAA TTAAACAAAG CCATAACTGA ACCAACGGTA	120
ATTAGTAGAT AAAGGGATCA AAATATTTTT TATTGCAGCA AGAATACCTT GGTATATTAG	180
AAAAACCAA AGTCATAGTC AAATCATCTT TTGATAACAA TCCCCAAATC TATAATTTAT	240
TATGAAATTA ATTGCTCCCT TGAAAAGATT AGTTTTTAAA ACTACAAGAC TACTATCAAT	300
CACTATCAGA TAGATTAAAA CAACCTTTAC AAGAAAAAAA TCTTACTACT ATTTTATTGT	360
AAATGTATTA TAAAATAAGT TCATGCAAAA ACTTACAATT TTTCACAACA AACTACAATA	420
AAATCATGTA AACAAACAAT TTCTTTGAAA ATTAAGCAAA TTTATAAATA TAAATTATAA	480
AGATATATAT TTTTATATGA TCAATAATAA AAATTAATAG GATACTTATT TGGAAAAATT	540
ATTGAAAAAA CAATAAGCAT GAATTGCCAC AATAAGCTAA TTGTCACCTA ATAATTCTTG	600
TTTACTAGAC CACATTAGTA TAAACTCAAA TATTGGCTAC TATAATATAG GGGCTTTATA	660
CGCCACATGT TTAATGATAA CATAAGAAAA TATTGCAATA ATAAAAAGAT TGAAATATCT	720
TTATTAGAAA AGAATCTCGA TAATTTAGAA AACAGAATAA AAATCATAAC TAATAAATAT	780
AACGTTGAAA AAAATATATT CAAACTTTAA CTATACAATT AATTACACCT TAAAAATGCG	840
TTACATAAAA ATTAAGGACT ACTATAAATA GAAAACACCA CATAACCTAC AGACTCTAAA	900
GGAATAATTA AATCCTCATA TTTCAGTTCT CCAAAGTTT AAATAGGGGC CTTTTACTTT	960

TCCTGATTAG CATATACATT ATTAAAGGCA TCTTCTTGGG CACTATCCTA AACTTTTTTA	1020
CATTATTATT ATTTTATTCT TTATTATTAC AAGATAATTC AAGAATCTAG ATTACAAGAT	1080
ATCAATCCTG CCATTAGTAG TTCAATAAAA CATTTAGAAT ATTTATACAT TATTTAATGT	1140
ATTTTTTTCA TTTTTGAAAT AATATTGTTA TAACTTAACT TAATAAGATA TTTGATTTCT	1200
TCAACTTGAG AATCCGATGT ACATAGAATC TGAACATCTC CTCTGCCCCA TTTGCCAATA	1260
TTCTTAATAT ATCTAGTAAA ACCCTCTTTT AAAATTATTT GATCTAGAGC AACAGTAATA	1320
GTAATATTAA TTTTATTTAC CCCAGGTCTA AAGCTAAAAT CTACAAAATA TCCGCCCTGT	1380
ACTTTAAATC CTGTATAGCA CTGTGTTTCA ACTTTCTCAA TTTCAATAAA ATTTAAACA	1440
AAAATAAAAT CTCTAATTC TTTATATATT GCTTTCATAT CGGAATTTAA TTTTCAAAT	1500
TTTTTTAAAT TTTCGGTTTT AATATTATTA TCTTTTATAC CAGAATCTGT GTCATCTTCT	1560
ATGTCACCTT TCTTGCTGTT TACTAATACA TCGCTTTTTT TTTCAATCAA AAACATACTA	1620
AAAATATTTT TAATAATATC ATTAAATATT TTATCTGAAT ATGTTTTTTT AAAACCAATT	1680
TTAGCTTTAA AAAAATCAAG CAAATCAACA CTTGGATTTT TTGTTTCCTT TTTTAAATAA	1740
GCTGAAAATT TGTCTGTATA TTTTTTTTCT AATGCAAAAG ATCTAGCCTC TTCAACATTC	1800
AAAGAATTC TAGAAACTT TTTAAGATAT TCAAAATCCT TAGATGTTAA TTTTCTAAA	1860
TTAACAACCA TAAAAGGCTC ATTGTCTAAC AAATTATCTT TATCTAGGTC AGTATAGAAT	1920
CTATATTCTA TGCCATCTGT TAATATACCA AATTCAACTC TCTTTGCTTG AGAACGAATA	1980
TTTTCAAAAT AAGGTTTTAA TTGCTTTAGA TGATTTTCAA GCTTTTCCCT GCTATTATGA	2040
TATTTGGCCT CTATTAAAAT AGTGGGTCTT TCATCCTTTT TTGTTGGATA AATAACATAA	2100
TCAACCCTTT TTAGTCCATC TTTAAGAATA TCTGCCTTCT CTTCAACTTT AACAATTGAA	2160
ATATCAGTAT GATCATAGCC CATCGCATCT AAAAATGGAT CAATAAGATT TTGTCTTGTT	2220
TGTGCTTCAT TTTCAATAAG ATCCTTATCC TTTTGAATTT TTCTACTTAC AGCTTTTATT	2280
GAATTTTCAA AATTTATATC TTTGTATTCA TTTGGCATAA TTATATTTTA CCAATAAAAT	2340
TAAAAATTAA TAATCTAAA AATAAATTC CAAAATGTTG TCTATTTTAA ACTCTTAACT	2400
GATACCTTAA TTCTTTTTTC TACCTAATTT TTTAGTTTAA AATCTTATTT TTTAATTTTA	2460
TTATTTTTTC CTTACCTTAT TTATACTAAA ATTTTTAGTA TTTAGCGAAT AATTTTCATA	2520
TCCTTTTATT AAAGACAAAA TATGATTTTC TCTTTTTTGT TTTTAAATAC CTTAAAATCA	2580
CTAAGCAAAG TAATAAAGTC TTCTTTGGTT AATGAATAAA AGACTAGCTA TAATAAAATT	2640
ATTTTATTTT TCTTTACTAA ATTCAAAATG CTCTAAATAA AGCAAATTAG AGAAATTCAA	2700

AGGATCATTTT	TTAGCTATTA	GCAGAGAAGT	GTTTTTTTACC	AAAGTTAGAC	ATAATGAACT	2760
AGCCAAAATT	TCTTCTTTGG	GTTGAGGCAT	TGGACATTGA	CAAAGAAATG	ATTTTACAAT	2820
GTCGGTATTT	TAAAACAAAT	CTTCTAATCA	TAAAATCAAA	TACAGTGCAT	TGAAAATAGA	2880
TATAATAAAC	AATTTTTTAT	AAAAAGATAT	TGGTATTTTC	TCACAATTCA	TATCTATTTT	2940
ATAGAAACAC	AATAATAATT	TTTAGGAGAT	AAAGTGCTAA	TCATGGTTCT	TTCATTTGTA	3000
TTGCTTGCAA	TTCTTCTATA	AAATATTCTT	TCATTTGGGT	ACTGATCATC	TTTAGTTAAG	3060
ATTTTTTCTA	AATCTTCTTT	ATATCCTATC	CATAAAAGCT	TATAACCTTC	TTTTACATAA	3120
TCATAAGTAA	AAAATCTTAA	ATTAAATTGA	TAGATATTAG	CCCCAGAATA	AAGAAATATA	3180
AAGTTTTTCAT	TATTATATTC	CTTTAATAAA	GATTTCGGAT	TCTTTATACT	TGGATCTGGC	3240
CCTTTTTTAA	AATTAATATC	TTCTTTACTA	AGAATACTAA	ATGAACTAAA	TATTTTGTTC	3300
AATTTGGCCC	ATGTTTAATT	CAATTCCTTT	ATAAGGATTT	TCTTTGCAGT	CTTTTAAGTC	3360
TCTAGTTATT	CCTTAATAAT	ATTATCACTA	CTTTGAATAA	CAAATTTTGC	TTTAAAATTT	3420
AATGTAAAAG	TTTATTACTA	CGAGGAAATA	TCGCAAATTT	AAACTTTGAA	TGCATATCTT	3480
AAAACCTTTT	TTTGTTTTCA	AACGTGATAA	TAAGTTAAGT	TTATAATTAC	TAAATATATG	3540
CTTTCTTAGC	AAGCTAAGAC	CAAATATCAC	AATAGAAGTA	ATTCTCAATA	AACAAAATAC	3600
AAAAAGTAGT	TATCATATCG	TCTTTAACCT	TAAATAAGGT	TGCTATAAAC	AACCAAGATA	3660
TTTAATTTCT	TTTAAAACCC	TTATTCAATC	TTTTTAAGCA	TAGGATCTTA	TAATTATAAG	3720
AATATAATTT	TATTTACATC	TCTATATTAA	TAGAAAGATG	CAAATATGTG	ATCAAATTGT	3780
TATTTTTGTA	ATATGGAATA	GTCCTTTATA	GGGACGCTTA	ATGCTCTATA	CTTAAGATTG	3840
GAATTCTCTA	TGAAAATATA	TACTCGCTAC	CCATGTAAAG	CTGACTTATT	TTAGCACGTA	3900
TCGCTTAAAC	AATTATATTT	ATATTATCTT	TTATAAAGTT	AATTTTTTCT	TGTAGATTAT	3960
TTTTTAATAA	AAAAGGCACA	AATTACCACA	ACAAGTTCCA	GTATAAATTA	ATAGTTCTTA	4020
TCTCAACACT	AAAGTACATA	AACATCAAAT	ATCAAAAATA	TATAAGAACA	ACATACTACA	4080
TTGTTTTAAT	GAAAACCTTA	AAAGGAATGG	TTAAACTCTC	ATTAAGCTAA	AACCAATGCA	4140
AAAATATCTT	TATAAATTAG	CAAAAGAACT	AAAAGTCACA	AACAACTACC	ATAAAAAATTT	4200
GGTAGTAAAT	TCTGGAAGTG	AAATTTACTA	TAAACTCAAT	TATTCTAAAA	AAAATATTGC	4260
CTTAAATTAA	AGAATGCCTT	AAAAAAACAA	AATGCTCTGA	TTTAAACCTA	TACCCAAAAT	4320
ACAAATTTAC	TAAAGAAGAA	GATATAGATT	TAGAGAAGAT	CTTAATAATA	AAAATATTAA	4380
TATAAAAGTT	GCTCAGTATG	CTAAAGGCAA	AGAGTTTAAG	TCAAGTTTAG	AAATTACAAA	4440
GAGTAAACT	ATAAACTTCC	TTTAAGAATG	AAAATTTATT	TTTATACTTA	CTTGGCTTAA	4500

TATTAAGATT	TTTTTATTCT	TTTCATAATA	ATCTCTTCTA	TCACTTAACA	TTTTGCTATA	4560
CAAAAATCTT	ACACATCTAA	ATACTTTTTA	AAAAAATTG	ATTAGTGTTA	GAATATATTC	4620
TATATTTATA	AACTTTATTA	GCACTCATAA	TTTTACTAAA	TTAATATATT	ATATTTAATT	4680
TATTTTTAAA	ATTTATCTCC	ATTTACCAAA	AAAACATAAA	TAAAACCTCTC	CAAACCTATA	4740
AATAAAAAAA	TAAGGCAAAA	CCCCAACAAA	CTCAAGATCT	ATAATACAAA	AATACAATAT	4800
AAGAATCCCA	AGCTTAAAAA	CAACCCCCTA	AAATCTTTTT	TTATTGGCGT	TTTTAAATAA	4860
TGGTAATAAA	GAATTCCAAT	CAACACGATC	CCCCCTACAA	CTTTTCAAAC	CCTATAGCTT	4920
GGCTTTTTAT	ATTATTTTTA	AATTTACATG	TCACAACAAT	AGATAATGCA	TAAAATAAGT	4980
ATTAATAAAA	CAAATACATT	TATAGAACCT	ATACAATTAT	TGAGCATATG	GCTAGTACTA	5040
AAAATGAAAA	TGTACAAGAT	AATATGCTAT	TAATAAAAAT	TAATGGCTAC	TAAAACTTTT	5100
GAATCCACAT	TTTTTCTTTA	AAAAAATTCT	AAATTATTAA	AATAAATAGA	AATTAAAATT	5160
ACCAAAAATA	TTATTATAGT	AATAAATATG	TAAAGCTATT	TTTATTAAAA	CTGATAATAA	5220
AAATATAATA	GCTAAAATAA	CATAAATTAA	CTTTAAATTA	TATCAAAGAC	TTAGATTTAA	5280
AATATTTAAT	AAAAGGCAAA	GCTATAAACA	CCATATACTT	ATTTTATTAT	TTTTTTCATT	5340
TTATTTAAAT	TAATTTAAAT	AAGACTCAAT	CAAATAATCA	ATCAAACATA	TTGGGTGAAG	5400
AAAAAATAGG	GTATTCTTGG	TGAATCGTTT	TAAAAGGGGG	TATAGTAAGC	TAAAAAACTC	5460
TTATTAAAGA	GGATGTTTAT	AGACTTAAAA	GTCTAATTCA	ATATGAAAGA	GGCTTTTTAA	5520
AGCTAAAAAT	GTAAAGAAA	ATCAAATTAA	GCAACAAGAT	GGTTTTGTTT	CTATAAATAG	5580
TTTTAAAGAA	TATATACATT	TGCACATACC	CTTCATTATA	ACATCTACTA	ATTACACAAT	5640
AAAAATAAAA	ATGATTTATT	AAGAATTATT	AGTAACTTAT	AAAAACTTTA	TAAGTTACAT	5700
AGTCAAAAAT	ATAAAAAATT	AAAACAAAAA	ATTAACGATA	TGGAAAAATT	GTATTTTATA	5760
GAAATAGAAA	TATATTTGCA	TTAAACAAC	ATGAATTTAT	AAAGATTCTA	GTAGGAGAGA	5820
AAATATGAAA	AAAAAAATT	TATCAATTTA	CATGATAATG	CTAATAAGTT	TATTATCATG	5880
TAATACAAGT	GACCCCAATG	AATTAAC	TAAAAAATG	CAAGACAAGA	ACGTGAAAAAT	5940
TTTAGGATTT	TTAGAGAAAA	TTCAAGCAGA	TAATAAAGAA	ATTGTTGAAA	AACATATAGA	6000
AAAAAAAGAA	AAACAAATGG	TGCAGGCTGC	TTCTGTAGCA	CCTATTAATG	TAGAGAGTAA	6060
TTTCCCATAT	TATCTTCAAG	AAGAAATAGA	GATAAAAGAA	GAAGAGTTGG	TTCCAAATAC	6120
TGATGAAGAA	AAGAAGGCAG	AGAAGGCAAT	TAGCGATGGG	AGTCTTGAAT	TTGCTAAATT	6180
AGTTGATGAT	GAAAATAAAC	TTAAAAATGA	ATCTGCGCAA	TTAGAATCTA	GTTTTAATAA	6240

TGTTTATAAA	GAAATCTTAG	AACTTGCAGA	TTTAATACAA	GCAGAGGTGC	ATGTTGCAGG	6300
AAGGATAAAT	AGCTATATAA	AAAAAAGAAA	GACCACTAAA	GAAAAAGAAT	ATAAGAAGAG	6360
AGAAATTAAG	AATAAGATAG	AAAAACAGGC	TCTAATTAAG	TTGTTCAATC	AGTTATTAGA	6420
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ATCTGCAAAA	TACTTTTTTG	AGAAAGCCAA	AGAACTTTA	AAAGCTGCTA	TTACTGAAAG	6540
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AATACAGGCA	AAAAATGAGG	CAGAGGATGC	TTTAAACCAA	TTAAGTACTT	CTTCTTTTAG	6660
GATACTTGAA	GCAATGAAAA	TAAAGGAAGA	TGTA AACAG	CTTCTTGAAG	AAGTAAAATC	6720
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GTAAAGGAA	GACTTTTTTA	TAATTTTATT	TAAATAACGA	AAAGCTTGAT	AGTTAAAAAA	6900
TCTTTTTTAT	TAAAAATATG	TTTACTAAAC	AGAGCTCAAA	AATGACTATA	TTTAGTATCT	6960
CTATAAAAGA	ATTTTTC AAT	ATTTTAAAAA	ATTTATAGAT	AAACATAATC	TAAAACCATG	7020
CATTAATACA	AACCTAAAAC	ATACTTGGTC	ACTTGTA AAA	GTAAATTGTA	TCTAACTTTT	7080
TTTATTTTATT	GAATATACGT	AAAAATCTT	TATAATTTCT	ATTTTAAAAC	GCTGCTATTT	7140
AGCAATACAA	TAAAAGGCAT	TACAGATTGC	AATCAAACAA	ACTAAAGTTT	AAATAAAATA	7200
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AAACTTTAAA	AGAACTTGTC	GAAAATAATA	TTTCTCTTAA	AAAAGGTTCT	AATCTTTTAT	7320
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AAAATAGAGA	TAAAAAACTC	AATCATAAAT	AATGGTAAAA	CAAAC TTAAA	CCACGTACCA	7560
TAAC TCAATC	TGGATATCCC	CAATACAGCC	ATTATAACTC	CGCTGGTAGG	TGTTATCAAA	7620
TTAATAAGCC	CAGATGCAGT	CTGCATGGCA	ATAACAAC TG	AAGCTCTTGG	AATTGACAAA	7680
AAATCGGCAA	GAGGAGCCAT	TAT TGGCATA	GTGAGACTAG	CATGTCCTGA	TGAAGATGGA	7740
ACAACAAATC	CTATAAATAT	TTGAATAATT	TCATTCAATA	TGATAAAAAG	GGGTC TTGGA	7800
AGATTGTATA	AAAAATTAGT	AGCAGCATTT	AACATAGTAT	CTGTAATCAA	CCCATCATCA	7860
CATACTATCA	TAACACCTCT	AGCAAGTCCA	ATAACAAGAG	CAGCGGTTAG	CAGACTTTCA	7920
GAACCTTTCA	CAAACGCATC	CCACATTTCA	GTTTCACCTA	ATTTACAAAT	AAAAGCCGAT	7980
ATAATAGCAA	CTCCAAGATA	CAACATTGTC	ATTTCTTGCA	TCCACCAACC	AAGATTAACA	8040

ATGCTAAATA	TCAAAATCAA	TATCATAAAT	CCAAATAAAA	GTAAAACTAA	TTTATGAGCA	8100
AAAGTAAACT	CAAGAGCATT	CTGAGCATTA	TCTCCGGTAG	AAAGTCCATC	TTTTTTAACA	8160
AAATATTGAT	AATGTTTCATC	TTTTTGAGAA	TACACAAGCG	ATTTTGAGGG	ATCCTTTTTA	8220
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ACAATTCTAA	AATAAAATCC	ATCCTGCAAG	CTAATAGAAG	CTATTGCAGA	TGCAATTCCT	8340
GTCGCAAATG	GATTTACAGT	AGAAGCCATA	GTTCCCACTC	CAGCTCCTAA	AGCAATAATA	8400
GCCGCTCCAA	CAAGACTATC	ATAACCCAAA	GCTACTATCA	AGGGAATCAT	AACAAAATAA	8460
AAAGGAAGGG	TCTCTTCACT	CATTCCGGTT	ACAGTTCCAC	CAATTGAAAA	AATAAACATT	8520
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ACATCTATTG	CTCCAGTTTT	CATAATAATC	CCATAAGCAC	CCCCAACAAAT	TAAAACAAAA	8640
ACAATAACTT	CAACTGCATG	TTCCATCCCC	TTTGACATTG	CGGTTAAAAAT	AGTCATAATA	8700
GGATGTAAAA	ATCCCCTAGA	GCCTCGATCT	ACATATTGAT	AAGTTCCAGC	AACAATTATT	8760
TCCCTTTTAG	ATCCATCACC	CATTGCTTA	AATTCTTTAT	CAAACCTACC	GGCAGGAATC	8820
ACATACGTTA	AAATGGTAAC	AAATACAATT	AAAGAAAATA	TTATTGTAAA	ACTACTTGGC	8880
ATTTTGATCA	TAACGTTTCT	CCTAAATAAT	TTCATAAATT	TAATTTCACA	TAAAAAATAC	8940
TGTTATCCCA	AAGTTGATAC	CATAATAGCT	TTAATGGTAT	GCACCCTATT	TTCAGCCACA	9000
TCAAAAACAA	CTGAATTTTT	ACTTTCAAAA	ATTTCTTCTG	TAACCTCAAT	TCCATCAAGT	9060
CCGTATTTAT	CAAAAATATC	CTTACCAATC	ACAGTGTTTA	AGTCATGAAA	AGCAGGCAAG	9120
CAATGCATAA	ATATTGCATC	ATCTTTTGCC	ATGCACATTA	TCTCTTTATT	AACCTGATAA	9180
GCCTTTAGAA	GATTTATTCT	ATCTTCCCAA	TTACTCTCCC	CCATAGATAC	CCACACGTCT	9240
GTATACACAA	CATCAGCACA	TTTAACAGCC	TCTTCTTTAG	AATCTGTAAT	TGTAATTTTA	9300
CCCCCACTCT	CTAGGGCTAA	AGACCTAGCC	TTAAGCGTCA	AATCGGGGTC	TGGAAAAAGC	9360
TCTTTGGGAG	CAAAAATTCT	AAAATCAAGC	CCCATAATAG	CACAGCCTTT	CAATAAAGAA	9420
TTAGCAACAT	TCCCCCTACC	ATCGCCACAA	AACACTATTT	TAATCCCTTT	CAAACCTCCC	9480
TTATGTTCTT	TTATTGTCAT	TAAATCGGCT	AGTATTTGGG	TTGGGTGAGA	AATATCTGTC	9540
AATCCATTGT	AAACAGGAAC	ATTAGAATAA	TTCGCCAAAC	ATTCAACAGT	CTGTTGAGAA	9600
AAGCCTCTAA	ATCCAATAGC	ATCATACATG	CGTCCCAAAA	CTCTAGCGGT	ATCTATCATA	9660
GACTCTTTTG	AGCCCATTTG	ATTACCCTTA	GATCCCAAAT	AAGTAATATT	TGCCCCCTGA	9720
TCATAGGCTG	CGATCTCAAA	AGCACACCGG	GTCCTTGTTG	AATCTTTCTC	GAAAATTATA	9780

163

ACTATATTTT	TACCTTTAAG	TTTTTGCACT	TCAATTCCTG	CATATTTTGA	CTTTTTTAAA	9840
TTAATCGATA	AATCAAGTAA	ATATTTAATA	TCTTTGCTTG	TAAAATCTAA	AAGATTTAAA	9900
AAGCTCCTAT	TTCGTAAATT	ATACATCAAC	CACCAACCTT	TACAATCAAG	TTTTTAAAAA	9960
CTCATTTAAC	TCATGCTTAA	ACATGCTTAA	ATATTAAATA	TCCTCTCTTA	CTAAAGACAT	10020
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TTCTCCTGGA	GCTATCGCCA	AAACATTAGC	ACCATCATTC	CATTGTTCTC	TTGCACCATG	10200
TATTAAATCT	CCACCCGCAC	ATTTTATTAT	GTCAATTTTT	CTGCCATAAT	AAAAGCTCAA	10260
AACATCTTTA	AGCTTGGCTT	TTTCTTTTTT	AATATTAATT	TTATTAGAAT	TTGAATTGTA	10320
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CTCATCCCCA	CCTTCCAAAG	AAGTTTCTTC	CCATCTATTA	AACCAAATTG	GAACATTTTC	10620
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CATATTATCA	ACGGTTAAAT	TAGAAAAATA	ATCTTTTAAA	ATATTAATTA	CACCATCTGT	10920
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AGCAAGAACT	TCACTAACAA	GATCCTCAAC	ATACTCAATT	TCAACTGAAT	TATCTTTTAA	11040
AATATTTACA	AAAACCTCAT	GCTCTTGTCT	TGCAACTTTA	AGATAAGGAA	TATCATCAAA	11100
TAAAAAATTT	TTCATAATCA	AGGGTGTCAG	ATTTTCTAAT	TCTTCTCCTG	GCCTATGAAG	11160
CAAACTTTT	TTCAAACGAC	CTATTTCCGA	AAATATATTT	ATTGGATTTA	AATATTCTTC	11220
TTCCATCGAT	TTCCCCCTTT	ATGAAAATTG	TCATATATTA	AAATACTATA	GTTTATATTA	11280
AAAAACATCA	ACTATTTTAA	ATAATATTAA	AAATATAATA	TAAATATAAA	AAATTGAAAA	11340
AATAAAAGTT	CTAAAAAACT	TCAAATCAAA	AACATAAACA	AAAAATTATG	CTAAAATACT	11400
AATCATGAAG	AATATTAATA	GATTAATATT	ATTAATATTA	ACTACACACA	CTTTATTATT	11460
CTCTTGCGCC	TTAATTGCAG	ATAATAAGTC	AAAAAATTTA	AGCACATCAG	AAATCATATT	11520
AACACAAAAA	ACACTACTAG	AAAGCTCTTT	AATAAAAAAT	CCTTCTAATG	TAGAATATCG	11580

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TAGCGTCAAT	GGAAATTTAA	CAATTAAAAT	TGATACTGCT	TTTGAAAAAA	AAACAAATTT	11820
TAATCATACA	AATTCAGATA	ATGAAAATTT	AACAGAACTA	ATAGAACTAC	AAATGCATCT	11880
GGAAAAAGAA	ATTTTAAACT	TAATTGAGCA	AACATTTTCAT	GATAAAAAAT	TAGGATATAT	11940
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AATAATAGAT	GGAAAAAGAT	ATATTGCACC	GCACATAATA	GCAAAATCAAT	TATTAAAAAT	12060
AAAAGATAAA	AAATATTTTG	AACAATTTAT	GCACTTTTTA	AAAGTTGAAA	ACAGCAAAAT	12120
AAAAACAATA	ATTGAAAAAC	AAAAAATTTT	AGATCTTCAC	AATGAACTGT	ATTATTCAAA	12180
ACAATCCCCG	CCCAGAAGAA	GAAAAAGGTC	AACTGCCGAT	TCCGATAATA	ACAATAAATA	12240
CGATATAATA	CCAAAAATAA	TAGACCCAAA	TACAGGCATT	GAAATAACTC	CTAAAAATTT	12300
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ACAATCAAGA	ATATTAAAAA	TATTCTCACC	AATAACAGAC	ATAAGAACAA	TTCAAAAAGC	12600
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AATTTGCGGA	ATAATTACTC	CTGGAGAAAT	AAATGCAGCA	GCTTACAATT	TTTACATGTC	12840
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GAAAGAAAAA	ATTTTGGGA	GAGCTTGCAA	CATTACAAAT	CTCTGGTGCT	CAGGAAGTTA	13020
ATACTACCCA	TGAACAAATA	TTATGCCTGT	ATTTTGATTA	ACAGCAATGA	AAAAATTATT	13080
TTCAAATCCT	GGGAAGAATG	CAAACCGCT	ATTAAAGGAA	AAAACAATAA	AATAAAAAGC	13140
TTCAAAACAA	TAGAACAAGC	TCAAAATTGG	CTATTTAATA	ATGAGAATAA	AATTCACCAT	13200
CACCCAAATG	GAATATATTT	TGATTCTGGA	ACGGGAAGAG	GAAAGGCAT	AGAAATTAGA	13260
GTTGTAAACG	AAAAAAGAT	TTCAATATTG	GATAAAATCT	TAGATAAATC	CTTGATTAAT	13320

165

GAATATGGAA	ATTATTATGT	CAAAAATTTT	CAAGGAATTA	GCAATAATTT	TGGGGAAGTG	13380
CTTGCCCTAT	ATACAGCTCT	CAAAATAGCA	TTAAAAGAAA	ATATAATAAA	CATATTTGGG	13440
GACAGTAAAT	TAATAATGA	CTATTGGTCA	AAAGGAATCT	ATAATAGCAA	AAAATTAACA	13500
CAAATTACTA	TTAATTTAAT	CAAAAAGACA	ACTGAACTAA	GGAAAAAATT	TGAAGAACAA	13560
GGTGGAAAAA	TTTCTTTTAT	TCCAGGAAAT	GAAAATATTG	CAGATCTTGG	TTTTCATAAA	13620
ACTAAGTAGA	AATATTGTCA	AAAAATACAT	AAAAACAATA	TTTCTGATTT	CAATGGTTTA	13680
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TAACAACGAT	AAGATCGTCT	TAAAAAAGA	AGATCTTACA	ATAACAATG	AAACAGGGTA	13920
TAAAAATAAA	TACAGAGAGT	TTTTTATTGG	TCCTAAAACT	TCATTTAAAT	TTAAAGTATA	13980
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GAGAATAAAT	CCCATCAGAT	CCCCTTAATA	AATCTGGTTC	TAAATTATAT	TCTCCAACAA	14340
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CCCCAAGGT	AAAAGAAAGC	TTATTGTCAA	AAAAAGTTAA	AACGTACAAT	TCCTTTTTGT	14700
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CTTTTAAAGG	ATCATAATTA	TATTCAAAGT	CGTCTTTCAT	AGCAAACAAA	AATTGAAAAT	14820
CAAAAACATT	AAGCTTAAAA	GAAAGTTCAG	AAACTCTATT	TATCAAAGGA	TCATAGGCCA	14880
CTAAAAAACT	AAATTTAAAA	TAATCCAAAT	ATCTCGGCTC	AATTTTATAA	TACAAAGCAG	14940
GAGACATTTC	TAAATTTTAA	TAAGGCGATG	ATGGTTTTTG	AGGCTCCAAA	GGACTTTGAA	15000
CAGCAGAAAT	TCCAGAGTTT	TTCATAGCAT	CTTCTTTAAA	CTTTTTATAA	TATTTAATTC	15060
CAATCCCAGC	TTCTTGTAGC	AAATAAGGAA	AATCTAAAGA	AAGTTTAAGC	TCAGAAGAAG	15120

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TCCTGGTAAA ACCCAATCCA AAATTTCTTT CCAAAGTTTT AAAATGCCCC AAAGTATTGC	16440
CCAAATTAAA ATCAATTCCA GAATAAAATC CCAGATTAGC ATAAATGTCA AAAATAAGCT	16500
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CATTTCTTAT ATAAGGTTTT TTACCCGAAT TATAAACAGA ATTGAAATCA AAATCCAAAA	16620
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167

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GAAGAATAAC	ATTTTTTAAT	AAAAAATTTT	GAGAATCAAA	ATCGACAAGA	AATTCATTGC	17040
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CATAAAGTTT	TTTAGAGTTC	TTATTAAGGA	CTATTCTGTC	GCCTTTAATA	TTGTGCTTTT	17160
TATTTTCTTT	AATATCTTCA	ACCAAGATAT	TAACCTCTCC	TTCAAAAATA	ATACTTTCAT	17220
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ATAGGAATTC	TCGCATTTTG	CAACCTCTTC	AGGAATACCA	GAAACAACGA	TATTTCCCCC	17640
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171

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177

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277

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291

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323

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347

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351

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355

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361

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365

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381

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403

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437

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451

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455

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457

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AAAACTATT	TGTCATGTGT	TTTAATTTTT	TTAGTAATTG	CTTGACTTTC	AAAAGATAGC	536640
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471

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475

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501

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505

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507

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527

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TGAAGCTCGA	GAAAAAGGTG	CTATGGCTCT	TTTTGGAGAA	AAATATGACG	ATTTGGTGAG	685740
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557

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563

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567

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571

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577

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581

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591

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607

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611

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613

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615

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623

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625

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627

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AACCCTTTGT	GATTCGCCTC	CTGAGAGCTC	TGAAGGGTAA	TGATTTGCTC	TGTTTTCTAT	834540
TTTAAATATT	TTCAATTAGAT	CTAAAGCTTT	TTTATTTATT	GTTTCTTTTG	TTTTTTGGCC	834600

TGAGATAATT	TGGGGTAAAA	TTATATTTTC	AATTACACTA	AATTCATTTA	TTAAATTATA	834660
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GTTTTTCAAA	AATATTCAC	ACGATATTAT	CTCTCCAGAA	TCTATTTTAT	CAATTCCTGA	834780
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TTTCAATGTT	TTTTTGACTT	CCAATTTTTT	TTGTGCTT	CATACTTGAA	TACATTGTAG	835020
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TATTTTTTAC	TATTTGTATT	TTAATGCCAT	CTATTTTTAA	AGCCAATATT	TGATTTAAAA	835140
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CAATGAAAAT	GCTTGCTAAA	ATAATTAACA	TTGTATTTCT	TTCTATTTTT	AATATTTTAT	835440
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CCTATTTTAT	TGCAGATTAT	TAAATCTATT	CTCCCATATT	TGCTTCTTTA	ATATATTTCTA	838140

631

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633

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635

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637

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647

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649

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653

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TGAGTGAATT	TCCTGTAATT	AAGTTTCTT	CATTTGATAT	TTGATAAAAT	TTGTCAATTT	883800
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AAACTTCTAA	TTCTTCTTCT	TTGTTTTGCG	CTAAAAGATA	GGTTTTTCCA	GATATATTTA	884040
CAATGTCGTT	TATAAACTCA	TAAGAATTGC	TCAAATCAAT	TTTTTCAATC	TTGCCGTTTT	884100
CTTTTTTAAA	TAAATGCATG	GCTGCAATGT	AGAGAGTTTC	TCCTACTAGA	GAAATTCCTC	884160

657

TTGGACTTGA	ACTGCCCAAA	ATATTGTATT	CATGTTTTAT	TTTTTGCAGA	TTTCCTAATT	884220
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661

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665

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669

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CTTGATTAAA	AGTGTAATTT	TTTGCAATCT	CAAAAAAGAA	GATGTTTTTCA	CAGCTGTTCA	908160
ACCTTTAGTT	TATTGTTATG	AAAAACTGAA	TAGCTCCAAT	TATCAATATT	TTACTCTCAA	908220
AGATAATAAA	AATGCTAATT	CTATTTTGGC	TTTGCCTGCC	GGTCATGGTC	AAAATTTTAA	908280
AATTTTAAAA	GATATTTATT	TAAAGCTTTA	TGAATCTGGT	AAAAGATTTA	TATATATTGG	908340
TAATGTTGAT	AATATGGGCT	TTACAATTAA	TTTTTAAAGCA	CTTGCTTTTAA	TGGCTTTGAC	908400
TAATGTTTCT	TCTGGGTTTG	AATTTAGTTT	TAAAAGCAAA	GCGGATTTTA	AGGGAGGGAT	908460
ATTGGCAGTA	AATGGTGAAA	ATCGTTTAAC	TTGTGTTGAT	ATTGGCGGGG	GGATTTCTTC	908520
AGAGATTGTG	CAAGAGTTTG	AAAATAAGGG	TAATAGACTG	CTGTTTAATT	GTGCAACTGG	908580
ACTTTTTAAT	TTAGAGTATT	TGATAAAAAA	TATTGATGAA	ATAATAGAAA	AAATGCCCAT	908640
TAGAATTATA	GAGCAAGATA	AAGAAATTGG	TAAATATATT	TCGGTTGAGC	AAATAACGTG	908700
GGAAGTGTTA	AAATTAATAG	AAAATCCATT	AATTTTAAACG	GTTGATAGAA	ATAGAAGATT	908760
CCTTCCTGCA	AAGTTATTTA	TTAACATGTT	GCTTAATAGT	AATCTTGAAG	ATATATGTGG	908820
ATATTGTTGT	AAAAAGGGGA	TCGATAATTC	TGCTAAGAAT	TTTAGCGCTC	TTCTGATTTT	908880
GTTATCAAAA	GATTATGGTT	TGCTTTGTGG	GCTATATAAA	TGGACTTTTTT	AAAAACCTTT	908940

671

TCTTTTTTGT	TTTTTAGCTT	TTTTTGCTTA	AATTTAATTG	CGATAGAATC	TTTACCAGAA	909000
ATAGATTATG	AATATTTTAA	CAAGGATAAA	TCAGATCTTG	TAGATTTGAT	AAAATTCTTA	909060
GGTGAATTAG	ATTTTCAAAC	TATTTTAAAA	GATAGAAATT	TATTTATTGG	GATTAGAAAT	909120
TTAACAAATT	TTAAGAATGT	TCAAGAGCTT	AATATCGATG	ATATTAATAG	AATAAAAAAG	909180
ATTAATCCAA	TTGGTATAAT	TTTATTTAGA	GAAAATTTAA	AAGATGCGGA	GCAGACAAAG	909240
GGATTGATTA	ATGCAATAAA	GAGTCATATT	GGACATGATA	TTTTTATTGC	TATTGATGAA	909300
GAGGGGGGAA	TAGTTAGTAG	AGCTAGTGAA	AATAAAAAAA	TGGGGGTTTA	TAATTTTCCG	909360
GCCATGGAGC	ATGTGGGGGG	TGTTAAAGAT	TTGCATCTTA	TTTATAAAAT	TGGTGAAGTT	909420
CTTGCTAAAC	AATTGCGTAG	ATTGGGTATT	AATTTAAATA	TGGCTCCAGT	TGCCGATATA	909480
AAATTTGCAC	CACATACTCC	TTTAITTAAT	AGGACATTTG	GAGGATATTC	CGCTTATAAT	909540
ATTGGACTTA	TGGTAGAAGC	TTTTATTGAT	GGTATGCAGA	ATAATGGAGT	ATTTTCGGCA	909600
ATCAAACATT	TTCTTGGATT	AGGGGGAACA	ACTACAGATA	CACATAAATA	TTTAGCATTT	909660
TTGCCTTATA	GTAAAAGCTT	TTTAATGTTA	AATAATTTTG	TTCCATTTGT	TTTTGGTAGA	909720
GCTGCTAAAT	TTATTATGAT	TGGTCATGTA	AATGTTCCCTA	AAATTTCTAA	AGATATAACT	909780
AGCATGTCTA	AAAGTATTGT	TAATATTATA	AGGGAAAATT	TAAATATTAC	TAGTATTATG	909840
ATGACAGATT	CTTATGATAT	GGGAGCAATT	ACAAGAAGTT	TTTCTAATAT	TGAAAATGCT	909900
ATTA AAAAGT	CTTTGAGTTC	GGGTGTCAAT	ATAGTACTCA	TTCTTAGTGA	AAATTGTTTTT	909960
GAAAATTTGT	TTTTGGTCTT	TTTACAATTT	GTGTTAAATA	ATTTATACCA	TAAAAAAAGT	910020
TCTATAATAA	AAAAAGGATT	ATATAAATAT	AGAAATTCCT	AGATCTAAAA	GGATAAATTC	910080
TTTAAAAGAA	GTCGATAATT	TATAGTAAAT	ACTATAGTTA	TTAGGTATGA	AATCAATTTT	910140
AAATTTGAAG	GTAATTATGG	GAAGAAATTGG	ATAGAGAAAT	GCATGAGTTG	TTTTTCCTGT	910200
AAATATAGTA	GTTCTCAGAG	TTAAATCGAT	TTGGGTTCCTA	ATAAAAAATT	TTATAGCAAG	910260
TGTATCAGTT	AAAATGAAT	ACTTGGAAT	GTAAATAGTG	AAAGCTAAAT	TGAAATAAGT	910320
ATTTGAAATA	AAATCTTTAT	TTGTTGGGAT	AGTAAAAAAA	TTTATGGGGC	TAAATTGTAT	910380
TTCAATCCAT	TCATTATAAG	ATGTCAATAT	TCCGATAAAG	GCAATGTATT	TATAATTTTC	910440
ATTGTAAAAG	ATAGAATTTA	TGTAATTATG	GTAAATTATG	CCTATTTTPTA	TTTTTTTTTTT	910500
AATTAAATCT	TCTTTAGGGA	ATTCCCATCG	AGAAGTAGTT	AATTTATTTT	GAAAACAAAA	910560
TAAATTAACG	CTACATATTA	ATAAAATAGC	ACTATACTTC	ATTAGTATCA	TAGTAGTTGC	910620
TTAATATTAT	ATATAATAAT	ATTATATTAT	ACAAACAGTT	TTTTAAACTA	TTATTAATTT	910680
GATTTAATTT	TTTTTATACT	ATTAAATTAT	ATTTA			910715

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116217 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

TAAATCCAAA CACTACAAGA TTCCATATAA CAAAAAAAAA TTTCAAAAAG AATGCTTTAA	60
AATTAAGATT TTCTGACTTC TTAAATCAA AAATTCAAAA TGGAAAAATT ATAAAAGCTT	120
TCCAAATGAA AAATGAAAGA ATCATTTCTC TTGAGATTTT GCAAAAAGAT ATGATTATCT	180
TATTTATTAA ATTGTGGCCA TCCTCGCCCA ATATAATAGC TACAAATTCA AACTTTAAAA	240
TACTAGATGC ATATTACAGA AGGCCAAAAA TAAAAGAAAC AACAGGTGAA ATCTTTTTAA	300
AAGCTAAAGA AATACATGAA AGCAATAAAA TGTCTGATAA AAAAAATTATG GAACATAAGG	360
AAGAATATAA TAATACCAGC TATACATCTT ATTCTGAATT TCTTGAAAAT TACTACGAAT	420
CGCTTAATGA TCAAATTTAA AAAACCAATA TAAAAGAATT GCTTATTGAA AAATATAAAA	480
AAGAGTTAAT TGTTTTAGAA AAAAGAATAG ACTCTTTTAA ACAACAAATT AAACGCTTG	540
AAAACATTGA AAACGAAAAG GAAAAAGGCG AATTGATTTT ATTAAATATT AACAAAATAC	600
AAAAAGGGAT TAAAGAAATA AACCTCTTAA ATTATAAAGA AGAAAAAATT AAAATATCCT	660
TAAACCAATC ATTATCACCA AAAGAAAATG CCTTGCAATA TTTTAAAGCA TATAAAAAGG	720
GCAAAAATTC TTTCAAAACC ATACAAAATC AATTAAAAGA TAATCTAGAT AAATTTAATT	780
TAATTCAATC AAAAATAACA ATGTTAAAAG TCGAAAATTT AATTCCGGAA GAAGAATATA	840
ATCAAGAAAA AACTGCTATT AAAGAAAAAG AAAAAACGCC AAAAAATAGGC TTGCATTTTA	900
CCTATTGTGG ATTTGAAATT CTATTGGAA GAAACGCAA AGAAAACGAT AAACTTTTAA	960
GACATTGCGT TAAAGGAAAT GACTATTGGC TTCATACAAG AGATTATCCT GGAGCTTATG	1020
TTTTTATTAA AAATCAAAAA AATAAACTC CTAGCCTTGA TGTCCTTTTA GGTGCTGGTA	1080
ATTTATGCGT ATTTTACACA AAATTAGCAA AAAAAATCGGG AAAAGCCGAT CTTTACTACA	1140
CTCAAGTTAA AAATTTAAGA AGAGTTAAAA ATAAAAAGCT GGGCCTTGTA ATTCCAAAAG	1200
CAGAAAAAAA TTTACATATT AAGCTAGATG AAAATCTAAT AAAAAAATA AAAAATCAAA	1260
CCTAAACACT GCTTATAGCA AAGTAAAGTT TTGAATTTTT TACAAAATAT TGTTATTCAA	1320
TGACAAAAAG CATAAAATTT ATAAAAGTGG AGGAAGAACT TTATGATTTC AAAGTTAACA	1380

673

AAAATTGTAG	CAACAATATC	TGATCTTAGA	TGCGAACCAG	AACATATAAA	AGATTTACAC	1440
GATGCAGGGG	TAAATGTTAT	AAGACTAAAT	ACTGCTCATC	AATCACACGA	AGATACAATA	1500
AAAGTAATAG	ACAATGTTAG	AAAAATTTCA	AATAAAATAG	CTTTAATGAT	TGATACAAAA	1560
GGACCAGAAG	TTAGAACAGC	AAATATTGAA	AATCCTATTA	TTGTAAAAAC	TGGAGACAAG	1620
GTAATCATTT	CAACCTCGCC	TATTAATGAG	CCTAATAACT	TTCAAACCAA	TTATGATGGA	1680
TTTGTTAAAG	AAGTACCCCA	AGGATCTAAA	GTGCTAATTG	ATGACGGTGA	ACTTGAAATG	1740
ACTGTTGTTG	CCAAATTGCC	TGACAGATTA	ATTTGTGAAA	TTAAAAATGA	CGGCCAAATT	1800
AAAAATAAAA	AATCAATCAA	TACCCCGGA	ATTTCTCTTA	AGCTACAATC	AGTAACCGAA	1860
AAAGACAAAG	GATTTATTGA	GCTTGCAGCA	AAATATAATG	TTGATTTTAT	TGCCCATTCG	1920
TTTGTAAGAC	ATTCCAAAGA	CGTTCAAGAT	GTTCAGAAA	TTTTAACTGC	CTCTGGAAAT	1980
CCTGATGTAA	AAATTATATC	CAAAATCGAA	AATCAAGAGG	GAATTGACAA	CATTGAAGAA	2040
ATTGCAAAAG	CTTCTTACGG	AATAATGGTT	GCAAGGGGAG	ACATGGGAGT	TGAAATTCCT	2100
GCAGAAGATG	TACCCATTGC	TCAACTTAAA	ATAACACAAA	CCTGTATAAA	GTATGGAATA	2160
CCCGTGATTA	CAGCAACTCA	AATGCTTCAT	ACAATGATTG	AAAATCCAAG	ACCTACTAGA	2220
GCAGAAGTGT	CTGACATCGC	TAACGCTATT	TTAAACGGCA	CAGACGCAAT	TATGTTATCC	2280
GGAGAAACCG	CCTACGGGAA	ATATCCAATT	GAAGCTGTAA	AAATGATGAC	AAGCATTGCT	2340
AAAAAAGTTG	AAAAACACAG	AAAAATGACC	TTATATAAGG	ATGAACTTTT	TTACGATAAA	2400
AGTATCACAA	GAACTATAT	TATCAAATGT	GCAATTGATG	CCACAAAAC	TATGGACATA	2460
AAAGCAATTA	TTGTAGATTC	TCTAAAAGGC	AAAACCGCAA	GAATAATGGC	AACCTACAGA	2520
GCAAGTGTTT	CATTATTCAT	TACAACAAAT	AGCGAAAGAC	TAGCAAGAGA	ATTAGCATT	2580
TCTTACGGGG	TTTATTCTAA	TCTTGTAGAC	AATAATTTCA	AAAGAACTAC	CGAATTTGTA	2640
GTAACCTCTC	TTAAAAATGTT	AAAAGAACAA	GGTGTGTGTT	ATGACAAAGA	TACTGTAATA	2700
ATTATTTCTG	GAAATCCAAA	TAGAAATATT	GAAAAAGGAA	CAGAAATTTAT	GGAAATAAAC	2760
ACAGTAGAAG	ATGCAATCAA	AGGACGAAAT	ATATAAGCA	AGCTAGAAAC	TCCTTGTTG	2820
AAAACATATT	TTATTCAGAT	AATACAAACG	ACTTGTCATT	TAAGTTGGAA	GAAAAAAAAA	2880
CTCACAAAGC	CCTCCTAACA	AGTTATGGGA	GCTATGAGTT	TTTTTTAAAA	AATGAATGCT	2940
TGTTTTAAAA	AATAATATCA	AATCAAAC	ATAATGTATT	TATAATCTCT	GAGGCCAAAA	3000
GCAATTTTTT	AATTAATATA	TCCAATCACA	ATGTGTGGAA	AATTTTAAAT	AAAAATATTA	3060
AAGTAAACCT	AAAGATATTA	AAATTATTAA	AAACCTTAAA	TTTTATTAAT	ATAGACGATA	3120
AATTAATCGA	AAATGATCAT	AAAATTGAAA	TTACATTGAA	TTTTATTAGC	AACATAAAGG	3180

AAAACATAAA AATAATTCCA ATAATTTTTG GAAAACTTG CAATAAACAT TTACTAAAAT	3240
TTTGCAGAGTT TTTAAAACCT TTTATAAACA GAGAAGAAAA TTCATTTATT TTTCTATCTT	3300
GCTTTATTTC AAAATCTACA AATATAAAAA AAGCCTTAAA GTTTGAAGAA AATTTAAAGC	3360
ATATCCTTCT TGAAAAAAA TTGCCTAATC TTAACCTAAT ACTAGAAAAC TATAAATCAA	3420
AAAAAATATT TCCGGAAAAT ATAAATGCAA TCATGACCAT TTCAAGCCTT TTTAAACATT	3480
TCGAATTTAC AGACTCAAAA ATAACATTTA ACTCCCCAGA ATACTTGATA TCAAACAGTA	3540
TTCTAATAAG ATAAAATTAT CAAAATAAAA ATTTATAAAA AGTTTTCTAT TTTTTTGCAG	3600
TTTTTCTTTA AAAAAGCATC AAGCCCTATC TTTGAAATAC TTCTTAGCGC ATTAGCAGAA	3660
ACCTTAATAC TAACACTTCT TCCAAGATTT GGAATAAAAA ATTTTTTATT TATTAAATTA	3720
ACCTTAAAGG TTCTTTTGGT TTTTACTCCA ATATGTTGTC CAGCTCCACC TTTTTTCTTG	3780
GCAAGCCCTT TCCTTGGAAC ATTGTTTCCA AACATAGTTT TTTTTCCTGT TATCTCACAC	3840
TTCTTAGCCA TTTTAACACT CCTTCAAATT AAGATTTTTT CTCCAAATAT AAATCCATTA	3900
ACTTTAAAAA TAAAGCTAAA CTACCCAAAA TATTTTTCAT CATACCTCCA AAGTTTAAAT	3960
TGTTTCCATA GCTTTTAGCA AGATCCATAT CAAGCTCTTT CCAATTATAA ATCAGCTCTC	4020
TTTCCAAAGA GACTTTTGAA TAGTCTGAAA GACAATCTTG CAAACGCTGC TCAATAGAAT	4080
ATATTTTGGG ATAATATTCTG CTTGATATAG CAAACGCCCT TTTATTAACA TCTGCTATTA	4140
TATTTAACAA CAATTTCTCC GAAGATTTAT CCCCCAAGA AGCTCTGTGC AATAATGCAT	4200
TTATTTCTATT GCCATAACCG CCTTGTTCCT CCAAATTAGA ATCAAAATCA ATAAGACTTG	4260
CATAAATATT AATCAAAGCA TGCATGTCGT TAGACATTTT TCTTGAAAGC TCTATAAGCT	4320
TCCATTGTCC TTTAATAATA AGTAAATTAA TAATATCATT AAGATCTTTT TTAACAAAAT	4380
AAATAGTATA TGTCTCTAAA TAACTAAAA GTTCGCAATA AATATACCCC GTAGTGCTCA	4440
TAATTTTAGA TACAATCTTT TCATTCATTT TTTCATTATA ATTATCCAAA TTTAAAAAAG	4500
ATATTCCTGG GAAAAGCTGC TCGGCTAATA TTTTAGATTT ATTATTTTTT TGCAAAACTT	4560
TAATCTTTTC AATTTTCTAGT GCAACATGCT TAGTAAGATC ATTAACAAAAC ATTCTTGCTA	4620
TTGGATTGGG TTTTGTCCCA ACAGAAATAG GGAAATAATC TGGATCCCCA CTAACATATC	4680
TTATTAGATA TAAAATTCTT TTAATCTTAT TTATATCCAA AATAGAAGAA ATAACCTTAA	4740
TCCATACATT AGACTTAATA GGAAAATCTT CTTTATTTCC ATAAATTTCT AAAATAATGT	4800
CATAAAGGTT TTTCCAAATA GAAATATTCT TAATGCAAGA AATACATTCT AACAAATCTT	4860
TAAGATCATC TATAATAACT CCACAACCTA TAGAGCTGAA TCTAGGCCTA TACACAAAAT	4920

675

CATCTTCTGG	AAGCAAGTTG	TCAAAATTTT	TAAGAACCAA	ATGATATTGA	TATAAGACTA	4980
AATCAAAAAA	ATTATGCAAA	GCTTCATAAG	TTTCATCTAT	CAATTTAATT	TGTTCTTGAG	5040
TTATGTTTTT	AAACAAATAA	GATAAATTAT	TATGTAAGTT	TTTAGGAAGA	TCTGAGGCAA	5100
AATTTATGTT	ATCGCTTGCA	GAAAAAGAAT	AAATATAATC	TAAAGACTTC	TTTTGGTTTT	5160
CATTTAAGTA	TTTTTCAACA	ACAAAATGAA	CAATTTTATT	AGAATTTTTA	TATCTTTGTG	5220
CAAATGGCCT	TAAGGGAGAA	AAAATTTTAT	AAAAATTATA	AAGAAATCTA	GAAAATTGAG	5280
GTAAAGCCTG	AATTTTTGAA	GCATTAAAAA	AATTACTTAC	TCTGCCTAAA	CTAACTTTAA	5340
CTTCTTTTAA	CCTTTTTTGC	TTTATTTGCT	CAGAAGTAAG	TTCTTTATTA	ATACTAAACA	5400
TAGAAAGTAT	AAAATCAAAT	AAACCCAAAT	TCATCATCCC	CCTAAAAGCT	CTTAAGCCAC	5460
CTTACTCTAA	TTTCCAATTA	AGCATGGAAA	TTAATATAAC	TATAAAAATT	ATACATAATT	5520
TATTGTAAAA	TAAAAGAAAA	AACTTGAATA	ATTTTATGAG	AATAAAAAAT	TTAATACTAA	5580
TAGCAATTTT	ATTAATTAGC	CCTAGCTGTT	CAACAAATAA	GAACATCGTT	GTACTAACTG	5640
ACAATAAAAC	AATACCATTT	TATATAAATC	AATTTAATAT	AGAAAAATAA	GCAAA'TTTTA	5700
TAATTAAGTT	TAGAAATAAT	ATTGATCTGC	AAACAATAGA	AAAAGAAAAT	GCACAAATAA	5760
TTATTTCTAA	AAACATTGGT	AACACAAATA	TTGCTAACCA	TTTTAAATCT	GTAAAAATCA	5820
ATTATAATCC	AGATTATCCT	ATCTTAAAGC	ATATTTTCAA	GCAATTTAAC	TACAAAATTA	5880
TTCCATTGGG	CTTGACATT	CCTATTTTAA	TCATAAAAAA	TACACATCAT	ATTAAAAAAT	5940
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GATTTTCTTT	TGAAAAAAT	AAATTAAATT	ATAATGAGAA	TCAAATTTTA	AAAATGCTAG	6120
AATATTTCTC	ATCATTTTTA	AATACAAAAC	AAATGGACTT	GCAAAAAGAT	TTCTTTAATA	6180
AATACGGCTA	CCTAAAGTTA	AATAAAATAT	TGCTTAATAA	AAAATCTCTT	TTAATAGCAG	6240
GATTGAGCGA	TATAACCTTC	TACAATAGCT	TAAGCGAACA	AGAGAAAGTCA	CAAATAAAAT	6300
TTTCCTATTT	AATAAACGAT	AACAATGAAA	TTGTTATCTC	AAACCCAAAT	TTTATTGGCA	6360
TTTTAGAAAC	ATCTGTTTTA	ACTAAAAAAT	TTATCAACTG	GATATTGTAT	AAAAAACTC	6420
AAAAAACCTT	AATTGGATTT	AACAATCAAT	CCCAATCAAA	TATATGTTTT	GGATTTGCCA	6480
ATGGTTTTAC	CCCTTACAAA	GAATTAATTT	TAAAAATAAA	ACATTCAATT	GATGGAATAT	6540
CTCCTTTTAT	TATTGACGAA	ACTCAAATCA	ATAGCCATTC	CTATGTATTA	AGCAAAAAAA	6600
CAATTGAAAA	AGAAAACCTA	CTAATAAATG	AATGGTTTTT	CTCTAAAGCT	AATAATCTAA	6660
AAAAAAATAA	AAATTAAATA	AGTCTTTCCT	TGTAATTCAA	AGTAATTATT	TTAAAAATAA	6720

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TAAGAAGAGA GGTAAAAACA ATTAGAAAAAT AATTTACAAA AAGACAAGTA ATCCCTGAGA	6840
AAATAGCTAT CATTAATGAA ACTAGAAAAA TCATAGCCTT GGAATTGAAA TTAAATCTTA	6900
TTTTAGAAAA CAAAGAGATA AAAAATGCCC CTATTAAAAAC TAGCGAAATA GGAGAAATCA	6960
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GAAAAGCGCT TGGCAAATTT TGAATTTTTA AAAAAAATCC AAAGTACGTA AAATTTGAAA	7080
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CTAAAATATT TTGATACACA GAATTACCCT TCAAAGTAGC AAATGGAATT TTAATATGTA	7260
ATATAACATT CCCTGTATTA TTAAATCTAA TAAGTTCAAA ATTTTTTATT ATTTTAGAAT	7320
GATTGTTAAA GGCCACAAC TTTTGCATAT AAATATAATC ATAAAAACCT CTCTTAGAAT	7380
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CAAAAAAAG ATATCTTTTC CTAAGCTTTT CAAGAGATTT ATTTTTATAA TTCAAAATTT	7500
CATTATCGCT GGGCAATAAC TTATAAAGAT TCGAAAACCC GTAATAAGCT AATTTAAATT	7560
TTTCAGTATT AAGAAACAAA AAATTTTTTT GCTTTTCTTC GGAAATCAAC TGCATTTTTT	7620
CTTTTTCAAA ATTCCTGTTT TCATTAAATA ACTTTAAAGT CAAATTTAAA AGCACAACAA	7680
AATTATCGTC TTTTGTGCA ACATAAGCAA TATAAGCAA ATAATTGGCT GTATAATAAT	7740
CATTTTTAGA AATAAATCA TTGACAATAT TAAAAAATC TTGCTTTTTA AGACTTTGCA	7800
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TACTATATTC AGATTTCACT AAATAATAAT TTGTTAAAAG CTCTTCATTA TTTACATAAA	7920
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TAAAAAGAG TCCTATAATA AAAAATAATA GTAAAAATGC ATAAAGCCTG GAAAAATAAT	8220
ATCCATTATG CGATTTTAAA TGAATCTTTA TTTCTTGCTG AACAAAAAA GCAAAGTAAA	8280
TACAAACAAT AAAAATAAAA AACCCAAAAA AATACTTATA AAAAAGCAAA ATAGAATCAA	8340
AAAAAGTTGC TATTAATTTA TGCTTTTCTA AAAAATTTTC TCCAAAAAA TATGAATAAC	8400
TAAAGAGCAA ACCTAGAAAA AAACACATAA AAATAATAAA ATTGCTCAAA AATGCATATA	8460

677

TTTCTCTTTT	CATAAGCTTT	AAGAATTAAC	TACCCCTTATA	TAAATTATTA	TCCAAATCTT	8520
TGCTGATTTT	AATATATTCT	GAAACAAAAC	CAAATAAATA	GGTAGAAAAA	AAAGTTAAAA	8580
CACAAAAAAT	AAAAGGAATA	AAATCAGAGA	TCATGCTCTT	TCCTATTATT	ACATTGTAAA	8640
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GATAAAGAAA	TATTGCAAAA	CTATTTGAAA	AAATAAGATT	AAAAACATAA	GAAAAAGCAA	8760
ATAACAATAA	AGAAATTCCC	AATATATTAA	AAATTAAATT	TAAATAATTT	AGCGAGAGTA	8820
GAAAATTATT	CAAAATTTTT	AAATCTCTGA	AAAGAAAATC	AACAAAATTA	TTATAAATCT	8880
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GGTAAGAAAA	ACCTTTATCC	CCTTTGTCAT	TCTCCGAAAC	GATTAAAACT	CCATTAAAAAC	9000
CATAAATTCT	AGGCCTATTA	CTAGAAAATA	TTATCTTATC	ATTTAAAAAA	TGCACAATCT	9060
CATCTTTAAG	GATAAAATTA	TCATTTCTAT	TGCTATTAAT	ATAGTAAGAA	TGAAAACTAT	9120
GACTAACTAA	AAATCCTAAA	TAAGAAAACA	ATAAAATAAG	AACAAAGATA	ATACAATAAA	9180
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TAAAAGTAAC	AACAAGGGAC	AAAGGAAAAG	AATAAATATA	AGCATTGTAA	TAAAGACTAT	9300
AGCTAAAAAT	AGAAAAATTA	AAATACAAAA	ACTTATATTT	CAAATAAAAT	GTACATATAA	9360
ACATTAAAGA	AAAAAGGCAA	AATATTAAGA	TAAACCTACA	AATTATTAAA	AAGATCAATC	9420
TTAAAGAATC	AAACACAGCA	AATCCTCCCC	CCTCGAAAAT	TGAAAAAACT	TTAAGCCTTT	9480
TTGTTATCGA	CCAAAATATT	TTAATCTTC	TTTTTAGCCT	CTTCAAAGCT	AATTTGCAAA	9540
GCTAAGCTAA	TCTCGTGCTC	CAATATTAAC	TCAAAATCAT	TCAAAATCCT	TTTTTCGTAA	9600
AAAGGAAGTT	CTTTTTGAGT	AGATTTTTTA	TATAAAAACT	TATATAACTT	TGCTGTATCT	9660
AAAATATCGC	TTTTTTTATA	AAATTCATGA	CCACCATCTT	TTATTTTTTT	TGAATCTATT	9720
TGCCCTTCAA	ACTCTTTAAT	AACATCAAAA	ACTTCTTCTA	CCTTTTCCCT	GCTAACCAAA	9780
GCTCTAATTC	CAAAATCATC	AACTTTAGCA	ACAGGAACCA	TAAAAATCAT	ATCATTAAAT	9840
GGAAAATGTA	TTTCATAATA	ATCAATAATC	TCACCATTA	ACTCTTTAGT	CCTAATATCC	9900
TTAATCGTAC	CTACTCCATG	CATTGGATAA	ACTACTGATT	GATTTAGCAA	AAATGCCATA	9960
CTTACCTCAT	AAAATATAGA	TAGTTAAAT	TTAAAAGTTC	ATAAAAAAC	ACTTAAATTG	10020
GTTCTAATAT	TAAATTTATT	TTCATAAAAT	AAATTTTCAA	GATATCTATC	ATTACAAAAG	10080
CTTATTATTA	CACTAGGAGT	AAGTTTATTA	ATATTTGCAA	AAAACATTTT	TTTATTTCTC	10140
TTTACAGCTT	TTAAATCATA	ATACCCAATA	AAACTAATTT	CTTTATGAGA	TTCTTTCAAT	10200
CTTAAAAAT	TTTTCTTTGA	AATCACTTTA	TCCTTGTC	TAATATAACA	TGTTTTATGG	10260

GCATTTTCTA	GTAATTTCCAT	TAAAATGAGA	AGAACTGTAT	TTGAATCATA	ACAATCAATA	10320
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TGCTAAACAA	TTCTCATCCA	AAACAATTTG	CTTCACAATT	TAATTACCTA	ATTTAGACAA	11340
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679

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685

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689

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691

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693

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CATGTACCCCT	ACAAGCCAAA	TCAAGTCTGA	GCCATTCCCTT	TTTAAATTAT	CAAGATCTGA	37080
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695

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TAAGGAATTA	TTCTAGCAGA	ATACAAATCT	TTTTCTTTAT	AAAAAACAAC	TCCTGGGGAT	49080
CTGTGAATCT	GAGAAACAAC	AACCCTCTCA	GCCCCATTAA	TAATAAAAGT	GCCTCTTTCT	49140
GTCATTAAAG	GAATAGTTCC	CATGTATACG	TCTTTTGGCC	TTATTTCCCC	AGTAGTCAAA	49200

AATTGCAAAT	TCAATCTTAC	TTTTAAAACA	GCCTCATAAC	TTTGACCCTT	TCTTTTACAT	49260
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TGAACTCTTT	TTATCATTAA	AAGACTCCTT	TTTTAAGACA	TAACAAGCCG	CACATCATAA	49560
CGACATGCGG	AATAACAAC	TTGATATATT	TTTAATTTTT	TATTTAACTT	CAACTTTTGC	49620
GCCAACTGCC	TCAAGTTTCT	TTTTTAATTC	TTCAGCATCT	GACTTAGAAA	GACCTTCTTT	49680
AATAGCTTTA	GGAGCGGCTT	CAACTAACGC	CTTAGCTTCT	CCAAGACCAA	GTCCTGTAAT	49740
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AGCAACAGCG	GCAGTTACTC	CAAACCTTTC	CTCAATAGCT	GTTACAAGGT	CAACAACCTC	49920
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TCCTTATATA	TTTTTCATTT	ACAGTGATAG	CATGCACTCA	AAAATTAAGA	CTAACACTGT	50040
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CTTGAACCTT	AGCCTCATCA	TAAACTCTC	CTAATACAAA	ACCGCCCTTT	ACTTTTAAAG	50220
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TAACAACAAC	TGTAGGGCCA	ACCAAACAAG	AATCAACAAC	ATTAATATTC	TTTTCTTTTA	50340
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701

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715

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727

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731

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AGTTTATTAA	ATCCTAAAAA	GAGTGCTGGG	ATAAAGCAAA	ATATACTTTT	AGTAATTATT	112680
GCTATTGCGC	TAATTGCTAA	TCCTAAAATA	AGAACTTCCT	TTGAAAGTAT	TTTATTAAATA	112740
TCTGACATAA	GTCCGATTGA	TGTAAAAAAG	ATCGGGATAA	AGAATCTTTC	AAAGATTGTT	112800
AGTTTGCTCT	GAATTACGTA	TACAATGTCT	GTTTTTGACA	TAGCAAGTCC	AAATACATAA	112860
GCCCCAACAA	CAAAAGACAT	TCCTAAATTT	TGGAAAATGC	TTGCAATAGT	AAGGGCTAGA	112920

GAGAGCGTTA	TTACGGTTGC	TAAGGTGACA	CTGTTTAATT	TTTTCAACAG	TCTTGAGAGT	112980
GTTTCTGATA	TATATATTAA	AGAGAAAGTT	AAGCATAGCC	AAATTACTAT	GTTTTGAAC	113040
ATAGCTTTTA	TTGAGCTTGC	TATATCAAGA	TCTGATATAG	ATCTTGATAT	AGTTATTACA	113100
CTTGTAAGCA	TAAGCATTGA	AAGCACATCA	TCAATAATTG	AAGTTGAGAT	TATTGTCACT	113160
CCTTCTGAGG	TACTCATTTT	TTTCTTTGCC	GAGAGTATGC	TTGCTGCGAT	TCCTGCTGAT	113220
GTGGGGGTTT	CAATTATTCC	AATAAAAAGT	GAGGTTGGGC	TTATTAGGGG	AACGTTAAAA	113280
ATTATGCTTG	CCATTAGTAC	AAAACCTGTG	AAGGTTCCAA	CAACCTCTGT	TATTCCAATA	113340
ATTCCTCCGC	GTGGCAAAAA	TTTGATAAAC	AATTTTAAGT	CAGTTTCAAG	TCCTGCTGTG	113400
AAAAGCAATA	TTATTGAAGC	TATGGTAGAG	ATTGCAAATA	TTTTTTCATT	TATTAAATAA	113460
TTTTCTCCAA	TTTGAGTTAT	TCCCAATGGG	AATAATAAAG	GTATTTGAAT	TTTTCCAAAG	113520
GCATTCCGAC	TTAGAATTAT	TCCCGCTGTT	ATTTGCCCTA	TTACTTTTGG	AATTCCTATT	113580
TTAGCTACTA	GATTGCCTAT	TGAAATAGAT	GAGATTACGA	TGATTGCCAG	ACTCATGACA	113640
AAAGCCGACA	TTTTTACTTC	AATGTCGTAT	TTGTGTTGAGT	ATGAAAATAG	AAGATTAGGT	113700
AAGTGCAGCA	GTATTGTTAT	GTAAAAAATT	TTTTTGTTC	TTTTTAAAGC	TCTTTTGAAA	113760
AATTATATTT	TAGCAAGTTT	AATAAATTTT	TAATTGCTAG	TTTTTCTTTT	TTTCCAACGA	113820
CTGTTATTTT	TATTTTTTCT	TTGTATATTA	TACCCAATAT	GATAATTTCT	ATTGTGGACT	113880
TTGCGTCAGC	TTTTCTGCCA	TCTTTTGTG	TTATTTTTAT	GTCGCACGAA	GAATGTTTAT	113940
TTGCGAATTC	AGCAATGATG	TTTGCCGACC	TTGAATGTAT	TCCATCTTTA	TTTATTATCT	114000
CAATTTCTAC	TTCTTGCAAT	TTTTACTTAT	CTTATTTGTT	GTTTTTTTTT	TCCTTCTCTT	114060
TGGTTGCTGT	TTGTAAAGT	CTTGCTATTG	CACTATCAAT	AAGATTAAGA	AGTATTTTCC	114120
CATCTTCTCT	TATATGTATT	ATTTTCCCCC	AATTAAAGTG	AATATGTGCG	TCTAATTTAA	114180
AAAGTTCATG	TTCTTTTTTA	ATTGTAATTT	TAAATTATC	AATATGTTTT	TTGATATGAG	114240
TATCAAATTT	TTCTAGCTTT	TTGAGAATAA	AATTTTTTTC	ATTCTCATTC	AAGCTGTAAT	114300
TAACCGTTTG	AATTTTAGGT	TCCATAATAT	GTCTCCCTT	TCTCAGATTT	TAATTCATTT	114360
CTGTATTTAT	TTACTGTTCT	TCTAGAAATA	GAGATTCCTT	TGGACTTTAG	TATAACAGAA	114420
ATCTCTTTGT	CTGACATCTT	TTTATTTGCT	TCTAATAACT	TTTTTACTGT	TATTTTGATG	114480
CTTAATTTTG	AAAATTCATT	TGTTTTTGCT	CCACCAACAG	AGCTAAAAAG	CTCTTTGATT	114540
AATATTGTAC	CCCATTCGCA	TTTAAAGTAT	TTATTTTTTA	TTGCTCTTGA	TATTGTTGAT	114600
TTGATACAC	TAATTTTTTC	TGATAAAATG	CTCAAGTTCA	TTGGCCTTAA	GCTTTTAAAT	114660

737

CCTCTTCTTA	GAAATTCCTT	TTGCAATGTA	TATATAGCTA	TTCCTATTTT	TGCAAGTATT	114720
TCGTCTCTAT	ATCGTAGGGA	TTGATTAAAC	CACTTTGCTT	TTTTTTGTTT	TTGGGGGTTT	114780
TCACTGTGCC	TTTTAAGTTC	TTTTTTAAAG	ATATTAACTT	CTTTGATTTT	AATTTTAAAT	114840
TTATTATTGT	GATTTATTAT	TAATATATCT	GGATCAACAT	AAAAATTAGT	GTCGTTTGGG	114900
TCTTTAAATT	CGAGCGTTGG	GTTGGGGTTA	AGTTTTTGTC	TGATAATTTT	TAAAGCCGTG	114960
TTAAATTCCT	TGCTTCTTAT	TTTAAGTTCC	TCTTTTAACT	TTTTTTGAGT	TTTTTTCAAGA	115020
AGCTCTGCTT	TTTCAAGAAT	TTTAATAATA	TTAGTTTCTA	ATTTATGATG	CTTTGCTTGC	115080
AAAATTAACG	ATTCATTAT	GTTGGGGACA	CAAATTCCAA	TTGGATCAAA	TTTTTTGAATA	115140
AGTTCAATTA	TTTTTTTAC	TTTTTCTTTT	TCTTCCTTTT	TAAAAAGATC	GTAAGGGTTT	115200
ATTATATGAA	AACCTTTGCT	GTTTAGATTG	TTTATGAGTA	TTTCGCCTAT	TTTAATTTCA	115260
TCTTCATTTA	TTCTTTGAAT	TCTTAATTGC	AGTAAAAGGT	GTTCTTTTAA	AGAAGTATTT	115320
GTTTGTGTTT	TTTCAAGAGC	TATGTCGTGT	TGATTTTTTA	TCATATCATC	TTCTTTATAA	115380
AAACTTTTTT	TAAACCTATA	TGTTTTCAAT	GTTTCAAAAA	ATATTTTATT	TGAGTTTATT	115440
TCTAGACATT	CATTATTTTC	GCTTTCTTCT	AGTATAAGCT	TTGTTAATTC	TTTTTTGGTTA	115500
AGGCTTAATA	TTTTTATTGT	TTGTATTGTA	ATTGAGTTTA	AATTTTGAGA	TATTTTTAAT	115560
TTTTGTTTAA	TCATATTTAT	ATTAATGTAT	AAAAAATCC	ACTAAGTATA	ATTACTAATG	115620
CTGGACTTAT	TTTATTATAA	AAAAATAAAA	TAAAAAAATT	AATTCCTACA	ATAGCCAGAG	115680
TTTTCAAAAG	TTCTGTTTTG	TTGTTTTCTA	TTTTTTAAATA	TGTATTTTCA	AGCAAAATGA	115740
TTATTGTAAT	TATCCACAGC	GCAACAATAA	TAGGTTTTAG	ATTTTCTAGG	CAATAATTTA	115800
AAAAGCCGAT	TTTATGTAGT	ATTAGGAGGA	TTATAATCAT	TATTATTATT	GGGGCTGTTA	115860
TTAATGCTAC	TGTAGCAATT	ATTGCTCCCG	CAATTCCTGC	AGTTTTTCATT	CCAACGTATG	115920
TTGCTATGTT	TGTTGCAATA	GGCCCAGGGG	TTATTCTTGA	TATTGTAATC	ATATTGACAA	115980
ATTCTTCTTT	TGTTATCCAA	TGTTTATTAT	TAATTATTTC	GTTGTTTATT	ATTGCTGCAA	116040
TTCCATTACC	GCCTCCGAAA	TTTAATAATC	CGATTTTTAA	GAATGTAATG	AATAAATTTA	116100
TTAAAAATCAA	CCGATATCCT	TTTTCTATTT	AGTTAATATT	TTTTTTATTG	TTATATATTT	116160
AAATGTGTAT	ACTAAAAAGA	AAATTAACAA	TATGTATGAT	ATTTTTATTT	TTAATTT	116217

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111309 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GTATCTATTA GTAGATTTTT ATATCTATTT GTTAGTGGGT ATAAATTGAG TTCGTTTTTA	60
AACTCGTTTA AGTATTTTAA GGCAACAATA GTTGAATTTT TTATTGATTT TGATGAGTTT	120
ATCATTTCTG TTGAGTTTAA ATATTTCTTT TCTTGCTTTG GTAGTTTGG TATTTTTTAT	180
TTGATTGAAT TTTGAAATAA TTTTGGTTC AAACTTTTT TCTTGTA AAAA AATAAATTAT	240
TGGCAAACTT TTTTCCCTT CGAGTAAATC ATCTCCGAAT TCTTTACCAT TAATTTTATT	300
TTTAATGTTT TTAATATCGT CTATTATTG GAAATAAACA CCAAGCTTTA AAAATGTACT	360
GTAAATTTTT TTAGCTTTGT CTTCAATTATT TGTGAGTATT GCAGCTAGAA AGCTGGCCAT	420
TCCAAAAAGT GAAGCTGTTT TTAATTCTAC TAAAGAGATG TATTCTTTAA TACTTGGGAT	480
GTATGACTCA TTGTGAAATT TAATATCAAT TCCTTGTCCT AGGTGGAGAT TTGAAAGAGT	540
TGTAAAGAAA TTTTCATAAA TTAATAATTT TTGATTTTCT TTTAAATTTG ATTTTTCTAT	600
TAATTTTGCA GGTAAAAAAT AAATTAAATT GCCAGCATTT AACTGTTAT CTATTCCATA	660
GATTAAATGT ATTGCTGATG CACCGCGTCT TTTTAGTGAA TTGTCTTCAA TGTCATCAAT	720
AATCAAGCTT CCAGAAATGAG GAAGTTCAAG CAGCAAGCTT AATTTATATA TTAGTTTGGT	780
ATTTTTTCT TTTAAACCCA ATGCATATGC TAAAGAATC ATTATCATTG GTCTTATTCG	840
TTTTCCGCCC CTATTAACAA TTTCAATTGC TGGTGCTTTA ATATAATCAA GGGTTTCCTT	900
TTTTATTTTA AAAGTAAATT TTAATCGTT ATCTTTGAAT AAATTTAGAA AATTAGTTGT	960
TGAAAAGATT TTATTAATAT TTTTTCAT ATTTTTTAAA AATAGTTTAT TTTGCATAAT	1020
AAGAATTATA ATGAAAAAGT ATAATAAAGT GTATTAAAGG GATTGATGTG TATCGCTTGG	1080
ATGATGAATA TTCTAAAAAA GCCAAAAGAG AAGGATATTT GGCAAGGTCT GTATATAAGT	1140
TGATAGAAAT TAATGAAAAA TTTTCTTTAT TTTCTTCTGG CAATGTTTTA GATATTGGCG	1200
CATCACCTGG CAGCTTTTCT CAGTATGCTT ATAAAAAGCT TAAAAGAGGA ATTCTAGTAT	1260
CTGTTGATAT TAATGATATT GGCCTTAGAT ATGATGATAA TTTTATTTT ATAAAGGGAG	1320
ATATCTTTTT AGATGATACA GTTTTTAAAA TTAATACGTT TAAACCTTAT AGTCTTGTA	1380
TTAGTGATGT GGCTCCCAAG ACTACTGGAA ATAGACTTGT AGATACCAGC AATTCTTTTA	1440
ATTTAAGCAT GAGAATAATA GATTTATCAC TTGAAGTTT ACTTAAAAAA GGAATTTAC	1500
TTGTTAAAGT TTTTCAGGGA GGAGACGAGA TGCAAATTTT TAAAAAGTTT GAAAAATATT	1560
TTAAATTTGT AAAAAAATT AGACCCAAAG CTGTAAGGAA AAATTCTTTT GAAATTTATT	1620

TTTTAGGCAA	AAGTTTTGGC	AAGTAGCAAA	TTAATCAAAT	TGTTATAAAC	AGATTTAAAG	1680
GTATAAAATA	TGTTTAGAAA	AGAAAGTTCT	AAAGACAGCA	GATCACAGCT	TCAAGTTGCA	1740
GGTTTTAAAA	TAGGAAAAGA	AAGCTATGGG	GTGTCAATAG	AGCACATTAG	AGAAATTATT	1800
AAAGTTCCAT	CAGAAGGAGT	TTATGCTATA	CCAAATGTTT	CCGAATATAT	TATAGGTATT	1860
TATAATCTTA	GAGGCAGTAT	TATTCCTTTA	ATTAATTTAA	ATATTAAATT	TGGAGTTCCT	1920
TCTATTTCCG	TAACAGAAGA	AGACATGCTT	TTAACAGGAT	ACTTAATAGT	TAAGATTAAA	1980
AATAAGCTTT	TAGGCATTTT	TGTTGATAGA	GTTCTTAAAG	TTATTAGCTT	TGATGATTCT	2040
AGGGTTCAAG	AACCTCCCGC	TACTTTACAA	ACTTTAGATA	GAAAATATAT	ATCTGGAGTT	2100
GTAAAGCTTG	ACGAGGCTGA	TAATCTTGAG	AGTGAATACT	TAGTATTAAT	TGATATAGCA	2160
AAAATTTTTG	ATAAATGCGA	ATTTGACGAC	ATTCCCTATA	AAGATCAATA	TGAAGAATAA	2220
AGTTCCTCTT	TGCATTAATA	CTTTAAAGTC	GGGAGCTAGT	ATTTTAGGCA	ATGATGTTAA	2280
AGTTTATTTA	GAAACCAAGT	ATTTTGTTGA	AGTAGTGTTA	ATAGATGTTG	GCAGACCTTT	2340
ATTTTCTTTT	CCAAAAGAAA	ATTTTCTTTT	TTTGATAACT	TTAGGAGGAG	ATGGCACAGT	2400
TCTTTTGGCT	GTAAATTTGC	TTCTTGAAAA	TGAAAACATT	GATATTCCAA	TTATTTCAAT	2460
TAATATGGGC	AATGTGGGAT	TTTTAGCAGA	TATTAAGATT	GAAGATTTTA	AAAAAGTCAT	2520
AGATAGATTT	TTTAACAATT	CTTTGGTTAT	TAATAAAAAA	TTTTTGCTTC	ATGTAACAGT	2580
TTCTCAACAC	GGTAAAGATT	TAATTTCTAA	ATATGCTTTA	AACGATATTA	TTATTCGCTC	2640
AAGCGTCTT	AATAAAATGA	TTTATGTAGA	TCTTATGGTT	AATTCTGAGA	GTTTTTTATC	2700
ATACAAAAGT	GATGGGATAA	TTGTGTCTAC	TCCAACAGGC	TCAACAGGAT	ATTCCTTCTC	2760
AGCAGGGGGT	CCTATTTTAG	AAGCAGATCT	TGAGGGATTT	TTACTTACGC	CTATTTCTCC	2820
ACATTCGTG	TATAATCGTT	CTTTTGTTG	CTCTAAATTA	AGTAAACTTT	CCATTTCTTT	2880
TTCAAAGGAA	TATTTTATAG	CAGCAGCATC	AATTTTTTTA	GATGGAATTA	ATTTTGGTTC	2940
TTTCGGAGTT	GACGTTGTTT	TTGAATTTAA	AATTTCTTCT	CAAAGCTTGA	ATTTTGTTC	3000
ATTTTGTACG	GATACTTTTG	TTAAGAGATT	AAAAAACAAA	TTATTGTAAG	TTCAATGTTT	3060
TTTTAAACAG	TGTTCTTTTT	AATAAAAATT	TTTCTTGTTT	GTTGTTTGAA	TGTTTGGTTT	3120
AATCTAATCT	TTAATAAGGT	TAGAGGATTT	TACATGTTTT	ATTATAAGGA	TTTTAATGTT	3180
TGTTTATTC	GCAGAGTTAA	TGTTTAAAGG	GTGTTTTTTA	TAAATTTATA	ACTTGTTAAA	3240
ATATTTAATA	TATTTTGTGC	TAAAATCAAT	ATATTAGATA	GCTGATAAAT	CACCCTTTTA	3300
TGAGTTTLAG	GCAGGTGTTT	ATGGATTTAA	TTGATAATGA	AAATTATAAA	AAAATAGTGT	3360
ACATTAATAA	TCTTGTTTTA	AGGACTTTAA	ATGATATAGC	AGCTATAAAA	GAGACTGGCG	3420

AATTTACATC	AAATGCTAAA	CTTTCATTTA	ATCTTATTGA	TTTCAATTTA	AATGTTTTAA	3480
GTTATATTTT	TTCTTTTAAAT	TATTTTTTATA	CTAGGCCTAG	ATTGAAAGTA	AATTATTCTA	3540
TAAAAAAAT	TTTGTCTGGG	TTGATTTCTG	ATTTTAGTTT	AGTTATTAGC	CCTGTTCTTA	3600
GTATTACTCC	AAGAGAGTTG	ATTGAAATGC	CTCAGGCTCT	TAATTTTAAAT	CCAGAAGAGA	3660
GGTTTTTAAT	TATTAAAAAA	TTAGGTTATT	TAATTGATTT	GGCTAAAATT	TTTAGCAAAA	3720
AAGATTCTAA	AACACTTGTT	TTCTTGAGG	ATATGTATCT	CAAATTTATT	GTTTTTCTA	3780
AAAATATTAT	TGATTTTAGA	GATTTTTCTA	AGAATTTAAA	ACTTGAGAGT	CCTTATTATA	3840
AATTTCAATT	TGAACACCTT	ATTAAAGTGT	TGGAGCTTTT	AGAAGAAGGA	GC'TTTTATTT	3900
TAAGGGGCAA	ATATGAGATT	ACTGGATCTC	ATGAATTTGG	ACTGCATTCT	CTTGGTTATC	3960
TTGAAGCTGG	AAGAGCTTTG	GCTACTATAG	CCTCTCAAAA	AGAAGCTGCT	GAAAAATTTT	4020
CAAGGTTTCA	TGGAGTTTGG	TCTTCAAAGT	TTAGTTCAGA	TTTAATTAAA	GTAAAATAGA	4080
TAAATTAAGG	TGGGGAGAAA	GTAGTTATAT	TGAGTTTTAA	TGTAGAAGAG	GGCACTATTA	4140
AATTCAAAA	ATTAAAATTT	TTTTTGATTG	TAAGCTTGTT	TTTATTATTT	ATAATTTTGA	4200
TTGATTTTTT	TATAAGATCT	ACTATGAATG	TATCTAATTT	TTATGATTTT	AAGAATTTTG	4260
AAAATAAATC	TGATTGTAAA	AATATAAATT	TAAGTAAGAA	TGTTTTTGTA	TCAAATAAGG	4320
TTTTAAGTCT	TAATTTTCGGG	GAATCTTGTT	ATTCTCTTTT	AAGTGATAAC	TTAATAAGTT	4380
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AAAACAATAA	ATTTTTATTT	ACACTCAAGC	TAAAGGATTT	TGTTTTTGCA	ATAAATAATT	4500
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TGGTTTTGGG	ACTTCTAAT	GGTGAGATTT	ATATATATAA	ACAGGGTAAG	ATAATTTATA	4680
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AATATTGGT	TTCACTAAAA	GGCAGTTCTG	AGTATTTTTT	AGAAATAATT	GATTTAGAGA	4800
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TAAAAATAGA	TGATTATCAT	AATTTGTTTA	TTGAAGGCAA	AAATTCACCT	GCGGTGATAA	4920
ATATTAAAAG	TGGTAGAATA	TTTAAGGTTG	AAAATAAAAA	TTCTATTTTA	AGAGCGTCAT	4980
ATGATTATTT	TCAAAATATT	TATAGAGTAT	ATTTTTATTG	TGAGAGTGAA	AAAATCATT	5040
ATATAAAAC	TTATTCTGCA	AATCTTTTTA	AATTGTTTGA	TAATATTTTT	ATTAAAGATG	5100
AAATAAGCTC	TTTTGTTGAA	TTTGAAAGG	GACTTTTGTA	TTTTAATAGT	AATAATGATT	5160

TAAAATACTT	GGGATTGGCT	CAGTGATTTT	AATGTGTTTT	ATATTTTCT	TTAATATTTT	5220
AGATTTATAT	TCATTTTGG	AATTTAGAAA	TGATGAAAAG	TTTGCTTTAG	TTAAAGATTT	5280
TGGTGTGTTG	GATAATAATA	AGTTGAATAT	TAGCCTAAGG	TTAAGGCCCT	TGGAAAAAAC	5340
CGTATCTGTT	TTTCCAATA	ATTATAAAAT	TTTATATTCA	AAAAATAGTT	TAAATAGGGA	5400
TGGTAGTATT	TTAATTATTT	TTGATAATGA	TTTAAATCTA	AATTTAGAGG	TTTTTGGGGG	5460
ATTTCTTTAT	AAGCTTGGA	AAATTTTTTT	AAAAGATGAA	AAGAGTGTTA	TTGATTTGGT	5520
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CAATGTGGTT	GCTGAGACAG	TTTATACATT	GGTAGGGTT	TTTTTAAAAG	GAAAGGGCGA	5640
TGATGAAAGA	TTGGAATTAT	CCAAAAATAT	AAATTTAAAT	GTAGATTCTG	GTCAATACAG	5700
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GAACATTAAA	AAAGATGGGG	GATGTCTTAA	GATAAATGAT	CTTAATTTTG	TTAAGGGTAA	5940
GAATGAGCTT	AAAATAAAAT	ATGGCGATGT	TTATGGAAAT	GAAAAAATAA	TAATTTATAG	6000
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AAAGAGATCC	TCAAATTTTA	GAAAGAGCAA	GGCAGTTTCT	TTCTATTTTT	GAAGAGAGAA	6240
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CCAATTTTAT	TTTAGTTGAT	CTTGGTATTT	CTATGTTTCA	TTACAAGGGT	AGTAAAAAAG	6360
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CAAAAGTTAA	AATAAATCCA	GCTACAAAAA	CTTTTCAAGC	GTTAAGAATT	TATGTAAATG	6660
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GAATTTTAGC	TATTATTACG	TTTCATTCAA	TAGAGGACCG	TATTGTAAAA	GATTTTTTTA	6780
GAAGCTTGAG	CTGTGATTTG	TATGCTAAGA	TCTCAAAAAA	GCCCATTATG	CCAAGTTTGT	6840
ATGAGATTAA	AAAAAACAAA	CCTTCAAGGA	GTGCAAAACT	TAGAGTTGTA	AAAAAATTAT	6900
GAACAGCATA	AGTAAGATTG	AATTTAAAGT	TTATTGTATT	TTAGTTTTGA	TACTAACAGT	6960

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AAAAAAGCT	AATGAAGATA	TAAATATTTT	TGTTGAGTAA	AAGATTTTAG	AATGAGGTTT	7200
GAGTGCCTAT	AAAGATTAAAG	GATATTTTAA	TCTCTTCTAA	AGATGTGAAA	TTTGTGGGGA	7260
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ATGACAATAT	CAATGATAGT	CTTTATTTTG	CGTATAAGGG	AAATAAAGTA	GATGGATTTT	7380
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TTTCAAAGAA	ATACAAAAC	TACAAAAC	GGGGTAATTT	AAATCTGAT	ATTGGACTTC	7680
CTCTTAGTAT	TTTAAGGGTA	GAGGGTAATG	AAGAATATGC	TGTTTTTGAA	GTTGGAGTTA	7740
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CGAATATAAG	TTATGCGCAT	ATGCAAGCCT	TCAAGGAGTT	GCAAGCTATT	GCTTTTGAAA	7860
AAAGCAAAAT	AATTGGCAAA	AACATTGAAA	TCTTTGTTGT	AAATGAAATG	AATGATTATT	7920
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TGATTTTAAA	CGACTCTTAT	AATGGCAATA	TGGGTCTTTT	TATGGCCTTA	AAAAATATGA	8280
TTTTAGATCT	TAATATCCAA	AACAAAAAGT	TTATAGTTCT	TGGGCTTTT	AAAGAGCTTG	8340
GGGAATTGGC	ATACAAAAC	CACAAAGATT	TAATTCAAGA	GGCTATTTCA	ATGAATTTTG	8400
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TGGAACCTTC	AGTTTTTATT	GTCATTAAGG	GCTCAAGGTT	TAACAGGCTT	GAGAGAATTT	8580
TAAATATATT	TAGATGATAG	TGGGGTTTTT	ATGTTTTACC	TTTTAGGTTT	GCGTTTGCTC	8640
AAATATATTA	CCTTTAGAAT	GGCTTATGCT	ACAATTTTTG	CATTTTTACT	TTCTTTGATT	8700

743

GTGGGCCCTT ATATTATTTT AAAGTTAAAA AAATTAAGAG CTGATCAGAT TTTAAGAGAA	8760
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745

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GCAAAAAATA	AAAGGTCTTT	TAGTTGAGAG	TTAGGGCCT	CAGTGCCTA	TTGGAGATTT	22680
GTGTTTAATT	GATCAAAGAA	ATGGCAAAAA	GGTATGCGCA	GAGGTTTTAG	GATTTAATGG	22740
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751

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753

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755

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757

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CATTTTGCAG	TTGCTATTAA	ATGGGATAGC	GAAACAATGT	TAGCTCCAAA	GGTGCTTGCA	35160
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759

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763

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765

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771

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ATACTTTTAA	AATTTTGGTT	ATTTCACTGA	TTACGCTGTT	TATTGTTTCA	AAATTTTTTTT	62100
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GCCTGTCTCT	TTGTTTAGTA	AAATTTTGTC	TTTTATTTTT	CCATTTATTT	GCAAGACAAT	62520
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775

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777

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781

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ATCCCAAATT	GTCTTCTCTT	TGAAAAATGT	TTTTTACTAA	AGCTGCAATA	AATGTGCTTC	100200
CAAAAAATCC	GTAAACTACA	CTAGGGATTC	CTGCTAAAAG	CTCTATTACT	GTTTGTAAAA	100260
ATTGTCTATA	AAATCCTTTT	GCTTTTCAA	GTAAATATAT	CGCAAATCCC	AATCCAATTG	100320
GTAAAGCAAT	TAAAATAGAA	AAAAGTGTAG	TTAAAAAGGA	ATTAATAATG	AATGCCAAAA	100380
TACCATAAGA	TTTTTGTAAG	TTGCTAGTAG	GATCCCAATT	TGTGCTGAAT	AAAAAGTTTA	100440
AAATTTTAAT	TTTGTATTAT	AGAAATGGCA	TTATTCCAGT	TTTTAATATA	AACAAACCCA	100500
AAAACAATAT	TGATAGGGAG	CTGATTATTG	CAGATATAAG	AATAAAAGAT	TTGAAAATAA	100560
TTTCAATTAT	TTTTCTTTTT	GTCTTTAAGC	TCAGATGCAT	TTTTTAAAAG	AATCCCTTAA	100620
AGCTCATGCC	AATGTTAAAT	TGTATTACTT	GACTTGATCT	TAAGTCAAGT	TTTTTTTTCT	100680
TTAATTTAAT	TATGTTTTTA	TCCCTAAAAA	GCCTTGTTCT	TCAACAATAT	CTTGTCAGT	100740

795	
100800	TGAGCTTGTC ATGAAATCAA TAAATTGAGT TACGCTTTTA TCCTCGTATT TGTTAATTTGT
100860	AACTATTATT AAATTTCTTT TAATGGTGTA TTTATTGCTA TTTATTGTTT CTTTGTAGG
100920	ATATGTGCTG TTAACAGAAA GAATATTCAA ACCCTTTTCT ATTGAATTTT TTGCGTATCC
100980	AAGACCTATA TATCCTATTG AGTGGGGAGT AAGGCTTGTT TTTTCAATTA CCTCTCCATT
101040	AGATTTTACC ACTATTCCGT CTTGTCTAAA TTGAGCTTCT TCGTGAGTTT TGAATATTTT
101100	ATTAAGAAGT AGGTCTTTTA TAGACGAATA AGAACCAGAA GAAGAGTCTC GATTGATAAA
101160	GTTGATTTTA GCATCAGGAC CTCCCACTTG TTTCCAATTT TGAATTTCTC CATTTAGTAT
101220	TTTAGCTAGA TTTTCTTCTG TAATATTTGT AATTTTATT TCAGGGCTTG TAATGAAAAT
101280	TAAAGCATCA TAAGCAAATA CAGTTTCTTT TGCCCCTTGT TCAATTTCTT CTTTGTAA
101340	ATCTCTGAT GATATTGCTA TTTTATATAT TTTGTTAAAT AGCCCGTTTA TGCCAACACT
101400	ACTTCCTTGT GCATCGTATG TTACTTTAGT ATTATTGTTT ATTTTATTAT ATCTTAAAT
101460	CATTCGTCT AGTATTGGGC TTACAGTTGT AGATCCTCCA ATTGATACAA TTTTTCATT
101520	GTCTTGATTT TTACAGTTGT ATAATAAACT TGTTGATAGC ATAAAAATTA AGATAATAAC
101580	TTTTTTCATC AAGCAAATC CTTTGTAA GTATATAATA GCATTAATTT AAAATAAGTC
101640	AATTACAAAT TAACTTTATT GATTAAGTTA TAATTGAGGA ATAATAGCAA ATATTTTAAAT
101700	TTTTTGGTAT AAATTACTAC TAGATTTATA TGTTAAGTTT TGCGAGGTAT TTAAATGGCA
101760	GTAGTGAAAT CTAGTGAGAT TGAAAAAGGT TCTTTTTTAC TTATCAAAGG GGCTCCCCAT
101820	ATTGTTCTTG AAAGAGAATT CTCAAAAACA GGTAGGGGAG GGGCGATAGT AAGGTAAAG
101880	CTTAAGAACT TAAAAACAA ATTTGTCATT AGAGAACTT TAAAAGGGGC AGATACCGCA
101940	GAAGCTATTG AAATTTATGA AGTTAGTGCT CAGTATTTAT ACAAAGATAA AGACGTTTTG
102000	GTTTTTATGG ATTTAGAAAC TTATGATCAA GTTAGTTTGG ACTTAAAAGA AAGTGCTAAT
102060	TTACAAGATA AAGTGCCTTT TTTGCAGGAG TCTGAAATCT ATTCTCTTGT AACTTTTGAC
102120	AATGTGGTTA TTGATATTAA GCTGGCTCCA AAGATTGCTT TTGAAGTTGT AGAAGTTGAG
102180	GCGGCTGTTA AAGGTGATAC TGTAACAAAT GCAATGAAAA ATATTACTCT TAATACAGGG
102240	CTTGTAAGTAA AAGCTCCACT TTTTATTAAAC GTTGGAGATA AGGTTTAAAT TAATTCTGAA
102300	ACTAAAGAGT ATGCAGAGCG GATTAAAAAT TAAATTAATA TTGTTTTTTT GTTGTTTTGC
102360	TTGTTCTTGC GACATAAATT ATCCGGAGAT AAAAGAGCTT GATTATAAGA TAAATTATTA
102420	TTTACTGAA AATCGCTTAG ATTACTCTAT GAGTTTGTAT TTTGCAATTA AAGTTATAAA
102480	TTCAAAGAT GTTTTTAAAT TATCAATAGA GAATAAGAAC ACTAATGAGT TTATTCAAGT
102540	GATTAATAAT AATTATAGCT CTTTTTTTAT TGATTCTAGC CTTGGAAAGG ATATTCTATA

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GTCAAAATAT	GATTTAGATG	ATGTTACAA	TTATGTATAT	AAGTCTAAAG	ATATGGAAAT	102720
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TCCGGTCTCT	TCAGTTGTTA	GAATTGATTC	AATAGATATT	CTAGAGATTG	ATAAAGCATT	102840
TGATAATTAC	ATAAGTTTTT	ATTATGTCGA	AAAAAATTCA	AATCTTTTTT	TTAAAGTTGG	102900
CTGAAAAGAT	CAAAATGGGC	CCACCAGGAC	TTGAACCTGG	GACCTACCGA	TTATGAGTCG	102960
GGTGCTCTAA	CCAAC TGAGC	TATGGGCCCT	TAGCTTTAAT	TTATTATATT	TATTTTTTAT	103020
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GATTTATATT	CTTTTTTAAG	AATATAAATT	TTTTTGTTTA	AATTTTTTAA	TATGTTTTCA	103860
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CCAAGCTCAA	TTAAATTTTT	GTCTTTTCTT	ATCTTTAACA	AGTTGATTTT	TGATTTGATT	104040
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AAAAATTCAT	TTATTAAAAA	TTTACTAAAT	TCAGCGCTTA	GCATGTCATT	TCTTTTGACA	104220
GCCTTTCTAC	AGGCAATAGT	TGCGTATAAG	TCAGATTCAA	GAGAATTTAT	TGTCCTACTT	104280

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CCATTATCTA	TTATTAAGAT	TTTTTGAATT	CCCCCTTCTT	CAAGAAAAAC	CTCAATTTTA	105780
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CCATAATTTT	TATCAATTTG	TATTGCTTTC	TCAAAAGATT	CTATTGCTTT	TTTGTTTTTA	106800
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GATTTTGTGT	TTTCAAGATC	AATGGGTTTT	ATTGAATGAA	CCTTAGATTT	AAGGTCCTCC	107160
AGGTGTTGTA	TTTTATTAGC	TTGAGCTAAA	GTTTTAGAGG	CCTGGGCGTC	ATTGGGATTG	107220
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TCAATGGGTT	TTATTGAATG	AACCTTAGAT	TTAAGGTCCT	CyAGGTGTTG	TATTTTATTA	107340
GCTTGAGCTA	AAGTTTTAGA	GGCCTGrGCG	TCATTGGGAT	TGTTTTTyAA	GAATTCGTTT	107400
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GAGGCTGrG	CGTCATTGGG	ATTGTTTTTy	AAGAATTCGT	TTAGATCCTT	AATGGCTTGT	107580
TGGCGTGATT	TTGTGTTTTT	AAGATCAATG	GGTTTTATTG	AATGAACCTT	AGATTTAAGG	107640
TCCTCCAGGT	GTTGTATTTT	ATTAGCTTGA	GCTAAAGTTT	TAGAGGCCTG	GGCGTCATTG	107700
GGATTGTTTT	TTAAGAATTC	GTTTAGATCC	TTAATGGCTT	GTTGGCGTGA	TTTTGTGTTT	107760
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ATTGAATGAA	CCTTAGATTT	AAGGTCCTCT	AGGTGTTGTA	TTTTATTAGC	TTGAGCTAAA	108000
GTTTTAGAGG	CCTGAGCGTC	ATTGGGATTG	TTTTTCAAGA	ATTCGTTTAG	ATCCTTAATG	108060
GCTTGTTGGC	GTGATTTTGT	GTTTTCAAGA	TCAATGGGTT	TTATTGAATG	AACTTTAGAT	108120
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CTTCCGGTAT	TAATATCGTC	TAATATTTCA	TAGAGCTCTT	TTTTTATCAA	GTAGCTATAT	108420
GGCCTATAAA	TTTTCCCTAT	TATTGTTTGA	CTGGGTGGAG	AAAGCTCACT	TTCTTTTTTG	108480
GAATTTGAAG	AAATTTTTTT	TAAAGATGTA	GTATTGTTAT	TGTTTGAATA	TTTACTGTTG	108540
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TCATTTTCTA	TTTTTTGAGA	ATCGTTTAAA	ATATTTTCAC	TATTTGATTT	TCCACTTAAA	108660
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AGCATTATTT	CTCGATTTTT	GTCATTTAAT	TTGCTTTGAT	ATATATAGTA	ACCAAAGCCC	109200
CCAAATGATA	AGATAAGTAA	GAAAATTAAA	AGCAATAATA	CCGAAAAATT	TGTATGTTTT	109260
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TGTTTCTAGG	TTGTCTTTAA	AACTATCTTT	AAGTATTTGA	TTTTTATCTT	CTTTTGCCTA	109380
TACAATATGC	TCGGTTCGCC	CCTTCAAAC	TTTGTCAAGT	TGTTCAAGAT	TAATTTTTTC	109440
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CGCACTGTCA TAATTAGGTC TACTTTTAAT AGAATTAGAA TAATATTTTA TTGCTAAAGG	109680
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GATTTCACCC CCTACTGCAA TTCCATCGAG CAATGCTCCT TCTGCTTCTG TTAGTTGATT	109800
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GCCAATTCTA ATTAGCCTTT GAGAATATGC CAATTTTGAA TTTAATATTA AAATTAAAAA	109980
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ATACTTATTT TAGATTAAAT GCCTTTAGAT TTCATAAGCT CTTTTTTAAA ATTTATTTTT	110100
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TTTATCTTTC TATTGTTTTT TAATCTACC AAATCTCAC AATATATTAA ATAGCACATT	110220
GCAGGTAATA ATTTTTCTC ATTTTCATCT TCCAGTTTTT CAATAAGATT AAATCTTATA	110280
TTTTTGATAA TAATTTTTAA AATCCTTGAT CTTGTTTTTA GTGATTTTAT TAAAAGATAT	110340
GATTTTTGGT AATCTAGTTG GTTAGGATTT ATTTTTTGTA TTTTATTAT TTTTTAGGT	110400
ATTGTAATTT TATTTTCGTC AAGGTAGAGT AGTATGTCTG ATATAAATTT GAAATGCTTA	110460
TATTCAATAT TTGGGTAAAA AGATAGAAAA TATACAAATA TTTGATTTTG TATTTCAAAG	110520
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GCATAAATAT AGAATGCAAT CCAGCCATAA GTTCTATAT TCTGAGAATT TTTTTTGACA	110640
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TCGTATGGGT TGAAATTTGT TTTGTCAAAA GATATAAAAA AATCTTCTGT TTGAAATTTT	110760
GCAGTTATAA TTTCTTTTAT TTTTCTTTT ATGTTGATTA ATTTATGTTT TTCAATGTAT	110820
TCAAGTGCAT CTATGAAAGA TTCCCAATTA TTAGATATTT TGTTTGTGAA AAACCAAGTT	110880
AAATATTTTT TTGTTATTGT TTTTCAATT ACATATAAAT AACACTTTAA TGTGTCTTGA	110940
AAATCTTTTG GGGCGTATTG TGTGAAATCG CTAAAAAAT AATTAAAGCT AATATTTTTA	111000
CTCGAACCTT TATAAAAAAT TTCATTAAGA CTTAAAGTTT TTAGTGCACG TAAGTAGTTT	111060
AAAATTCAT TGTATTTTAG CGCTAGAATT TCTTCTTCCA AGTATTTGTA AGGTTTTATT	111120
AAAATTTTAA TAAAAATATT TTTGCTCAAA CATCCAACGT GCCAATATGT AAGTATTAGC	111180
ATTCTTTTTA ATTTATTAG TCTACTTTCT TTATTGGTTA AGCTTGATTT AAAAATTTT	111240
TGATTTTCTG GTCGATATTT TAAATTTTTA TTTAAATAT TTAATATTTT AATTAAATCC	111300
GGnTCCTAC	111309

801

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53585 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

AGCATTTAAT TTACAATTTA AACTATCTTT TAAAGATTAC ACCTTATGCT AAAAAATAAG	60
TTTTTGGTCG CAAAAATCGC AAATCCACAA TTTATCAACT AAATACTAAT ACACACTTAC	120
AATCAATCAA TTCCTAGCTT ATCTTTCAAT AAGTTCAATT TTTCAGCATC CATACTAAGC	180
TTATTTAAAT CCAAAGCATT AATAATTGCA ATTATCTCTT CGTGGGAAAA TCTCTTTCCT	240
CTTAAAAAAT GATTTTCAAA ACTGTTAAAA GCGATGGGCA CAATTTCTCT TACTATGCTT	300
ATCAATGCTT TAGCATATTC GCGCATTTCT TTTGGCGAAT TTTCTTTAAT TTCTTTTGGA	360
CTGTCTAGGG CTAATCGCAA TTTAATAAAA TGAAAAAGAT TATTTAAATC AATTTGCCAA	420
TACCATTCCG TATATAAACT TAAGGGCAAA ACTATTCTTG AGAGTTCCTT TGGAAATATTA	480
GCATTGATCA TATCTTGATA AAGCTCATAA GAATGTTTTT GATGATGCTT TATTTTGTC	540
GACAATTTTT CCAAAGACTT AAACCTTTTT TCAGAGCTAT TACTAGAAGT TTGACACTTT	600
AAATCTTCTT CTAAAGGGAC ATAAAATTCC TCTCTTGCCA AGCTGTAGCA TCCAGAAACT	660
TCATTAATCC TTGCCGTTCT ATGCCTCATC CATTGCCTTG CAACAAATAT TGGAGCTTTA	720
ACATGAAATG TAAAAACCAC CTGCTCCAAT GGGCTTGTTG GCCCATTTCT TATTAAATAG	780
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GAATATAAAT ATGCAAGTAA ATATTGAAAA TGTAAATATT CATAACGAAA ATATATTATA	1020
TCATAAGAAC AGCCTTAATA GGGAGATCAA TATTGATCTT ATTAAATAAA AAAGGCAGAA	1080
ACTAATACAA TTAGCTTCAA ACCTTTTTTG TTTAACCTCT AATTATTTAT AAATTTATAT	1140
ATCTAACTAT CTCATGTATA AAGAAATAGC CATTACTTTT GTAAGATCTC TTGCGCCTTG	1200
AGCTACCTTA ACAACATTAG AAATAGCCTT TGCAACATCT TTTTTTGCTA ATACTTGATC	1260
CTTATTTGAC GGATTCAAAC CATTAACCAT ATTGAGAACT TTTTGAGCCT CTTGAACTGT	1320
TTCATCCAAA GCCCTTTCAG AAGCCATTAA AGTTTCTTTA ACTTGCTCCA CTTTAGCAAA	1380
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CTCTATTAAA AATGTTGCTT CACCAGCAAC AGAAACAGCT TTTTGGGTTT CTTGAACAGC	1500
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CATTGAGCCT ACAAACTTTT TAACTACTCC TGCATCATTT GATTCTACCA ATTCAAGAGA	1680
TGATTCTCTA ACTCCCTCTA ATTTACTAGA AACATCTTCG GTTACCTTGT TAATAGTATC	1740
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803

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805

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807

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TAAATTATTT	GCATTTAAAA	CCTTATTTAA	ATTGGTCTCT	ACTTCTAAAG	CAGAATTAAT	29040
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CATAATTTTT	CAAATTTTTT	AATTCGTTGT	TACTCTCGCT	TTCAGTAAGC	ACTTTTTTTAA	29280
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CTTTATAAGA	TTTTTCGTAC	TCAGCTTTTA	AAGCTTCTTC	TCTACCATTA	ACACTCATTG	29640
CATCTTTTAA	AAAGACTTTT	AAAGACTCTA	GCTTTTCAGC	TTCTTCGGGA	GTTAAAGAAA	29700
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CAAAGAGGGA	TATATATTTG	TCTAATGTTA	TAAATCAACA	ATTCATTGAA	AACTTCTTTA	30120
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ATATTTTTTT	ATTATTTTAT	TATTTGTGTG	TTTTTTGGAA	TTTTTGTGTA	TATTTCTATA	41400
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AGTTTCACTT	CCAGAATTTT	TTCCCAAATG	TTTACAGTAG	TTTAGCGTGA	CTTTAAATTT	41640
TTTCTCTAGT	ATGTATAAAT	AGTTTTGTAG	TGTTTTGAGC	TTTATGAGTT	TTTGTTTATT	41700
TCPTTCAAGG	TTTTTATTTA	GTAAATAAAG	TATGTTTTTT	TGTGTGTATT	TTTTAAAGTT	41760
TAAGTTGATA	AAGTTAAGGG	TAGAGATTAA	TACAATCAAG	TTGTGTTGGA	AGTTCATGT	41820
GGTTTTTTTT	ACTCTTTTTG	TAGTGTGTTG	TGATTTCTTT	TTTAATGTTT	TCAATTTTAT	41880
ACTCCTAATA	TAAGTAGTTT	CTTTAATTAT	AATTTAATTA	ATAGTACAGT	TTCTTAAAAA	41940
AGTAAAGTAT	TTTTATATAA	AAAATAAAAA	AAAGTATATT	TAATACATAT	TTGTTAAATA	42000
TACTTTACAA	AAGTAAGTTT	TTGTAATAAA	ATATAATAAA	TAATAAACTT	ATATTAGGAG	42060
TAAATTATTT	TTACGCTTTA	ATTTTTATTT	AAAATAGTGA	GCTTATTAGC	GATGGGTTTA	42120

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GTGAAGGAAT	TATCCCCATT	AATTTTATTA	AATTTTATGC	ATTCAGTGTA	TTAGCGCTTT	42240
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GCTTGATTCT	CAGCTTTTTA	ATGTTGCTAT	GAAAAAATA	ATTGAAAAAT	ATCCTAAAAT	51540
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831

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ATTAAAAATA AAAATTGTAT TATGATTGGC ATGGGCTTCC tATTTTATAT TAATATCTTT	53580
TAATT	53585

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35515 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

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ACACCATTCA TTAGACAACC CCCACACAAG ATGGCGTTGA AGTTTCTCTT TTTAGTTTTT	120
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TTTTGATCCT ATCAAATTCA AATTCTCGAA CAACTCCCTG TTTTCTTAAT TGGCAGCCCA	300
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CAAATTTGTC TATTCCTAAT AGCAATAACA CTTCTGAATG GAGTTTGTGTT ACTAAAAGTT	480
CTTCTTCTCC tGCAACTTGT GCTTGTAAGC TTTCTTGTTT ACTCATTTTC ACTTACCTTA	540

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CCTAAAACAA AATCAATGTA TGAATGAGCT ACATCGGTTG AGTCTTTATC AACTTGTTCA	660
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ATCATCGGGG TGGAAAATTC GTCGCCAGT TCTAACTTTG AAAGTCCAGC CTCAATCTTT	960
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TGAATCGAAA CAGTCCCGGT TAATACAAAG TGATTAATAA GTTTAATAAT TTCACTACTT	1140
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835

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CAAACTATTC	ATAAAATCTC	CATATTATCC	TTTTAATTCT	TTATATTCTT	TCATAAGTTT	14220
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CAAAAATATT GGAATTTTTA TTTTAAATTT GTTCATATGA AATTCCAATA ATTCTAAACT	15060
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841

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843

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845

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TAAGTCTATA	TTTCTCAACA	CGCTCTCTTA	AGCTTTCAAA	TTTAGATTGT	CTACTAAGTT	27000
CTTTTTTCTT	GTCCGACAAA	TTATTTTTTA	CAATATCTTT	AGTGCTACCC	AAACTAGATT	27060

TTTTAGGTTT AAGATATTTT TCCATTTTAG AAATATCTTG TTCAATGGCC TTTTTGTGTG	27120
CAGCATGATC AAGAATACCT TTAAATTTAA TGGTGAATTT GTCGCTCACT AAGTCCTCAC	27180
TTGCTTAAAA TTAATTCATA CAATTCCTTT TCTAATTTAA TCTCAGCAAG TCTATTGACT	27240
TCTAAAAGCT CGTCATAAGG CAATTTTTTA ACCGAGTmGT ATGAGCAAAT ATTCATAATT	27300
ACTGGaAAAt AGTATTTATC GTTCTTAATC TCGTCAAGCA AGTTAAAATA TTTTTTCTA	27360
GTCTCATCAA GACTTGCAAT AGCTTTATCA ATATCTCTAT TTCTTTTGyT CATTTAGCAA	27420
CCAGCTCATT GGAATTTGAT GTAmTTGATG AAAGyGAAGT GGCTACTTTT TCATAATCAA	27480
AATTTTCATT AATATAGTCA AAAGCAACAA AATCACCAAC ATTATTTTCA TACTCACTCA	27540
AATATACTAA AGCGGGCTTT TTTAGATCAT TGTCTAAATG AAAAGTATTA AATTGTGCAG	27600
TGTAAATTAT TGCAACAAGA TAGTCCTTAT AATAAGAAAT AAATTCCTTA TTTTGATCCA	27660
AAATCACATA GAATTCGTCT AAAAAATTTG GACTTATCAT TAAGCTTG TG ATTTCTCTTA	27720
AGTATTTAAC CTCATTAAGC TTTAAAACAG CGTCACTTTG ATTAAATCCT AGCACTTTAT	27780
CCCATTCTA GACGGGAAGT ACTCTCAGCG GATATTCATA AGTTTTATTT TTAGTTAAAA	27840
TTTTCATTTT ATATCTCATT ATCATAATAA GAmTCTCCTT TTAAGwGTTG TTTGGTTTAG	27900
ATTTTTGGCA ATTAATAGCC CTAATTTCAA AAGATACTTT TTCGGCCTCA GCAGAATAAC	27960
TTCTTGAAGG CTCTTCAGTA AAAATTGCAT AGTTAGAAAT AATTTTGGTA GCAATTCAT	28020
CATTGAATGC TAAATCAAGC ATTTTATCCT CTTTTCTCAC ATCCATGTTG TAAAACGT	28080
CATCAGAAAG TTCAGTTAAC AAAATGTAGT CATGACTACC TAGTGTCAC TCAATGTTGA	28140
AAACATAAGT TATTGTTTTG GGATCTCTTA AGCTTATTAC AGGCATACCT TTATCTTCAC	28200
TACTAATCAC TGCTCTTGTT GTAGGTTTCGC TTGTAAGCTC TAGCTTGCCA CTATGTAAC	28260
GCGTACCACC AATTGAAAAA TAAACTTCTC TTAAATCATA AAATTGCATT TTTAGCCCCC	28320
CTTTTAAGCA CTTAAGCTGT TTTGATAATC AACTATATCT TGAGTAGTAA TTAATAAGC	28380
AACAGCATTA ATGCTAAAGT TATAAGTAAT ATTCACGCTA AGTTCTAATT TAAGTTGTGG	28440
CGTAGGAGAA AGAGTAAGCC TTAAATTTTT ATACTCTATT ATCAGTCCTC TATCCACAAA	28500
CCTTTTCAGT AAACATTCAA TTGCTGAAGT ATATGCATTG TCTCTAGCTC CACTAAGTTG	28560
TAGTGCAGAT AATTTGCTAT TTTGCCATAT GTTTTTGTTC CAAATTCATA TAAGCTCAAT	28620
AATCGCTTCr TTTTTTATAT AGTGGTATGT AAATTGTTTCG TCTATTGCAC CTCCAGCTAG	28680
GTCAACACCT TCTTTAAAkG CrGGTACACC ATCAAGCCCA GTTTCATTAA GAAGTGAATA	28740
AAAGTTGATT TTTGCAGTTC kCAACTTTCC AATTACAGTA TCATCAACAA GTGGTGTAGC	28800
AGCCAGCGGC ATGCCATAAG GATTTACAGC ATGAAAAATA CTAGCTTGAT GkArATATTG	28860

ACTTATAAAT	TTrAGGTGTA	AATTGCTCTT	ATTrTTTrCTG	TAAACAGCAA	TATTTCTTTT	28920
TTTTTCAGTA	TGCGCTTTAT	CTTTAAATAG	TTCTTTTATT	TCTTGTCTTT	TAGTCGAGAA	28980
TACAAAAAAA	rTTGAAGGyn	TTTTrAAyTT	ATyATArTCA	TCTTTTrTAA	TyTTAAGTCC	29040
ATCATCkGAm	kyATCnCCCT	CAGTrTTAAT	AAGTACAACA	AAAGTGTGTC	TATGTACTTT	29100
AAGATAWTTr	TTTArCTCTT	CrGGyTTATC	CTTATAAAATr	AAAAGATCGG	CTGATTTTAA	29160
yGATTCTTCr	CTTGAATTGA	AAAAATTyGA	CATTGCAGTT	TTAAGCAGTG	TTTTTTCTTT	29220
TCCAAACTGA	TCTTsTCCAT	TyCCATTmTC	TTTTTCTAAA	GTTTCAATTT	GTTTTTCATA	29280
rTTATTAACG	GTTAAATTCA	ATATTTTATA	GyTAGCAGCA	TCTTTATTAA	CTTTGATTTT	29340
AGCTGTTTTG	TAAACCAAAA	GTGGATTATA	ATAATTrGGC	CTACTAGCTT	GAATTCTAGA	29400
GTCAAGCAAA	CTTACACTAA	TGTATCTTG	CGGCAATTTy	GTATTCCTCC	TTTAAAAATT	29460
CAATTGCTTT	TACACTAGCA	TTAAATGCTA	TAGATGCACT	GTATGCATGG	TTGCTATATT	29520
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TAATTTTATT	AATATAKTCG	GGTTGTAGAC	TGGGCAAAKT	ATACTTATGA	GCTTTATTGT	29640
GTAGAAAGTC	ACTAAGCATA	CTATAAAGCA	TTAACATGCG	TGAATTAGCG	TCAAAGTCTT	29700
TGGCGTTTAA	CACTATTGCA	ATAATATATA	TTTGAAAATT	TATACTAAAT	TCCAAAGCAT	29760
TTTCATAAAA	TACACCGGCT	CTAKAATTAT	GATCAAATAG	ATTTTCTGTA	CCATCAAATT	29820
TCAATGCTAT	TATATTTGAG	CTAGCAGCTG	TGATTTTTGA	AAGATATGGA	TGATTGTAGG	29880
TATTTATGAT	ATCGCACTCA	AAATTATTTT	CAGTTGCATA	yGCCTTAAAC	CCTTTAAATA	29940
TTTGrGTTAA	ATGATTTAAT	ACCATATCTA	AAGTGAAAAT	CATTCAAGTG	TTACCTTATA	30000
AGTAATCTCT	GATAACATTT	TGGCTGTATC	AACAAGTGGA	ATTGCTGCAG	TGTTACTACC	30060
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TAGATAATTT	TCATAGTAyC	TTATAAAAGC	TTGTCCAATA	GCCTCCATTC	CCGATTTAGG	30180
GTCAAGATTA	AACTTAGAAT	TTATATAGCT	ATTATTGATA	TATTCTCTAA	ACTCAGAACT	30240
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TTTAGCAATA	CCTGCACGAC	CACCAAACCA	CCCAATTTCC	AATTCCATTT	TAAATTCTAG	30360
TTTGTCCATA	TAAATTCCTT	TAAAACCAAA	GTAAAATATC	CkATTGAAGA	GTCAATACTA	30420
AATATTTCAA	AGTAAACTAA	ATCTGCAATT	GATATTCGGT	CTTTTrGTTT	ATAGTTAAGG	30480
TCTTGATATG	TGTAAAGTTT	GGAATATCCT	TGAATATCAG	ACATATCAGA	ATCATAAAGA	30540
ATTGCAAGTT	CTTGTGGCTT	TATGTCAATA	ATAACTCCTG	CrAATTCArT	GTACTTAKTT	30600

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CTTTTCTCTAA CACCATTTCAT TAGACAACCC CCACACAAGA TGGCGTTGAA GTTCTCTTTT	30780
TTAGTTTTTC TAAAAATGCA TCAAGTTGTG AACAAAAATT CTGTTTTGAG CCACAACyCC	30840
CCTCGCCrCC TTCTTCGCCT CCACTGCTAC TAGGATAATA ATCAAGTTCA AGTTCATTGA	30900
ATTTCTCTTT TTTGATCCTA TCAAATTCAA ATTCTCGAAC AACTCCCTGT TTTCTTAATT	30960
GrCArCCCAT ATGGTAaAAG gTAAGTAAAA ATATTTGTTC ATAyGTmAGT GAACTrGCAT	31020
CAATACCrCG TGTTACTAGA ATAGCTTGAA GTAAAGATAA ATGAAGTAGA AAATTTTGyC	31080
TGCTTAATGC AAGTTTGCTT ATTCCTAGTA ACAATAACAC TTCaGAATrA AGTTTGTGTA	31140
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CTTGCTGCAC CCTGTGCTGC TGCGTATGGC TTTACGAGTT TGAGmGAAGT TGTAGGGTCA	31560
ACTATTACCA TCATAGGTGT AGAAAATTCTG TCTCCTAGCT CTAACTTTGA AAGTCCCGCC	31620
TCAATTTTTT CAAATATTTT ATCCATTTTG TCCTTATTAG CACTTTCAAC CTCTCTTTTT	31680
ACTTGATTga tGTGGCATAT TAAGAAGTCC ATACATATTG GGAAGTAGAC GTTTTGGATT	31740
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AATCTCGCTA CTGCAAGCT TATAGGCTTG AGAGAAAGGA AGTAArTTGT TATTAAATGTC	31860
ACCAAGATAT GAGTCTGAAG TGTAaaATTT TTCAGACGCC TGCTTTAAGT GCCTAAATTT	31920
GTAAGTGAAT TTTAAGTAAT TAAGTCTTAC CACTTCAGAA CTAAATCCAA TAGTTGAAAT	31980
AGTATTAACy TCATTAGCAA TCGTTGTAGG ATTAGCATTT AAAAACGCAT CCCACTTTAC	32040
AGTTCTTTGG TAGCCCATCT GAAGATCAAC ATCTTCAATT TGATCAGGCG AAAACCATTT	32100
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TTCAATCAAAT AATTCATAT TAAATCCTCC CAAATATCAT TAATTTTAC TTACAGCTTT	32220
ATTTCCAAAT ACTGCTACTT TTATTAAAwA AACATCGTTA CTAATTTGTT TTGCATCAGA	32280
CAACGCTATy GCATTAATAG TTGCCTTATT TGGTGGTGCT CCAGTCACCT TTTCAAGAGC	32340
ACCGTCTTTA TTAAAAACAA GTTTGTCTTT TACTTTAAGC GTAGAATCTT TTGCTACTAA	32400

ATAACCCTCA	AAATATTTG	TAATyGGAAC	AATAGTGGCT	GTTTTGCTAA	ACTCATCTAT	32460
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AATTTGATca	GCTTTTTCCT	CTTGAATAAC	TCTTTTTTACC	CCACGCTTrT	ATGGATAYCC	32580
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GGGATTTTTC	ATAAACTTTT	CAAGTTTACT	TckyTTmTCT	TGATAATCTT	TTAATAATTG	32760
CGTTGTGTCT	GCCATTTGTT	TAACTCCTTT	TATTGCCCAA	GGCTTAACCA	CCAGCTTCAG	32820
GTGTTACTGT	TTTCTCAAGG	CCTCTATTGC	CAAAAATTGC	AACTTTTATC	AAATTAATAG	32880
AATACTCTTG	TTTGGGATAT	CTAGCTTGAT	CTTGATGTTT	ATCTTCGGGT	GCAAAAATTGA	32940
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TGATAATAAC	CCCATTGTTA	TTTATATCCA	ATATTTCTCC	CATTTTTATA	CTCGGATTTT	33060
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ACTCACATAC	ATCTACACAT	ATCCCATACA	TATCAGTATC	AGCACCAACT	TCAACATATA	33180
TAGAGTTCTC	TTTTTGAACA	AGTTTAACCC	CACGCTTATA	TGAAAAACTA	TTTGCTGGAT	33240
CATAAAGGTA	TTCTTCTATT	TTGTCTGCAA	AGCTTGAACA	TGTAAAAGAA	TAAGCATTA	33300
CTCGKcATT	CTTTGATTTA	AAACAACCAC	CCGAACTACT	AAAAACCTTA	TTTTCAATCG	33360
AACTCATTGA	TTTTGAATAT	TTTTTAATTT	TAAAAGAAC	ATCGTCAAGT	TCTTTAACTG	33420
AATCTAAATA	AGGATCTTTT	GCTTGTACTT	CTTCAGCCTG	TCTTGTTTGA	CGTTTAGATC	33480
TAGGAGCAAC	TGGAATTTCT	GATTCTAACC	CTAATTGTGG	ATTATCATCA	ACATTAGGAG	33540
ATTTAGCTTG	CCCTTTGCCT	TTTAAAGCCA	TAATTTAATT	ACCTTTTAAA	GCTCTATTCC	33600
CAAAAACACT	AGCAAGCACT	ATrGATAACT	CTTCGGTTAA	TTTATGTACT	TTTGAAAGTG	33660
CTATAGCATT	AACAGATTTA	TCATTTCCCC	CATTCTTTTC	AAGCTCTCCT	TGTGCATTAA	33720
AATGCAGCTT	ATCACCyGGr	TTyACACCAT	TTgtCCATTT	TTCTTAAATG	TTAAATACCC	33780
CGTGAAGTTA	TTTrTAATTG	GAACACAGT	TGCCATGCCA	GTAAACTCAT	CTATATCAGT	33840
GCATATTCCG	TACAAGTCAT	CCCCACCACC	AGCCTCAACT	TCTAGTTCTG	TTGTACyATC	33900
TGCACTAAAA	CTAAGCTTGA	CTCCACGCTT	GTATGGATAC	CCTTTAGCAG	GATAATTTTC	33960
TATTTTrTCT	TTACTACTAG	TAAAAACTCC	ATCCGAATTG	GAGTAAATTA	GATTTTTATC	34020
TCTAAArTCT	ACAGAATTmC	TAAGCAAACC	AGCATCTTGC	TGAGGATTTT	TCATTAATGC	34080
TTTAATTTCT	GCAACTTTTT	TATCAAACCT	TTCTTTTATT	TTTGTAATAC	CATCGCTCAT	34140

851

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ATTCGTCTTT GCTTGTAAGT ATTACTTATC GCTTGTAACA ATTCTGTGAA ATTAATAGGT	34260
ACAAAATTAG AATCAAGCAA ACTTGCTCTC TCTTCTGATT TAACAACAAT ATTGCCTCTG	34320
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GCTAAAGAAA CAAGTTGCTC TAACATCTCT CCATCGATAT GACTTATGTC TGATACTTTG	34440
GCAATAGCTT TAATTTGCTC AATTGGAACG AACTTGCGCA CAAGTTCTCT ACGTTGTGCT	34500
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CTAAGATGTG CTTTTCGAAG TGTATCAATT TCATTTATGC GCTCAGCCTC TAGyAAyAAT	34620
TGCTTTTyAA TACGCTCCCK CTCTTCAACT TCTGCrAGTT CTTTGTATT TCGTTCATTT	34680
ATACTTAAAT CTCGACTTGT CTCTTTGGAT TTAATTTTGG CTTGCTCTTT AAAGCGCATG	34740
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TTGyTCTTCA CTTAACATAA TCAGmGAATT AAyTTCATA TCAAGCCCrA AATACTTTGT	35040
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TAAGTAACTA AGrTCGTATT TAATAACCTC TAACTAGCA CTAGGGGTGG CCGTATAAAA	35280
CATTCCCTCA TTATTTAGAT TrCTTTTtag CCTAGCAAGC TCCTGTGATA ATGAGTCATT	35340
AAGGTTTCTT AAATTAGAAA TATCTTTACT ATGATTGTTT GAATTTTGTt TTCTCAAAAA	35400
AGAAGATAAA ATGCCACTTC CCCTATCATT ATTrCTCTGA GTAAGGCAC TTAAAGAAGT	35460
TGTTGCGCTA GACAGTGGT CTTGTAGTTG TACTAAAGAT TCATCTTTGT AAAAC	35515

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26811 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

GTGTTTATA CATTATTACC TTCTTTGTAT AAAATCTATC CAATAGAAAA GTTTTAAAT

TTTTCTATTG GATTAGCTGT TTTTATATTA TATTTTAAAA ATTTTACATA AGCTTGTCGA	120
TTTCCATTTT TATATTATCG GACAATCCTC CAAATACAAT TTGAACACTA TTTCCCTTTT	180
TTAATATTCC ACTGGCACCT AGATTTTTGA AATAGGCGTC TGATTTAATG ACTTCTATTT	240
GTTTTAGATT GACTCTTAAT CTTGATGCAC ATGCATCAAT GTATGTAATA TTATCTTTTC	300
CTCCAAGACC CTCTAATACT TTTGAAGCGG TTTCTGATAA GCTTGTTTTT TCTGAACTCA	360
TCATGGTTTT TTCCATCTCT TCGTCTTCTC TTCCTATTGT TTTAAGATTG AATTCATGA	420
TTGCAAATTT AAATATAAAG TAAAATCCAA TAAAGTAGAA GATTCCCAAG ATAGGAATTG	480
CTATCCAATT TGTTTTGCTA TTTCCCTGAA GTATTCCAAA TAGGAACATA TCTATAAATC	540
CGCCAGAAAA TGTTAGTCCA ACTCCTACGT TTTAAAAGGTG TGTAAAAAGA TATGCTAGTC	600
CAAAAAGAGG AACATATATA AAGTAATAAA GTGCTGGTGC TGCAAAAAGG AATGCAAATT	660
CAAGAGGCTC TGTAATTCCT GTTAACATTG ATGTAAAGCT AGCAGATAGT AGCAATGAAG	720
CTACGTTTTT TTTATTTTCA GGTTTTGATG TATGGTACAT AGCAAGCGCC GCCCCAGGTA	780
ATCCAAAAAT CATAACAACA AATTCCTCCG TAAAAATCT TGTTCCTTTT GCAACTTCAA	840
AGTGTACAGT ATTGGGATCT GCAAGTTGTT TGAAAAATAT ATTTTGTGCT CCTGAGATTA	900
ATTCGTTATT TATTTCCAAT GTTCCCCCAA CAGCTGTTTG CCAAATGGC AAATAAAATA	960
TGTGGTGGAG TCCAAATGGA ATTAAAGATC TTTTATTGTC TCCATATGCA AATGTTCCAA	1020
AAAGTCCTGA TTGTTCTACA ATTCTTCCAA ACGAAGTCAT TGCACCTTGG ATAAAAGGCC	1080
AAATAAATGT TAAAAATATT CCTACCACAA ACATTGCCAT TGTAGTTACA ATTGGCACAA	1140
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GAAGAAAGAC AGCAACAAAT CCTGCTATCA ATCCTCCCAT TACGCTCATT TGAAGAGAGA	1260
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CTAATTCCAA TAGTGCTTTT AAGCTTGCGC TTTCTGGTGT GATTCCTTGT ATGTACAAAA	1380
TCCCATTAT AGTTTGATGC ATAACCAAAA ATCCCACTAC TCCTGCTAAA GCAGCTGTTC	1440
CTTTTCTAC TTTAGCAAGT CCGATTGGAA TTGCCGCTGC AAACATTAAG GGCAGATTAG	1500
CAAAAATTAC TTCCCTGTA TATTTCATAA GATAAAGTAT TGAGTTAGCA ACAGTTCCTT	1560
TTCCAAGGAC TTCTTCTAAT CCATAAGCCT GAATCATTGT TTCATTAGTA AATGCTCCCC	1620
CAATTCCTCA TAAAATCCA GCTGCTGGTA AAAGTGCTAT TGGAAGCATG AAGGCTTTTC	1680
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CCTTTTATT AAGTGCAAAT TAATTAATTA AAATAATTAA TTTGAATAAT ACGCTTAATA	1800

853

TC'TTAACAAG	ATTTT'TTAAT	CTTGTAATA	TCAGTATAGA	ATAAATGATA	GTATATTGAA	1860
TTGCTGTTTA	TAAAATTTTG	TATTTATAAA	AAACATTAAA	GATTGTTTTT	CCCTTTAATT	1920
TCATGGCATT	TGTTATAAAG	CATTGCTTAT	AATCTTCGTT	TTCATTGAAA	TTATTTTAAA	1980
TTAAATTTAG	AAATAAATCG	GATCAATTTG	GATTAGGGTG	TTTGCAATGG	AATTAATCAT	2040
CAATTAGCAT	TGTAAAGTTA	AATACCGATT	AAATATTTAT	AGATTTCACT	AGTTTTGTCA	2100
GAGTAATCTA	TGGGCAGTTT	ATTGTCGCCA	TCTCTGATAT	TTGGATTAGC	GCCTTTTTTCG	2160
ATAAGTGATT	TAATAAAATT	TAAATCATAT	TTTTGAATTA	TGGCACTATG	AAGAGCTGTT	2220
TGAGAATTTT	GATTTGTTAA	ATTAATATTA	AATTCTTTTG	TTATTAAATA	ATTTATAATA	2280
CTTTTGTCTT	TTACATTTAT	GGCATAAGTA	AATATTGGAT	TGCCGTTGGA	AAATATTGTA	2340
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TCAAACTAG	CATTAAACAC	TGTATATAGT	GGATCAAATT	TTGACATCAA	TTCCATTCTT	3000
ATTGGTACTG	GAAAATTTAG	TAGGTATTTT	TGAAAAAATT	GTTTCGTTTAT	TTTATGTATT	3060
TCGAAAAATT	CTTTTTTCGAA	AATATTAAAA	TCTTCTAATA	ATTGCTTTTC	GGTGAAGTAA	3120
TAAGATAAAT	TTGAACTAAT	AATAAAAAGA	GTAAAAAAG	TTAAATAATA	TAAAAAGTAT	3180
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AAAAATCCAA	TAACAAGGTA	CCCAGAATAT	AGAAATATTT	TGCTTAGCAC	ATAATAACTC	3300
ATTTTACATC	CTTTTAAAGT	TTATTTTTTAA	ATTATATCAA	AATATTTCTA	TATTTTTATT	3360
TACTTTACTT	TATTTTACTA	AAAGCATACA	ATTAGGCATT	AAATGAAGAA	GTTTTTAATA	3420
TCCGTTTATT	TTTTATGTGT	TTATGGTTGT	TCAACTATAT	CTTTGGTAAA	AATACCAGAA	3480
AAAGATAAAA	TAAATTTAAC	TGTTTTATCA	TCTTTAATGA	ATTATCCTGA	TTTGAAGATT	3540
TCAAATTTTA	AAATAAAAAGA	CTACGAACAT	TTGCATTATT	CATCTGATTT	TGAAAGCTTG	3600

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AGCTTGACCC	AAGGTGCATC	TTTTAAGGCA	GAAGTTTTAT	CTTATCTTGA	AAAACAAAAA	3780
ATTATGAAAA	ATTTTTCATT	GAAAATAAAT	TTTCCAACCTG	CTAAAAAATT	TATGGATAAT	3840
AAGTATTGGA	TTGTAATTGC	AAAAAACCAT	TTAGATTCTC	TTGTTAAGAG	TAAAAATTAT	3900
TTAGTCTTGG	CGAATGTAAA	GATGGAATAT	ATACTCAAAA	AGTTTTTAAC	TTGAGAAAGC	3960
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TTCTATTTTT	TCTTTTGTGT	TTTTAATTTT	TAAAAATTTT	TTACTCTTTT	TTATTTTATC	4140
TATTTTGACA	AGATCATTA	TTATGCTTAA	TTTTAAATAA	ATTATATTTT	CAGTTACTTG	4200
GAATTCCTTT	GCTATTGTTT	TTTGGGGATA	CTCTTTAGAT	TTATATTGAG	ATAATTTTAA	4260
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CATGTTTTCA	TTTATATATA	AAGATTTTTT	ATTTAATTGA	ATATATCCTG	GAAAACTTTT	4500
ATTCTTATCT	TGAAAACCTA	TTTCGAAAAT	TTTAAGATCT	TCTCCCATGG	CAATTTTTAC	4560
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CTGTATTGTA	TAATATAAGT	TAATTATGAA	ATACTGTTTT	TCTTTGATTT	TAATGGTTTT	4740
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AATTGAAAGA	GCAGATTATT	TTCTTTATTT	TTATCCAGAC	AGTCAAATAT	ACATTAAAAA	4860
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GGATTCTTTT	CAGGTTTGGA	CTAAGGATAC	CTTGCAATAT	GATCCAAGAT	TTATTGATGT	5160
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857

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GGCTTTATTT	ATTGTATAGT	AAGTAAACT	TCCATTGTTT	TTCCAAGTG	GATTGAAATG	18480
ACTTTTAATT	AATCCTAAAG	TTTCAAAAAT	TTTTATATCA	TTTTGTATCG	TCCTTTTAGT	18540
GACCCTTTTG	AATCCTTTTT	TTTCCAATAT	AGAATTGTC	ATTGCTACAA	CATTGCTTAG	18600
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TTCAATCTT	CGGTCTACTA	CTTTATTAAA	AGGCATCTTG	TTGGTTTTTA	TTTGATACAT	18720
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GTTAAAAATT	ATGCCTACTT	GATTGCAAAT	TTTTTATGCA	ATGATCTACT	TCTTTTAAGA	18900
ATTTTAAAAG	AAGTGGTTTA	TATATTTCAA	ATGTGAATTC	TCCCTTTTCT	CCGTAAGATT	18960
TTAATTTTAG	AGTAATATCT	TTTTCAATGT	TTTTTGCTAG	CTCTATTATT	TTTTGAGGAC	19020
TTAATACTAT	ATTTAATGTT	TCTTTTATTG	TTTTTGAATT	CTTTAAGGCT	CTCACAGGAG	19080
GCTCCATTTT	TAATTTTCTA	TCAITCTCAT	CATAAATAGA	GTTTAGAAAG	CGTAATTTAT	19140
CAGAGTATAA	GCTTAAATTC	AAAAACAGTA	TATTTAAATT	TTCACAGGGG	TAATAATTTG	19200
CTATAACAAA	TGTTTCGTAA	GTTTCAGAGG	GAGCGTCTGA	TTTTTCAAAT	AATTTTGGA	19260
TTTTCATACT	GTAGATGTAA	TAATCCTCTA	TTTCATTATA	TTCTGTTTTA	AGCTCTGTTT	19320
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TTTCTTTATC	AAAATCTGTT	ATATATGCTA	AAATATACTC	CTTATTAAAT	TTTATACTGT	19440
GCGATACGTT	CCAATTGTCC	TTAAAGTCAA	TGTTAATGTA	TTTCCCTGTG	CTTTTATCGT	19500

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GTAGATTGAA ATTACCATTT GGGATGGATT TGCAACCTAA AATTAACAAA AATAAGGAAA	19860
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CTCAACATT GTTATACCAA CAGTGGTATG TTGATTTAAT GGCTAAATAT AAAGGAAATC	22980
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865

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ACAGAATACT TATCAATAAT TTTAATTAT AAGCTATAGT TTTGTTTTT TTAATTCAG	25740
GCATTATCAA TATATTTGGG AAATATTAGG, AAATATTTTA TTAATAAGAT ATTATATAAT	25800
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TTTGATATAA ATCTATCCAT TAGAAAAGTT TTAATTTTT TCTATTGGAT TAGCTGTTTT	26580

867

TATATTATAT TTTAAAAATT TTACATAAGC TTGTGCGATT CCATTTTTAT ATTAACGGAC 26640
 AATCCTCCAA ATACAATTG AACACTATTT CCTTTTTTTA ATATTCCACT GGCACCTAGA 26700
 TTTTTGAAAT AGGCGTCTGA TTTAATGACT TCTATTTGTT TTAGATTGAC TCTTAATCTT 26760
 GATGCACATG CATCAATGTA TGTAAATATTA TCTTTTCCTC CAAGACCCTC T 26811

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26782 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GCATTTATAT CTCTATCATG CAAAGTGTTA CAACTACTAC AAGTCCACTT AGCATCACTT 60
 AATCTTAGAG TCGTATTTTT AATGTGACAA CTACTGCATA GTTTACTTGA TGGAAAATCT 120
 CTATCTACTT TATACAAAGA GGATCCATAC CACTCTGATT TGTATGATAA TTGTCTTACA 180
 AACTCAGACC ATCCTAAATC ATTAATACTT TTTCCAAACA TTCCTTTTGT CATGCCTTTA 240
 ATTGATAAAT TTTCTATTAC TATGTTTTTA TAATTGATA CAAAGTAATA AGATAATTTA 300
 TGCAAAAAGT CTTTCTTTTG ATTTGAAATT TTCTTATGCA GCTTAGCAAC TCTTAATCTA 360
 GATTTAGCCC TATTAATAGA ACCTTTTTCG TTTTTTGATA GTTTTCTTTG ATATTTTTTA 420
 AGTTTATTTT CATTTTTTAA TAAATATTTA GGATGATTGA TTTTCTCACC CCCACTACTT 480
 ACTAAAAAGT GTTTCATACT CATATCAATA CCAACTATCT CTTCTTTATC ACCTTTAGTT 540
 TCATTGTTAT TTTTAGTATC TAAGCACTCA ACTGTTATTG AAATATGATA TTTATCATCA 600
 GTATCTTTTT CTACTACTAC ATTTTAAACA AGCTCATTAT CTTTAATGCA CCTATGTAGA 660
 CACAACCTTA TAAACCTAT TTTAGGTAGT TTTTATAACC ATTTTCTATT CTTATTGAGT 720
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 CTTGCATTTT ATTTCTTTT TTAATTTCTC TAAAAAATT ACTATACGCA AAATTTAAGT 840
 CGATCCACGC ACTACAAAGA GCCAACTAT CAACTTCCTT TAAAAAAGGA AATTCTTCTT 900
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 CACTTAACAT TTTGTTATAC AAAAATCTTA CACATCCAAA TACTTTTGAA AAATATTTTT 1020
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AAAAAGTATT TAAAGTAACA ACTAACTACT ACAAACACTT AGGGATAAAT TTCGGAAGTG	1560
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869

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CCTTGATCCA CAAAACGCAG TTACAAGTTA TTTTATAACT CAAGATCATC CGAGAATGGA	3120
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CCTGCTTTTC	AAGTGCAGCT	ACAACCTGCC	TGTTAGACTC	GTTTCAGAGTT	TCGAAACTTT	5940
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AACATAACTT	TCAGCATCCA	CAGTACAAAT	TTCAATTTCT	TTAGTAATAA	CTTCGCTTTT	18540
CCAAATTGGA	AGTATTTGTA	GTTTGCCGAC	TGAAGAGAAA	GTGTATGCGT	ATCCGAATTC	18600
ATACAACAAG	GCTTGCAAAA	TAGTTTCTAC	ATCTTCTCCA	GAATCAATGA	TTACAGCGGG	18660
GACTTTGTCA	AGTATTGCTT	CGCTAGCATC	ATCATCAATA	AGGTCTTTTA	GTTTAGTTTT	18720
TTCTATTATT	AGATGGACAA	GTGAAAGTTC	TTTTGCTAAA	GGATTGTATA	CAAAAAGCCA	18780
GTCTGGTAAA	AAATTGATTG	GGAATTGAAC	TGGATTTTCG	AATGCAATCT	TTAGTAGGCT	18840
AGAGTAGTCG	TTAACGGTGA	ATGATACACT	TTTGGTGCTA	TTGAACAGAT	CTCTGCTGAA	18900

AAATTTTCT	AGAATCCCC	TAAAAACGGG	GTTATTCTTA	TCATTTACTT	TTACGAAAAT	18960
GTCTTCGTTT	CTGAAGAATA	AGAAATTCAA	AAATTCCTTCT	GATAGGCCGC	TTACACTAAA	19020
GCTGAACGTG	CTTGCTGCTG	TTTTTAGGCT	TGGATCAACT	ATTTTTCTT	CTAGAAACAAT	19080
GCTTGTAGTG	TCAACAAAAG	GGGTAAGTTC	AAAAATTTGA	CCCTCGTCCG	TGTAGAATAC	19140
AATATCAAGC	CCCAAAGAAG	TACAATTTTC	CGATGTATCT	TCTTTGGGAT	TTGAGATTTTC	19200
TTCAAGTTTCG	GCACCTTTTT	CGGTTTCTTG	ATTTAAGGCT	TCGGATTCTT	GACTTGAATT	19260
GTCTTGATCT	TTCAACTTAA	TACAATCCTT	ATCTTCTGCT	GTATTTTTTG	TAACACCCAA	19320
ATACAATCGG	TTCGGTTTTT	TCTATGTATC	GATTGTAGTA	GGTAATTCGA	TTTTTTAGTA	19380
TATTTGTTTC	TTTAGTTCCA	TTTTTCATCGC	CAAACACGGG	ATCAAAATTT	TCAAAACACAG	19440
GAAATTTGTC	ATTAGGATAG	TATTTGATCA	CATAAGATTT	TACAGTCAAA	AGCCAAACAT	19500
TTAGTGCGGT	TGAGTATCTA	AAAAGTTCTG	CTTCATCGAG	CATTAAATTT	TCAATATCTT	19560
CTTTGTTTGT	TAGGGTTGGT	TTTTGGGGAA	GTGATGGTAT	TGATTCGCAA	GAAAGAAATA	19620
GTAACAGTAG	CCAAAATATC	CCTAAAAAAT	TAATTTTTGT	CTTTAAATTT	TTCAATTATTT	19680
GCCCCCTTGA	ACTTGATTTT	GTAAATCTTT	TAACATTTTG	CTTGTGACTT	CGTCTCTAAG	19740
CTTTAAAAGC	TTTTTGATAT	CTGAAAAATC	ACCTCCAGAA	TCTTTGTAAG	CTTTATAAGC	19800
TTGTATTGAG	AGTTCAATTG	TATCTTTGAG	TCGTTTATCA	ATTTGCTCAA	CAGCTGCTTG	19860
ATCTTCATTG	TTTTTTTCGA	TTTTGTCTTT	AATGTAGAGT	ATGAATTTCA	AAAGTGAAC	19920
TGTAAATGTC	ATTCCTTCGT	TTACAATATC	TAATTTTTTCG	CTACCAAAAG	AACTTTCAAG	19980
TCCCTTTAGA	AGTGCATTTT	TGACGTCTAC	TGCGTCTAGT	AACTCATTAA	TGTTTTTAAT	20040
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TCATCAATAC	CCAAGTTTGC	AAATATTGCA	TTTGGAGAAT	TAACAAATGC	ATTGTCACCC	20400
CTTAGGCAGC	CTTTACTTAC	AAGACCTTTG	AAAAGTAAAT	CAATCTCAAA	ACAATCAAAA	20460
CATTTTTCAA	CGCTGTTTTT	GATTTCTTTT	ACCACAAGTC	CAATAAATAA	AATACAAAGA	20520
AAATAACATC	CAAATTTTGA	AATAACCTCA	TTTTGTTCTT	TGAATTGCAT	TTGCAAGGGC	20580
ACGGCAATTC	TGTGAATTTT	CACTTCTTTT	ACAGTTTCTT	TGTAAGAATT	TTTGAAACAT	20640

GCTGCACTTT	CGAGTAATTC	CGATTTGTAC	TTTTTTTATAA	AGTAGTCTTT	CAAAAGTTTG	20700
TAGAAAAAAT	TGTAAATGCA	TAAAAACATT	TTGTTATTCA	TTTGCTTTCT	CCAAGTTTTC	20760
TAAATTTTTT	TTCTATTTCT	TCTTTTAGAA	GTTCTTGTAT	TTTGATTCTGA	TC'TTTTGAGA	20820
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GGACTGAAGT	TTTTAGATCA	GCCATCACCC	CTTTAAAAGC	GTATGTGCCA	AGCCCAGAGA	21060
TAGATATTAC	TAGCATTGCT	ACAATGCTGC	CAATAATATT	TATTTGTTTT	TTTACTCTTG	21120
TCATATAATT	CCTTTATTTT	TTTAAATTTT	TAAAAAAACC	ATATTTTACT	TATTTTTTAA	21180
AAAATAAATA	AAATATGGTC	TAGCTAGACT	GGATTAAAAA	TCCAAGTGTT	ATCCAACAAT	21240
GTCAAAACTA	TTACATTATT	AGGTATTTTCG	TAATTGTATA	ACGTTTTTGC	TAAAAATCAA	21300
AAAACCAAAA	ATTTTTTGGA	TTTTTTTAAAG	ACAAAAAACA	CGAATTGATA	TATACTTTAC	21360
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AAAGTTTAAG	TCGCGCTGCA	TGCAGCGCGA	CTTAAGCCTC	GGACACAAAA	TAAAGTTTAT	21480
GTGTAAGAGG	ATATGTAAAC	ATATATGAAT	AAAATATTAT	TAAATAATGC	TAGACTTACT	21540
AAAGTGTTAT	TACATGAATT	GCTTACCAAA	TTGGTAGCTT	TAAACAGTAA	AAAAGAACAC	21600
TGTCCTAACA	CGATTAAAGT	GTCTCAAGTT	GAATCACTGA	TCAAAAAAAT	GAGATCAAAC	21660
CAATACGATA	GGCTTTTAAA	GGTTTATTGG	GTGATTGATG	TCAAAAAATCA	AAATTACAAA	21720
AACTCTTGTTG	GAGTTGATCG	TTATTCGGCG	TGCGATATTT	ATAGACTGGT	TGCTGATCTG	21780
CTCAAAAAAG	ATGGCAAAAA	GGTTGTTAGT	GTGCGCACTG	TGCAGCGGGA	TCTTAAACTG	21840
CTTAACGAAA	TTGGCTTGAT	TAAAACTAAG	TTAAGAAAGT	TCGGTAATAA	GGACAACAAA	21900
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TATAATGCTA	ACAATCCATT	AAAGGATCTT	TCCGATACGT	CCAATGGGGC	CTCTAATTTT	22140
TCTAACAATT	TTTCAGATAA	ATTTTCTAGA	CATTTCAGAAA	GATTATCTGA	AAATATTTTT	22200
TTGAAATCTT	CATGCGACAC	TGTCTTAACT	AATCAGGATG	TTGACAGTCG	CACCACAATG	22260
TCGCGCCACT	CGCCACCGGC	TGTATTTAAT	AAAGCTAATA	TAAGCTATAG	TAATTATAAG	22320
AATTCAAAGA	ATTCTTTATG	TAATTCAAAA	ATTCAAAAAA	ACAATATTAA	TTTTGAAAAA	22380
AAAGATATTG	AGACTAAATT	GATCGAAAGG	AATATCCCAA	AGGATTTTCT	TAGTCGCATA	22440

AAAGATCTTA	GCAATAATCC	TACAACTTAC	AAAAATGCAC	TGTATAATCT	GGATAAGGCC	22500
TTAGACGAGC	ACAATGAGAG	TAATTTGAAG	TATGTGCTTG	AACACTTTTT	GGATCAGTTT	22560
TCTATTTATC	GATATAAAGT	TTGGATGATG	ATGAAGCGTA	GGGATGGGGT	TATTAGCGAT	22620
TATGAGGTCA	TTTGGAAGGA	AAGGTTTGGG	GAGTTTGTTA	AGAAAAAGT	TGAGCTTAAT	22680
GATTATGTGA	AAAAAGTGCT	TTCAATGGAG	GCTAGAGAAA	GAGAACAGCG	TAGTAGAGAG	22740
CGTTTGAGGA	GGATTAATGG	TCAATCGCAA	GCACAAGTGC	AAACGCAAAC	AGGAGAATTG	22800
TCAAATAATC	AGGAGCAAGA	TAGCGTAAAT	ACGCCGCCCG	AGAGAATTTA	CTTAGGGGAG	22860
AATAGAAATA	ACATCTATGG	AAGAAGTAAC	ATCGTTAAGG	ATTCCTTGGG	CTTTAAGACA	22920
ATTAAAGGAA	TTACTCTTGA	AAGCCTTGGG	ATTGATAAAA	AAGCAATTTA	AGCCTAGGTG	22980
GCTTTAGGAG	GTAAAATGAG	AATAAGAATG	AAACATTTAG	TAAGAAGGCT	TTACTTAAGA	23040
AGGGACAAGA	TTTGGCATGT	TTACAGAAGT	ACGGAAATTC	AAAACAAAGC	TAAAGACAAA	23100
AGCATTACTA	ATTTTCCTAA	ATTAGAACCA	GAAGATTTTG	ACTATGAGTA	TATTTACAAG	23160
TTCGTGGATG	AGTGGATTCA	GAAGAAATAC	AACGATAAAT	TAGGGTTTAC	CATCCAAAAG	23220
GTAGATGGTC	TTGAATATAT	TTGTAAGGCA	AAAAGGTATG	CAAGTTTAAA	GAAAATATTG	23280
GCTAGGATTG	TCAAAGACTA	TAAAGATATA	TTTCTTGGCA	GGTTGCAAAA	GAATGTTGCT	23340
GGTGCAACAAG	CGGGATCCGG	GGGGAGTGGA	GGTAAGGGGA	GCAAGCCGGC	GGGAACAGGA	23400
GGATAATATT	AGTTCACAAA	AATAATAAGG	AGGAAAATAT	TAGCTTTAGA	ATAGTAAAAA	23460
GACCAGTAAA	ACCCGCAAGT	TCTGAAAAGG	TTGTTGAAAC	TGATAAACAG	CAGATACCTT	23520
TTCAGAATCA	TTCTTTTTTT	AAAAAGGAAA	TTATTGGCGA	TAAAACCAAT	TACCATACAA	23580
GGTTGATGAA	TATTTATAAG	GGTTGTCGGG	CCTATAAACA	TAAGTTCTGT	GCTTATTTTA	23640
TAAATACTTT	TAGCAAAGAG	AGAAGATTTA	TTATGCTGTA	CCCCATAAAG	GAGGGAGATG	23700
CGTTTTTAGG	TATATTTTAT	GGGTACAATA	AGGTAAAAAA	TAATCCATTT	TACAGAGATT	23760
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TTGAATTTAG	ATTTAAAAAG	GGGAGTGTGT	TTTGTATCT	CCACACTATA	GCTTATTTGC	23880
TTAGGGATAG	AGATAGCTAT	AATAGGGAGC	AGAAAAAATT	ACATATGCGT	CTGATGGAGC	23940
TAGAAAAAGG	AGTATTTAAG	TTTTATGGTC	GAGATTTGAA	TCCCCAGGGC	GAAGGTATTA	24000
TAACTAAGTG	GATAGATAAA	ATCAATCAGA	AAAAGTTGGG	CAAAGAGGAT	AATCCTAGTT	24060
TGCTTCGCAG	TCTGCTACGT	AGTCGACTGC	GTAGATTTTG	AATTTACAAT	GTTACTAAAG	24120
GGTAAATTAT	GAAAGTCGCT	AGTCTTATAA	GGTCAACTTG	TGAAAAATGAA	AATTTAATTT	24180

TGCGGAGCGG	ATTTAGAGAT	CTTGATGCTA	TTATACAAGG	CTTTAGGGAA	TCAAATTTTG	24240
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CTGTCACTCG	GAGGCTTTTG	TCGATGAATT	CGGGCATAGA	ACATAATAAG	TTGCTTGACA	24420
ATATCAGTTC	GCTAAATAAA	AGTGAAGTGG	ACGCTTACCA	TAAATCAGTT	TCTGAGGTTA	24480
GTAATTTTTT	TTTTTGGATT	AATAGCGTTT	GGGGTACTGA	CATACATGAG	TTAGAAGATA	24540
AAGCTAGACA	AATGAAATTG	AACCACGATG	TAAAAATTAT	CTTTATTGAT	TACATTAATT	24600
TGATTCCTGT	GTCACAGAAT	AATATTCCTC	GTTTTGAACA	AGTTGCATTT	TTGAGTCGTA	24660
ATATACGTTT	GCTTGCACTT	GAACCTGGAA	TTCCAATAAT	AGTTGTATCT	CAAGTTTCCA	24720
GAAGCGCTGA	GGTTGTAGAA	CCTAGTTTGG	CAACTTTGGG	AGAATCGGCA	GCATTACAAT	24780
GGCATGCAGA	TATTGTAATT	TTTTTACATC	AAGAGAGGAA	AAAACGTAAA	GGCGGAATA	24840
CTTCTAAAGG	TAATAATACA	ACTAAAGTAA	AAGTGATAGT	TGCTAAAAAT	AGAAACGGTT	24900
ATATTGGGAT	TGCCAATTTA	GGTTTTACTC	CAAAAACTAT	AAAATTTTCG	AATTGAAATT	24960
TAGATTTGTT	AGATTGTTAG	ATTTTGTAAA	TATTTCTGTTA	TTTGGCCTTA	ATTTGTGTTA	25020
CAATGTATTT	AGTAGGTGAG	TAAATATATG	AATCATCAGT	AGTGACAACA	AGTATTACTG	25080
AAGAGCAAAT	ATATAAAGAG	TTTCTGCGAC	TAGGTATGGA	ACAACATAATA	GCTCAAGATT	25140
TATCAAAAAG	ATATTATCAC	AATGAACTTA	CATATAGAGA	TTTAGAAAAT	TTAGAAAAGC	25200
AATTTGGCAT	AAAGTTTGAC	AATCTTGTTA	CTAAGATTGA	TACTGTTAAA	AGTGAACCTA	25260
CTACTAAGAT	TGATAATGTA	GAAAAGAATT	TACAAAAGGA	TATATCCAAC	TTAGACGTTA	25320
AGATTGATAC	TGTTAAAAGT	GAACCTACTA	CTAAGATTGA	TAACGTAGAA	AAGAATTTAC	25380
AAAAGGATAT	ATCCAACCTA	GACGTTAAGA	TTGATACTGT	TAAAAGTGAA	CTTACTACTA	25440
AGATTGATAA	CGTAGAAAAG	AATTTAGATA	CTAAGATTGA	TAACGTAGAA	AAGAATTTAG	25500
ATACTAAGAT	TGATAACGTA	GAAAAGAATT	TAGATACTAA	GATTGATAAC	GTAGAAAAGA	25560
ATTTGCAAAA	AGATATGTTT	AGTTTGAAC	AAAGGCTAGA	AATAAAGCTG	GAAGCCAATA	25620
ACAACTTCT	TTTGGAAAAG	CTGGAAGCCA	ATAACAACT	TCTTTTGGA	AAGCTGGAAG	25680
CCAATAGCAA	AGTTCTTTTG	GAAAAGCTAG	AAGCCAATAA	CAAAGTTTCT	TCAGAAAAGC	25740
TTAAAGTCAG	CAACAGAATA	GTTATTATTG	CAGTAGTAGT	TGTGCCCACT	GCTATATCTA	25800
TTCTAACTCC	CTTCATTACG	TCAATTAATTA	GCAATTATTT	CAAATAGAAA	TTGCAAAGAA	25860
TTCTTTACTT	TAATCAAGAA	AAAAAATTTT	AGATATAATG	CGCTTTTGTA	ATTTGCAAGT	25920
ATTTTGTAG	ATTCCCaGTT	TTTTTAGGTT	AGCATTAATG	TATAGCGTTA	GAGTATGTAA	25980

882

ATTTTGTCAA GGTTCCTTTT CAGCAATAAA ATTTGAAATC AAGTTTGTA TAGTAGATTT	26040
AAGCTCGTTG GAGCTGTTTT TATAATAATT CAGATTGTTT TGATTGAGCT TTAAAGGTGC	26100
AAATGATTTA ATATAGTTAA GCTTTTGTGA TAGATTTAAT ATGCACGGCG TGTAACTAA	26160
AAAGATGCTT TGTGAATTAG AGTTGTGCCT AACTTCATTT GGTGTTTCTT TAGACTTTGC	26220
AATCAAAGAG TAAACAATTC TCAGTTGTTT AGTAGTAATG TCAAAACCAA ATATCTTTTT	26280
TGCCACATAA TTAATTCTGG TTGTATTAAT AGATATCAAT CTATTTTGT CTAGATTTTC	26340
AATACATCTG GAAATTTTAT TAGAGCAAAT TAGGGAATGT GTTTGAATTT GTAAACCGCT	26400
GTCCAATGTA TAAGAAATTG TATCAGATTG GAAATTGTAA GGAGTTTTTA TGTTTTGATT	26460
TTTCAGATGA GTTAATGGAA TTCCAGCAGC CATAATAATT CCAAGTAAAT GGTGTTTAGT	26520
GCTAGAAGAA TTAATAAGAT TCTCGCTAAT TAAAATAAAT TCATTCGGAT TTATTTTATA	26580
AATTTTTTTT TGTTTGGCAA ATTTACCTTT TAAAAAATAA TTGCATAAAA ACATATAAAC	26640
ATTATATACT TTTTGTAAAG AATTTCAAAA GAAGTTATAA ATTTGTAATT TGGAGATAAG	26700
ATTTGGTATT CATGAAACAT CTAAATTAAA AATTTGTAAT TTGAGGTTAG TGCCTAGGGT	26760
TTTTGGTTTA AATGTTAACC CG	26782

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18359 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

CTATnTACAT CACAGCTTAC CAATGcTATT TAAATAAACT AGAAAGCAAA CCACAATACA	60
TGATTAAAAT GATATGGGCA ATAAACTTAA AAAGTTTAAC GATAATTTTG AAATCTTTAT	120
TAGAATCTAA TTAAAAATGT AAATTTATAT AAATTTTATA AATAAAGAGT CAAAGAAAAC	180
GCTTTATACT AGAAAGTCTT TATAAAGATA ATAAAATATA TTTTTTAGAA CTTTCTTCAA	240
AATATAAATC TTATATAAAG AATATAAAAA AGAAAATAGA ATTTCAAAAT CATTAATAT	300
CGAATGATAT TTTTAAAATA TAGTTTGAGG ACAAATAATA ATCGAATGAT TTTTGAAAAT	360
TAAATTATTT AGATATTTAG ATATGGAAAA AGCCCCAAA GGGGCATCTT TATCTGCGAT	420
GATAAACCCCT AGGAGAAAGA ATTGCCCTCTA CCCTAAATTA ACAATAGTAC TAAAGTATAG	480
CACAACATAA AAATACTTAA CAAGATTAGA TTGATTCAAA CTAGACTAAG AAAATTTAAC	540

883

AAAGATAATG TTGAACATGG AAGTGTGGC CAAGCATAAA GAAATAATTT AAC TTGGAAA	600
CATCTTGTTT CACTACTTGA AAAAAAATGA AAATAGCCGT GTCAATACGA ATACAGCCCA	660
AAATATCTAA AAACCTACAA AAATATTAGC TGATTATATC TATTTTTTTC TTAAGTGAAT	720
ATGAATAAAA AATTCTTTGT AATTCTATT TAAAAAATTT AGCAATTAGT AGCATAACAA	780
TATTTGTTAT GCTAGATATA GCAATGGGAA CTATTATTAC TGTAATAATA ATTATTATTC	840
TGTTGCTCAC CTTGAGTTTT TCCAATAAAA ATGACTATT AATTGAACT TCTTTTTTAA	900
GAGCTTGTC CAAATTAAAT ATGTCTTTTT GTAAATCTT TTCTACAGAA TCTATCTTAG	960
CATCTAAATT AAATATGTCT TTTTGTAAT TCTTTCTAC AGAATCTATC TTAGCATCTA	1020
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CGGTAATATT TGTCGTTGCC AAAACTGCTT TCATAATTCA CTCACCTACT ATATATATAT	1440
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TAATGCACAC AAATAAATA TATTTTCATA TTAAATCCCT CTTTATGAGA AAAACTTATT	1560
CCACTTTATT AGGACCGCTA CCCACCTTAA ATCCAATTTT TCTAAAAAAA TTTATTTTAT	1620
TCGTTGATAT TTTAGTAATT TATATAATAA TAAATTGAAA TTATTAGATA AAAAGCTAAA	1680
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CTAAGCGCTT TATATCTAAT AAAATTTATT CTTTGAAAC TCTCAATATC AATGCTTGGT	1800
AACTTTTTTA AACAATCAAA ATAACCTTGC ACATAATATT ATTGGCTCCA GAATCATAAA	1860
CAAAACTAC TTTATTCCTC TCATTGCCAT TAACTTGAGA CATACTGA AGCTTTGCTT	1920
TCTTTTTTTT AAAAAAGTCT ATCTACTTTA ACATCTGACT CATTAAATGCC TTCTTTGACT	1980
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CTACTTGCTA TTTCTTATCT TTTTGATAAT CATCTTCAA ATTTTATAGCT ACATAATTTT	2100
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GGCCAGCGAA GCATCAAATG CTTTCGCCTAA CCTTCTAAGC TGCTTGCCTT AAAGTCCTTA	2400
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CAATTAAAG TATCTCTATT TTTTATTTTA TTGCTAATAC CCTGAGAAAG CCTATCTACT	2580
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TAGGGTTTCT TTCTGCATGG GGGCTGCCTA AGACTTGATA TGCCACCATT ATAACACTTG	2760
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CCAGTAAGTT GGAAATTTA GAAAGCTTTC TAAAAACACA ACACGAAAAA GAAGCTTTTA	3540
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AGTTTAAGGA AGAATATTAC AAACTTTATA ATTTGTTTGA AGGCATACAA CAAAAATTC	3660
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CAGTTATATT TAAATCCTTT TCATCTATAG AGAAAGAAAT TAGAGATTTG AATTATAAGT	3780
TGmGTGAAAT CCAAAGTAAT TTTCAAATTG CAGATGTTAG CTGGAATAAT GCAAACCTC	3840
TTTTAAAAGA ATCTATAGAA AAATTAATTC AGGCAATTGA AAAAAGGTAT GACAATGAGA	3900
GTAGAAAGCA AGGTCAAAT GGTGGACCTG CTAATAGATG GGATAAAAAT CAAGCTGACA	3960
ATTTTGCTAA GGATGCAAAG TATAAGGCAG AACATTCAGC AAATGATTTG GAAAATGCAG	4020
CCAACATTT TAGATATAGT TGTTCAAATG AAAAAGAAGC TAAAAAGCTA TTAGAAGAAA	4080

885

TTAAAAAAG	ATTTGTACGA	ATTGGTATTA	GCCTATAAGT	AAATTTGAAT	ATTTCAATTT	4140
TAAGTATTAT	GCATAAATAT	TAGTAATAAC	CTAATATTAT	GCATAATATT	CCAATCTGAG	4200
ATTTCTCTAT	ATATTTTTTA	CTTTCCCAAC	TTTTATGTAT	GACCCTTTGT	ATTTCTTTTT	4260
TATAAAAAAT	ATCTTCTAAG	TAAATTTAAA	AGTATCGCGT	AAATAATATT	GTGTAGAAAC	4320
TATCAAAACC	AAAAAGTCAG	AAACAAGCTT	TAACACAAAA	TATCAAACCG	CCTTACCCAA	4380
CGGACTTTAT	GCACATTTCT	TATCAAATAA	ATCTAAGTTT	TTCATCTTTA	CTCTTAACAC	4440
TATATTCTGA	ATAATAAATC	CTTGCAAACT	CAACCAAGTA	TCAATTTTGT	AATAAAGAAT	4500
ATAAAATTTT	GGATAATGGG	GTTTTAAAGC	TTATTGATTT	TAAGAAGAGA	GGCAAGAGCT	4560
TGCTTAAGAT	AAATTTATCA	ACTTTTTCAG	AATATAAATA	CTATCTATAA	ACACAGCCTG	4620
GAGAGGGATT	AATATTAATC	TAAGCAAAAT	AAACACAATT	AAAAGGCGAA	AACTAATATA	4680
ATTGCTTTAA	ACTTTTTTGT	TTTAATCTTT	AAATATTAT	AAGTCTGCAT	TCAACTATCT	4740
CATATATAAA	GAAGTGGTAA	TTACTTTTGC	AAGAAATCTT	GTGCCTTGGG	TCACTTTAAC	4800
AACATTAGAA	ATGGATTTTA	TAACATCTTT	TTTTGCCACT	GCTTGATCCT	TATTTGATAG	4860
ACTTAGACTT	AAAAATCATT	AATAATAATA	TTGACCCTTC	TTTGGCCCCC	TTAAACCGCT	4920
TCATCTAGGG	CATCTTCAGA	AGCTATTAAA	GCTTTTTCAA	CTTCTTCTAC	TTTAACAAAT	4980
TCTTTTTTTG	TCAATTCTAA	TTCCTTATTA	TTTGGAGATT	TATTTGACAT	TATTTATCTC	5040
TCTATTAAAG	ATATTGCCTT	ATTCTACAAC	ATAACAGCC	TTTTAAGCTT	GAGCGGCCTT	5100
TTTAGAAATT	TTAACAACCC	TATTTAATCC	TTGGCAACAT	CAAAATCTTC	TTCCCTCCGA	5160
AAACTTTGCT	ACAATCGCTG	CTTCTTGTTA	TACAACAACA	GCTCTCTTGA	TAATAAATGA	5220
CATCAAAAAC	ATTGAACCTA	CAAACTTTTT	AACATATATC	TTGTCAGTAA	ATTTAATTAA	5280
CTAAAGAAGT	GATTCTTTAA	CACCTCTCCCT	AATTTACTAA	GAACACTCTC	TGTTAACTTT	5340
TTAATAGTAT	CTAAATATGG	ATTAACCCGA	TATTTTAAAT	CTACATTAA	CCATCTTTTT	5400
TATCTGATTG	TCCTAAAATA	TTAGATTGAA	ATTGAATAAT	ATTCACATTA	TTAAAACTG	5460
CAAACACATT	TAAATTCACA	AATCCAAACA	ACAATCCACT	AATTATTAAA	CATTTTAGAC	5520
ATTGTTAATT	CTCCTTGTTT	GAAGTATTTT	ATTTTAAACA	AAGATTATCA	AACTTAAATT	5580
TATATTAAAT	GGAAAAAACC	AGTTCTATTT	TATAATAGTT	GAATTTATTA	TTATAAAAAC	5640
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TGAACGATCT	CTAAATTAAC	AGAGACAATT	TTTAATAGAG	AAAAACTCTC	GCCCCACCTA	5760
AAAGACAATA	GTTTTACACA	AGCTAACTAT	TTAATGCTTT	ACCTGTCATA	TTTAATCTAA	5820
AAGAAAATAC	TAGATCATCA	ATCCATGTTA	TAAATGAAGC	CTTATGCACA	CCAAAAATAT	5880

CACATTTGCT	TGTGTTTTAA	ACAAAGTTTT	TTAATAACAA	TAAGAAGAAT	AATAAGAATG	5940
CGTTCAAACT	GTCAAAGTTT	TCAAGCTTGA	AAATAACCAA	ATCTTGTTT	AGCAAAAATA	6000
AAGGTGATGA	ACTTCATTTG	GTAGGCATTA	CTAGTGCAAG	ACCAAGCAAT	AATATCTAGA	6060
GAAATAAAG	TCGAGCTCAA	AAATCGTGCT	TTTAGCTTCC	TTATAGAGGA	TACTTTTTTG	6120
ACCAATATAC	TTATTCTCCC	CTTGACAAAA	AAATCAAATG	TAAAGGTGTT	AAAACTTTAT	6180
TTTGGTACTT	ACGTGGAAAA	TACTAAAAAC	AAAGAAGAAG	GCACTTGGGT	GATAAATGAC	6240
TAGAATTTTG	AGAATATCAT	AAAAAACTTC	AAGCCAATAA	TATCAAATTT	TGATTTGGTG	6300
CTGGAATAT	GGAAAAACA	GGAAATTATG	TTGACAAGCT	TTAAGAACCT	ATTGTTAAGA	6360
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GAAGTGGTGT	TTAGAAAACA	CTTGTCTCGA	ATTCTTGACC	ACCGAATTTA	CTAAGAAAGA	6540
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GATCTTAATT	TTCAAGGTGA	GTGAATCAGC	AAGATTAGCC	TCATTCAATC	ACTGTAATGT	6720
TGGTTGGCAT	TGATTAACAG	ATACCACTAG	ATTTTTGATC	AACATTATTG	ATCTTGATGA	6780
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TTACTATGTT	AACTATAAAC	ACTTTTGAAA	AAGGTCTTTG	GCTTTTTCCT	ATAGTCTTTT	7260
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TCAGTAATCA	ATTACTTAAA	TAAAGAATTT	AAAAAAAAT	ATAATACCTC	AATTAATAAA	7560
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887

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TCAAATAGCT TCGGAGAATT TAAAGGAAAG CTTTGTATAT ATAAAGTGTC GCCTATTGCA	7800
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GCTTGTCAGA	GATATATAAA	GAAAAATATG	TTAAAGAAAA	CCCAGAAGAA	GGTGTGGCA	10140
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CTTGATTAAA	ATTGTATAAT	ATATTATAAT	CAAAGTAGGT	TAGAGAGCTT	TTCTCTCTCC	10380
GTGTT CAGTA	GTAAAAATATT	TGCCCATAGG	GGGCTTTTTT	TGTGCCTACT	ATATATTAAA	10440
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AACAAAAGAT	TGTTAAAGTA	TTCTCACGAG	ATTAATCTTT	TATTAAGCAT	TTATGCTTTT	10560
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891

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AAAACAATAA	TTTGAATATA	TTAGATTTAG	CTAATGACTA	TAAAAAATA	AAAAATGAAT	17700
TAATAAAGAA	AAAAAGTTTA	ACAATGCTGA	ATTTTATTTA	TATTTTAACC	CATTAAACTT	17760
TATAAAGGAT	TTATCAAAT	CAATTTTITAG	CTTTCTAATA	TTATTTTAT	TAATAATAAT	17820
TCTTTAATGA	ATTCTCTTAT	TTTGCCCAAA	TTTAAATTCA	AAAAGCTTTC	CAGTTTAAAT	17880
AATAATCTTT	TCTGGAAGCA	GAAGAGAAAA	GTTCTAATGT	TAATAAATTG	TATTCTTTTA	17940
CAAACCCAT	TTTAGGTAGT	TTTATATAAC	CATTTTCTAT	TCTTATGAG	TTTTTTTGAT	18000
TATTAGTTCT	ATAAGTTTGC	CTATTTTTCT	TACTTTTATA	CTTAGGAAAT	CCTTGCACTC	18060
TATTTCTTTT	TTTAATTTCT	CTAAAAAAT	TACTATACGC	AAAATTTAAG	TCGATCCACG	18120
CGCTACAAAG	AGCCAAACTA	TCAACTTCCT	TTAAAAAGG	AAATCTTCT	TTATATTTAC	18180
TTGGATAGGT	AATAAGATTT	TGTCTATTAT	TTTTATAATA	ATCTTTCTTA	TCACTTAACA	18240

893

TTTTGTTATA CAAAAATCTT ACACATCCAA ATACTTTTGA AAAATATTTT TTTTGATTGG 18300
TGTTGGGATA TATTCTGCAC TTATAAGCTT TATTAGCATT CATTATTTTTT TATAATTAT 18359

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14752 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

GCAGGTCGAC TCTAGAGGAT CCCCTTACTT ATAATAGCTA TATACTACGA AATATACAAA 60
AGAAAAATAT ATAAATGCCG TTTATATATAA ATTACTTGGA TTAGAAAAAC AGGGAAAATT 120
ATTTCTTATA AACCATCAAA AAATATAAAA ACTTTCAAAA AGTATGAGGG AAAAAGTATT 180
AATTTACATC CCCCCAAAAG AAAAAATTG AAAATATTTT ATAACACCAA ACTTTTAAAA 240
AGTAACAACC CTAACAAATA TTTTCTCAAG TGCAATCTAT TAAAATTGGT CAAAATGCCA 300
TAACGTTTGA AGAGCTTGCA ATCAAATATA TAAAAATCCA ATAATATTGC CTAGCAAATC 360
TTATTATTTT AAAATTTTAA AAAACAAAT CCTAACTATG TCTTAAATCT GGATCAATAT 420
AATTTATTTA AAACATTAAA TAAAGATTAT ATAGATAATA TACTTATTAT TTTTAATTCA 480
AAGCCTAGAA GAGAAAAAAA GAATGCCCAT TAAATGTAAC AAGATAAGTA AAAAAGAGGA 540
AACAAAAAAA TTTTTTGTGT GGAAATTTTT CAAAAAATA ACATAGTTAA AAAGGCATTT 600
AAAAACACTC TCAAATATTA AAATTATAAC ATGCATTTAT ATAAATGCTA CAGAACTATC 660
GATAAACAAA AATGGAATTT TTTAAAAATT GAGATAGACT AAAATTGAAG GAGAATTAAA 720
ATTTTTATGA CAGCAATAAT CGTGTATTCA TGCTTGACTA TGTGTGTAAT ATATTTTCAC 780
TTGCAACTAA AAACATTTTT CACAAAATTA ATCAGATTTT GTAAAAATG TTTTGATATT 840
TTTTTATTAT TAATAGAAAT GTTAAAATTA ATTTTTTATC TATTAATTAT TAATAATAAG 900
TTTTTATATAT TTATTATAAT ATCAATAGCT TTAATTACAA TCAATACAAT GATTTAACTT 960
ATTGTATTGA TTGTAATTAA GCCAAATGTA TCCAACAAGC TAACTACTAT TTCTAAATCA 1020
AAGATCATTAA AAATAACTTA TTGCTTCATC TCATATGATA ACTTTTAAAA TTATTTTTTA 1080
TTAAGACCGG CCATCCGCCA AAACATAATC CCCCAAACCT TACTTTAGGA AGTTCTTACC 1140
TTGGTTTTTT ATTTCTTTAT AAAAAGAAAG TCTTAAGATT TAAAATTGCA TTTAAATCTC 1200
TATCATACAT ATTGAAACTT TACTAAAAACA TTCCTTTTTG TATAAAATTA ATTGATTAAA 1260
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TTAGCTCTAT	TAATAGCGCC	CTTTGTCTTT	TTAATAGTTT	TCTTCCAGTA	TTTTTAAGTT	1440
TACTTTTATT	TTTTATAAAT	ATTTAGAATG	ATTGTTTTTT	TACTTTCACG	ACTCTTTTTT	1500
ATTATTTTTT	TTATTGTTAT	TTTAAATATT	TAAGCTCTCA	ACTACTACTG	AAATATAATA	1560
TTTATTATCG	GTATTTTTTC	TACTACTAAA	TTTTTAATAA	CTTTATTATT	ATAATGATCC	1620
TATGTAGACA	TAACTTTACA	AATCCTATTT	TAGATAAGCT	TTATATTCAT	TTTCTATTCT	1680
TATTGGGTTT	TTCATTTTAT	ATTTAGGAAA	TCCTTACGTT	TGCTTCCCT	TTTTAATTTA	1740
TCTAAAAAAT	TATTATCTGC	GAGGCTTTAA	TCAATCCATG	CACAAAAAAG	AGTTAAAGTA	1800
TTAATCTCCT	TTAAGAGTGA	AAATTTATTT	TTATATTTGC	CTAGATTAAT	GCTAAAACTT	1860
TTCTTGTTTT	TTTATAAGAA	TCTTTCCTAT	CACTTAACAT	TTTGTCATAC	AAAAATCTTA	1920
CAAATCTAAA	TACTTTTAAA	AATTTTTTTG	ATTAGTGTTA	GAATATATTC	TGTTTTTACA	1980
AACTTTATCG	GCACTTATAT	ACTCTATTAT	TTTATAATAA	TTACTTAGTG	TATATAGAAA	2040
TGAGATAGCT	TTTAATAATC	ACTGCATATA	TTTAGTTAAT	TATCCCCCCC	CCCCGAGTAC	2100
TAGTTACTAA	CCATAGACAC	AAATGATGAG	CTTATGCCCT	GTCTCACAAA	ATAATACTTT	2160
TATATTCCTT	ATGGAAAATA	ACCATTAATG	AATTAAATTG	CAATAAAGAT	CACATTGCCA	2220
ATATTCATC	TTCTAAATTC	ATCAATAATT	TAATACAATA	TCTTCATCAA	AGCTTATAAG	2280
AAAAAATATT	CTAATTATTT	ATGCATTGCT	GAAAATCTTA	TTTTTAATCT	AAAACTACT	2340
GACTTATTTA	TACTAGAGAG	AAAGTTTTTC	CGATATGATC	AAAAAGCATA	TTCCGAATCA	2400
AAATAAATCC	ATTTACTAAC	AAATTCATAT	CTACCTAAAT	TTACACAGAA	TCATAGGTAG	2460
ATAATTCTTT	ATTATTTTTT	TGTTAAAAAT	TTAAATAACA	AAATTATTAT	TTTTTTAGAAG	2520
CTTCTATATA	TTCCATAATT	AAAGTTCTTA	TAAACCAGA	AGCTGTTAAT	CCCTTTTTGT	2580
CTAAAATAGA	ATAAAATTCA	ATCCAATATT	CATATTTTCA	TCCTACACTT	ATTTGCTTGA	2640
TCGTCATTTT	TGATCTAATA	GGCTTAACAT	TTGGAATGTT	ATTGCTAATA	ACATCATTAT	2700
CACGAAAAGC	AAATTTAGAT	TTGCTAACAT	TTTGTTTAAT	AATTTCTTCT	AAATTAACCT	2760
CTTTGCTTAT	AGGCATAAAG	CATCTCCCAA	TCTTGAAAGT	TCTAAGACAG	ATCTACTCTC	2820
CGGATAATAA	TCAAAAATCG	ACTTCTTATA	TAGCTGAGAT	TCTGCTATTT	TAGCATCTTG	2880
TCCAACCTCA	TAAAGATCAT	ATCCAAAAGT	TTTAAATTGC	CTTAGATGCA	AATTATGTCT	2940
TTTAAAACTT	TTATTAAGCA	TATTGCAAAT	AATCTTCTCA	TGTTTAACCT	TTTTTCTATA	3000
AGATTTTAAC	AAAGACTCAA	ACTCTTCTTT	AAAAATATTA	ATTCTTCAA	GGCTTAAAAA	3060

TTCTGGGGTC	AGTGGAGTAA	TAAC TTCACA	CATTGCAAGA	ATAATTCTTC	GCTCCCAAAG	3120
CTCAAAACTG	GGAGATAAAT	CAAAAATTGC	AAATTCAAAT	CCCAATTTCT	CCAATTCCAA	3180
ACAAAAATCA	TCTATCAAAT	ATGGAAAATC	TTGCAATTCA	TGTTGCACAT	CTCTTCTAAA	3240
AGTTCCACTC	GGCACACATG	GCAAAATATA	AAAATTTTTT	TGTATTTGTC	TTACTACTTG	3300
ATCTACATCC	ATCTTCTTCA	AAAGAAAATC	TTTAATATCC	AGCTTAAGAA	TTTCATGATT	3360
AAGAAACCAT	GTAGAAGAAC	TTGCTTGCTG	TATATCACAA	TCAACTAATA	TAAC TTTTTT	3420
TGTTTTAGAT	AAATAACTTG	CAATATTTCC	GCTTAAGGTA	GTTTTCCCAA	CACCACCTTT	3480
TTGAATATGA	AATGCTATTT	TTTTCATACA	AACTTCCTTT	TAATTATTTT	ATATCACATA	3540
TTAATTATTT	TATATCACAT	ATTAATTATT	TTATATCACA	TATTAATTAT	TTTATATCAC	3600
ATATTAATTA	TTTTATATCA	CATATTAATT	ATTTTATATC	ACATATTAAT	TATTTTATAT	3660
CACATATTAA	TTATTTTATA	TCACATATTA	ATTACTTTAA	TCTCTACCTA	TGAAGCCCCCT	3720
TTCACAAAAT	TTTTTAATGA	ATTAGATCTG	ATGTGGCCTT	AAAAGCTAGC	AAACTACTAT	3780
CTCTATATTC	ACGGCTTTTG	TCTCATTCTA	CGATAACTTT	TTAGTTCTTT	TTATATCTTA	3840
TTTTTCACACC	AATAGCATGA	TTAACAAGCC	TAAATTCGGA	AAATTCCTGT	CTTAGCTTTT	3900
ATTTCTTTAT	AGCAATAAAA	CTTAAGATTT	AGAATTGCAT	TTATATCTTT	ATTATACAAA	3960
ACGCTGTAAG	TTTACCTAGC	ACCACTTAAT	TTTAGAATTG	TATTTTTTAAC	ACCACAATTA	4020
CAAATAGCTT	GCTTGATGAA	AAATATATAC	CTACTTTATA	CAAAAAGGAT	CCATACCATT	4080
CTGATTTATA	CTATAATCGT	CTTACAAGTT	TATAACATCC	TAAATTATTA	ATACTTTACC	4140
CAAACATTCA	CATATCTTTA	ATTAATAAGT	TCTCTATTGC	TATATTTTTA	TAAATAACTA	4200
TAAAGCAAAA	AATACCTTGT	GTAAAAAGGT	TTTTTGATTT	ACAATTTTCT	CATGTAAC TT	4260
AGTAATCTCT	AATATAGATT	TAGCTCCATT	AATAGAAGTT	TTTTGTTTTT	TTGATAATTT	4320
TTTTTAGTATT	CTTTAAGTTT	ATTTTCGTTG	TTTTTTTTATT	ATTAGCTTTA	AAAGCTTGCT	4380
TATTTTCTCT	GCTCTTATGT	TTAAGAAATC	CTTGTGTTCT	ATCCCTCTTT	AAATTTCTCT	4440
AAAAGAATTT	ATATATAGAG	CTTAAGTCAA	TCCATGCATA	CAAAAGGCCA	AACTATAAAC	4500
TTTTTTTAGC	AATAGAAGCT	CTTATTTATA	TTTATTTGAA	CAAGTAATAA	GATTTTGCTT	4560
ATTTTTTTTA	ATAAAAATCT	ATCTTGCCGC	TTTAACACTG	TATTATATAA	AAATCCTACA	4620
CATCTAAATA	CTTTTAAAAA	GTATTTCTTT	TGGTTGGTGT	TAAAATATAT	TCTGTACTTA	4680
TAAATGCCAA	CCTTCTCTTT	GCCAAATAAT	ACTTATTTTA	TGTTCTTTAT	AGAAAAAAGA	4740
ACTTTTATTA	AAAAAATTTA	AATTATGATA	AAAATAAAAT	TCATTTATCA	CCAGAATTTA	4800
CTTACAATAT	TTAACCTTCT	AAATTAATTA	ATAATCTAAA	AACGGCACCT	AAGCTATTGT	4860

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ATCTATTTTA CAAACCTACC CCCCGCCCAA ATTTATTTTG AAATTTAGGC GGGCAATTCT	4980
TCATTATTCT TTATTAAAT TATAAAAAGT CCTAAGAAAT TTCTCTCTTA AGGACTTTTT	5040
ATAAATGGTT AAAGGTTAAA GATAAGTTAA AATCTACAAC AGTTTAGAAA AAAAAACAAA	5100
TTAAAAATAT TTTTTTTATT TATACTATGT ATTAATTGAT ATATAATATC AATTAATACA	5160
TAGTATTATA TTATATTAAT ATATTTTAA AGGATAAAAA TGCAAAAAGA AATAACAATA	5220
AACTATAATG AATATACAAT TGGGGGCATA AAAGGAACCT TCTTTGAAA TTCTCAATAT	5280
GAAGCTAATT ATCGAGCAAA AATAAATGGC TTTATAATTG ACTTTTTTAA AATTCCCATA	5340
AGTTTAAAGA AAAAATATGA ACTTAATATT AAAGCCCTTA GTGATCCTAA TTTTTCATCC	5400
ACAAATATTG CAATGAATTG CATAAATACT TTCAAGCTTA TAGTTGATAT TGTTAATATG	5460
CAAACCGGTG AAAATTACGA TTATGACACA TTTATTACCA AAACAGACAC AGAAAAATG	5520
CTTAAATATG GAACAAAAAT AATTGCCGCA CTAGCAAGGC ACTTCGACGA ACAAACAAA	5580
ACCAACTTTA ATGAAAGCTA TTATGAATGG GAAAAAGGCT GGATAGATAA AAAATGGATA	5640
AATTATGAAC CAACTGCAGA AGAAATTAAA GAAATTCAA TAATGAATCA AAAATTAAAT	5700
CCTTTAAAC TCAACATAG AAAAAAAC CTTAATAACG GCCAAATAAG GCTTTTACAA	5760
GCCATCAATA AAATTGAAGA TCAATCACA CAACAGGCTA CTAAATCAA TAGCAAACT	5820
AAAAAATTAA AAGGAAATCA TGGGGAAAA ACCAAATTT AACATTTTAC TTAAAAGCGT	5880
TTAATTTTAT TTATTATTAT TAAATAATAT TTACAAAATT AAAAAATAA AATATTATAT	5940
ATGTAAGGTA GAAAACGATC TACCAATAGT CCCCAACACC CCTATTAATC CTCTCCAAAT	6000
AAGATCGGGG GTAGGGACTT CTTTTTTAAA AAAATAAAAA CTAAAATATT TGGTGCCTAA	6060
ATTAATAAGT TTATAGCAAA TAAGAAAAAT GAAATCTAA AAAACATAAA TTAACATAAA	6120
ATTTGCATTG TGAATATAAA ATTTTAACAA TGCTTTAAGA TTTAAATTAC TATTTCTAAA	6180
TCAAAGATTA TAGAAACAAA TCCTCGATTT ATTTTCATGGC AGCTTTCTAA ACTATTTAAA	6240
AGAACAGTAT TTACCAATAC ATGATCTAGC CTTACTTAAG GCAGCTCCTG TCTTAGCTTT	6300
TATTTCTTTA TAAATAAGAC TTAAGATTG GATTGAATT TAGATTCTA TCACCTAGAA	6360
CTACAACCTG CAAAAGGCCA ACTGGTTTCT CTTAATTTTA GAGTTGTATT TTTAATACCA	6420
TAATTACTAC ATAGTTTACT TAATAGGAAA CATCTATCTG CTTTATGTAA ATAAATCCA	6480
TAACAACCTA ATTTATATAA TAATTATCTT GCGACTCTCT ATACCACCAT AAACCACCA	6540
TACTTTTCTT TTGCTATACA AAAATCTTAC AGATCTAAAT ACTTTTGAAA ATTTCTTTTG	6600

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GCAITATTTA	GGGTTTATGA	AATAATATTT	TTGCATTTCT	TATTCGTTTA	TATTTCTTTA	6720
TAAGAAATATA	TAATTTTGTT	CGAATTCGTC	TTTAAAAAAT	GGTTAATTTA	GAATATAATT	6780
CTAATGGCTA	AAATGCTAAA	AATGGATATA	AATTTGGACT	AATTTTATTA	TATTGAAAAA	6840
CAAATTATCT	GTATATACTA	CAATAATGCT	TAACTTTAAA	TTTTTAAAAAT	GTGTTTACTT	6900
GTGCTTTATG	GTTTTTGTAA	GGTTAATTTT	AATAATCAAA	TTTAGGGGAA	AGAAATTTAT	6960
GAATAGAAAA	TTTGTATTAT	CATTATTATT	TATAATATTA	ACTTTTTTAT	TAATATTGGG	7020
TTGTGATTTA	TCAATAAATA	ACGATCGAAA	CAAGATAGAT	GGGGCTTCTC	ATTTTAAAAA	7080
GAAATATATG	GATAATTTGA	ATTATCAATG	TTTAAGCAAA	AAAGAGTCTG	AGGCTAAAAA	7140
TTCTCAAATT	AAACTGGATG	AGAATAATAA	TAAAAATCAT	TTTTATTCTT	CCAGAGTATC	7200
TAATGTTTCA	AATTACTATG	ATAGAACTCA	TATATCTTGC	AAAAAAAATG	ATTGATTTTT	7260
TTTGAAAAAT	AAAAGCATGC	TTTGTTTACA	ATCTGATTTT	AAAAAATTTT	AGTTTAGTTG	7320
GTAAATATGA	GTTTTTCAGT	GTCTTTTATA	TAGAAATGCA	TATATATATA	TGAACTGTAA	7380
GAAAAATATAT	TAAATGTTC	TAAAGTAAAA	AAATTCCTAG	AATAGGGCCT	ATATATAATA	7440
ATACTTTTTA	TATATGTAAA	TAGCAATTAA	TTTTGATTAA	TTTTAATTTT	GCTGATTCCT	7500
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TTATTTTCTT	TTTCATAATT	ACTTCTATAT	TGTTTTTTTA	AATTTTTTAT	TAAAAACGTT	7620
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TCTTCAATTT	TATATTCTTC	CTTATATTTT	TCTATTGCCA	ACTTTAAGTT	TCTTAATGCA	7800
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GAATATGTTT	TAAGTTTGTT	AGATTTATAG	TATTGTTTGT	TTTTAAGGTC	AATTGCCCCAG	8400

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ATATGATAAA	TTGAAAAATA	AAAGGGAATA	TTTTATTTTA	GTTAGAGTTG	AATCTAGAAA	10620
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TAATATCTAA	TCTTTTGAAA	AATTAATAAA	TTCTAGTATC	GCTTTTTTCAT	TTCTCAGCAA	11160
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TTCAATTACCG	GCTCTAATTA	CATCTTGCTC	ATTTTAAATA	GAAGTTGCAA	TTTTTTTGTC	11580
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TATTAAGAAT	ATAAAAGTTT	TATTTTTTCAT	TATACAACTT	ATTATATGAT	AGCAGTCTTG	11820
AATAATTTTA	GTAAACCTTT	TTTATAGATT	AAGTCTGAAA	TTTATAAAAA	TTTTAGTTAT	11880
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CTGGATAGCT ATACAATAAT TGTCTTACAA TTTTCATGCAA TTCTAAATCA TTAATACTCT	12060
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ATTAGCCATA AATATAGGCA TAAATGTGTA AATTCTAAGC TTTTCATCTTT TTTTATCCAA	12180
ATAATACTTT ATTTTCTGTT CTGTGTAGAA AAGAACCCTT AATAAATCCA ATTATGACAA	12240
TGATTACATT CATTTATTAT TAGAATTTGC CTCCAATATT TAACTTTCTA AATTCATCAA	12300
TAACCCAAAG ATAGTAATCT TAAAGATTTA TAAGAAAAA TATTTTATTT ATTTATATGA	12360
GCATTACTTA AGCCATTATT CTAGCTTTGA ATAATATTG ATCTTCTCTG CAAAAATCTA	12420
ATTTAAAAA AAATTTTAAA AATACATGGT AATACTCAAT TATTGAACTA ATAATTGAGT	12480
ATTAAATATT CTCCTTTTTT AAAATTAAAA GAATTTATTA TCAATATTTA CTTCATACCA	12540
TACATTCTTT TAAATAAACC TCTTATCTTT AAGGGGTTTT CTTTTTATTA AATCTTTAAG	12600
ATTACTATCT TTGGGTATT GATGAATTTA GAAAGTTAAA TATTGGAGGC AAATTC TAAT	12660
AATAAATGAA TGTAATCATT GTCATAATTG GATTTATTAA GGGTCTTTT ACATAAAGAA	12720
TTTGCTATGC AATTTTAATT TTTGTTTGTA ATCGCCAATT ATTAAAAATA AAATTATPAA	12780
AGGGAATTAA TGTA AAATTA ATTACCTTTA AATATACTTC TTTTAGAGAA TATATCATT	12840
CTAATATTAA TCTATTACTA ATGATATTAT TAAATTAAAG ATCTATAGAA ACATCAGTTT	12900
ACTTATTATT AGAATTAAAG TTTATGTAAA TTATAGGTTA AAAATTTTTT GTAATCTTTA	12960
GTAAGAATGT TAAACCTATC TTTTATTAAA GACAGGCTTT GTATTATAAC AATTTCAATA	13020
TGCAATTTAA AGGCTACTAT ATATTGAATA TATGTCATTT TTTAGTTTTT CTGCTTCTTT	13080
TCTTTTTTCT GAGACTTGAT TGCAAATATC TTCTGTATGA GATTTAAGTG CATTTTCATC	13140
TGTTTGATG TTATTATAT TATTTTGATA GTCTAATAAG AGTTGCTGCA TCATTTCTGA	13200
GACTGTTGTT TTTGTAGATA AAAATTTTCC CAAATAATAT TTAAGCAATA CAAGATTTAG	13260
TAAAGCGTAT ATTTTATTTT TTTGATTTAA TTTCAGTTAT TTTTAGGATT TTTATTATTT	13320
TAATCATATT TTCTTTATCA ATATTTAATG TTAATAAAAT TGAAATAATT TCTTTACATA	13380
AAAAGTCACA TTTATTGAAA TGCTTTATTA CTTGATACTT TTCTATTTCTG TTAATTTTTT	13440
TTTCTTCTTT TATATTATTA TTACAATTCT CCAATTGTAC ACTACCCATT TTTGTATCAG	13500
AATTTTATT AAAATAGTTG GCAACTCTAT TTTGAAATCT TTTTCTTTT TTTTCTTTAA	13560
AGTGTGGTT TATCTTATGG TAACAATCTT TTTTAGGATA ATTAAGCTT TAATAAATTT	13620
CyGTACCCGA ATTTACCCCC ATATGTTGAT AGTAGTTTGT TGTGACTTTT ATTTCTTTTT	13680

901

GTAGTCTATA GATATACTTT TGCATAGTTC TTAGTGTAGA AATAGTTTGA CCGTTTTTTC	13740
TTAGATTTTC ATTAAAGTAA TAGAGTATGG TTTTTTGTGT ATATTTCTTA TGTGTTTTGT	13800
TTAGATAGCA TATTGTTGAA ATAAGAATA TTAATTTGTG TTGAACTTTA TTATAGCAAT	13860
TTCTATTGGT TTTATTTGTT GTTTTTGAAT TCATAGAGAC TTCTCCTTAC AATTATGGTG	13920
ATCATTTTAC AATATAACTA AAATTGCTAT AAAAGTAAAT ACTCTTATAG CAATTTTAGT	13980
TATATTGTAA AGTTTTAGTA ATTGAGATTA AAATTTATTT AAAATACAAC TTGACTATGG	14040
TTTAATTTTT GTTATACTAT AAATAGTTCG ACGAGAGTTC GAATTACAAA GAAGTGATCG	14100
TGAAATAGGG CTTAAAGCAA GTTTTTTATA AAGAATTTGT CTTAAGCCCT ATTCATTTTA	14160
TGTAACACTA ATTTTCCCAG TTTAAGTTTT ATTTTGTPTT GGGCACTATA ATAATGATTT	14220
TTTTAGATTA AAAATTTTCT AGAATTTAAA GATATATTGG ATTTATTTTG TATTTAGCTT	14280
TATATTGGTA ATTAAGTAAT TATTTATGTT CAAAATCCAT AAAAGACATA TAGTCCTTTA	14340
TGGATTGATC ATTTATAGAT CAAAATATTC TTTATTGGGC CTATTATAGG CCATAATATA	14400
CTAGGATAGA TATTGGTTTA CTATTTATAT AATCGATTAT AGTAAATTTT CTGGATTATA	14460
TTAGCTTAAA TATTAGGATG AAGATTATAA ATTTTAGTGC AACAACTTC TAAAGGGTAA	14520
AGGAGTGTAT AACGGCCTAT AAAGCTTTCA TTTTCTTTAT TTGTGGGACA TTTTACGATT	14580
ACTTTTGGAT TTTTCTCTAA TATTTCAAGA TATTCTAATA GGGTTTtATA ATTAACTCGT	14640
GTTGAGTCGT TTtAGCTAGA GCAAGATTAA ACTTGCTTTT TATTAATAAA TGAGTATAAT	14700
CTTTGTTTTC ACTATAGAAC AATTCTTGAT TCATGTGATC TAGTGTTTTG AC	14752

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10749 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

CTTTTTTACT TTtAAATTTA GTAAATTGTA AATTGATAG TCTTAATTTA TCTACAAAAA	60
GCGTAGATGA CAAAAACAAT TCTATAGCCA AGCTTCTTCA ACACCTATCA AAAAGTGAAG	120
ACCAAGCCAA TAAACTTCT ACCTCAGAAG ACCAAAAGGA ATTAGAAATT ACGGAAAACA	180
AAGAACAGGA ACATGAAAAA CTTTCACAAG TAGCACAAACA TGCTCCAAAC TCAAAAATTG	240
AAAAAGTAAA ATCCGATGGA AAACCTGTTC CTGGGGACAA AATCTTTCT TCAAATAAAG	300
ATATTTACAA TTCTTATATC CCAGAAGTAA AAGAGGAAAT TGTTTATGAA ATTCTTGAAG	360

AAGTGATAAT TCCCGAAACA AAAATTCCCTG AAATTACTGA AGAAGTGATA ATGCCTATTC	420
CACAAACAAT AGATTTTTTAT ATTGAACCAA GGCCAATAAG TAGTTTCCTT ACTCAAGGGA	480
CATCACCAAG TATTACAAGT ACAATAAAAT CATATAAAGA ACTCGCTAAA GAAAAAATTA	540
ATAATGGCTT GAATATAGTA CAGAAAATAA CTCAAAATAT TGATAATATT ACAGAAAATT	600
TAAATTCTAA AGAAACACCA AAGGAAATAT CGGGGAAAGA AGTTGAAGAA AAAATTACAC	660
ACCCCATATT TGATCACATT ACTGGAAGCG GTAATAATCC CGGACAAGAT TCTATATCCA	720
ATACATGGGG CGAAGGACTT GAAATTGGTG GTGATAGCAA TTTCTTTACC AATTTAGAAG	780
AAGTAAGAAG CTCTATAAGA ACAAAAATCA AAGTTTCTGA TGGCACTGAG CAAACCAAAG	840
ACAAGGTGGA AATAGATGAA ATTATAGAAG ATTTGCAAAA ACTAAAAGAA TTTCTAGAAA	900
AACTCAAGAA ATATCTTAAA GATACAAATA ATCTTAGCGC AATCGAAGAA AGTGTAAGG	960
GTTTAAGTTA AAAGAACAAT CGGATTTTTA ACTTAAAGTC GAAATTACAT ATACCTATAT	1020
TAATGACTTA AAAACCTAAT TACAAAACT TTAGTAATTG GGTTTAAATT AAAACACATT	1080
ATTTAGTAGA GGCTACATCA TTTTCTACAT CTAAAATTGA TTCGTAAAAC TTATAAACAA	1140
GTTTTTATAT CTTTTAAAC ACAATCTCA ATAAAATATT TTTGATTTTA GAATTACTAC	1200
TAAACAATA AAAATTATTC ATTCTTTGAT TACTAGGGCA AAAGAAACAC TACATGAAAT	1260
CAGATATAAC TCTCATTCAA AAAACTTCTT TTTAGCTAAA ACACCTTGTA TTTTAAATCT	1320
GTACCAAAAG CTCAAATATA TCAAGTCATT CGCACCTTTA AAGCTCAATC AAAATAATCT	1380
AAATTATTAT CGAAATAGCT CCAATGAGCT TACATCTACT ATTACAAATT TAATTTCAA	1440
TTTTTTTAAT GAAATGAGT CTTGCAAAAA TTTGTATAAT CTAACGTTAT ACATTAATGC	1500
CAACCTAAAA AAACGGGAA TCTATAAAAA TACTTGTAAG TTGCAAAAAC AAATTATATC	1560
TAAAATTTTT ATTCTTGATT AAGGTAAAA TTCTTTGTAA TTTCTACTTG AAATAGTTGC	1620
CAATTAATGT CATAATTAAG GACGACAAAA TAGATAAAAC AATGGGCGAA ACTACTGATG	1680
CAATAACAAC TGACACTCTG TTTTTCACGC TAAGCTTTTC CAAAAGAACT TTGTTATTGG	1740
ATTCAGCTT TTCCAAAAGA ACTTTGTTAT TGGATTCCAG TTTTCCAAA AGAACTTTGT	1800
TATTGGCTTC CAGCTTTGCT TCTAGCCTTT GTTCCAAATT AACATATCT TTTTGTAAT	1860
TCTTTTCTAA GTTATCAATC TTAGTAGTAA GTTCGCTTTT AACAGTATCA ATCTTAGTAG	1920
TAAGTTCACT TTAAACAGTA TCAATCTTAG TATCTAAATT ATCTATTTTT AGATTTAAAT	1980
TCTTTTCTAC GTTATCAATC TTAGTAACAA GATTGTCAAA CTTTATACCA AATTGCTTTT	2040
CTAAATTTTC TAAATCTCTA TATGTTAGTT CATTGTAATA ATATCTTTTT GACAAATCTT	2100

903

GAGCTATTAG TTGTTCATA CTCAATCGTA GAAACTCTCT ATATATTTGT TCTTCAGTAA	2160
ATTATGAAAA AAAATCAAAA AAACAAGTGC TCAGAAATAG AAAAAACACA ATTAGAAATA	2220
ATAAATACCC AATCAGAAAT AGAAAAACAA CTCCATCAAT TAGAAATTGA GTTTACTGGG	2280
GTATGCCTGC TTTATGTGGC AATACATTAT TAAATCTAGA ATTGAATAAT TATTCTCAAA	2340
AAAAACTATT AAAATTTTAC AACGAAATTC TTAAAAAAGA TAATAAAAAT TCTTGCGATC	2400
TACCAACAAT GAGTAAATAT CTTGATATAT TAGAAAACAC AAAAACCATA ATAAAGCTAT	2460
CTTTTAAAA TCATCCCAA TATATAATTT ATTATAAAAT TAATTACCCC CTTAAAGTGT	2520
TTTGTTC AAC AATACAAGAC TACTATCAAA CAATAGCAAA CAACTAAAA CTACGGCTAT	2580
AACTAACTA TCCTACTACT ATTTAATCGT AAAAAATAT TTCTTTGCAA ATTAATCAAT	2640
TTAGAAATAT AAATGTAAAG ACATATCTTT TTATTTGATA AATAATAAAA ATTACTGGGG	2700
CACTATTTGG AAAAATTTTT AAAAGAAATA TTAAGTATGA ATAGCAAAAA TAGGCTATCT	2760
TCACACTTAA,TAATTCCTTAT TTACACGCTA AACAACATTG ACCTAAATTC AAAAAATATT	2820
GGGTACAAAG AGTTGAAGA GTTAAATAAA GCACATGAAG CTGCTTTAAG TAGTAGAGAA	2880
TCTTAGCTAG TGTAGCTTCA AAGAAGACAT GACACTTACT TATAAATAAG GAAGCTTTTG	2940
GATTTTAAAC AAAATAGTCT GGCTTTTTTG CACATATAAA ACAACTCCAT TATTTCTAAG	3000
ATAAATATTT TAAGCTCCCT GGTAAAGTAA TTCATTATC CTAGATTAC TCTTCCACTT	3060
CTATACGTCC CGTCCTGCTT AATCATTAAT TTTTAAAATT AAATGTTTCT TTCTAGTTAC	3120
GCACTATATT GTTACTATAA CAAAAATTGA ATCTTAAAAA TTAACATATT ACTTTAAAAA	3180
AGTATACTTA TAGGAGATGC TTATAAAGCT TAACAACTT ATTTTACCA ATATATATAT	3240
CTAAATCTC TTATACTTAG TTGCTCAATA TCTAAAGATT TAAGTGATAA GCTCTCTTCA	3300
CTAAATCTA ATGATTTTTT TAATTCAGAC ACTTTAGTTT mTGATTCTAG CAATTATGCT	3360
CCTTTATTAG AAAATTCAAC TACTGGCAAT ACTGCCTTTA GTAGCAAAGA TGTGCTACT	3420
GCACTACCAC AAGAGATTGC AATAGAAAAT CTTTAAAAAG AAAAAATGTA TGAAATTAAT	3480
CAGATTTCTT CAGAAGATAT TCCAAATATT GATGATAAAA TTACTTCTTT GGAAGCTTTA	3540
AAAAAGCAAT TAGAAGACAA ATTAGAAATC AAATTATCTA ATCAAACACA CATAAAACAA	3600
GACGATAGCT TTAATAAGCA AGCTCAATTA CAACAATTGA ACCCAGGTGT TTCACAAAAA	3660
CAAGAAATAG ATAAAAAAC ATAGAAAAAA GAAGCCTAGA CAATTCCTTCA CAAGAAAAAG	3720
AACTCACAAA CCCTGCTTAT TCAACACAAG AACATACAAA AAGTGCTACA AACTTAGACT	3780
CAAAAAAGA TGCTCTTATT AAAGAACTC TTGAAGCTAT AAAGGAAAAA ATTAAAGAAG	3840
AAAAGAAAAG CTATTCTAGA AGAGCAGCAA AGACAGAAAC AACAAGAGCT TGATAAGATT	3900

AAAGCACAAT ATGAGGAAGA GAGGAGAAAT AGAAAAGAAA GCAAGACTTC AAAAATTCAT	3960
GCAAACTACT TCTGACTTAA CTAATCTTGT TAAGATGGCT GGGCTTGAGG CTTATAGCAT	4020
TTCCCATAAA TTAAAAGATC TTGAAAAAGG TATTGAAAAT TATGAAGACA ACAATAATTC	4080
TACTAAAGAC AACTAAACC AATCTCTTAA AGATGTTATT TATGAGATTA CAAAGCTTAG	4140
TAGTCTTATA GAAGCAAAAG ATAAGATTGA TCAGCGTAAG AAATTGGGTT ATCAGACAGA	4200
ACAAGAGTTT GATGCTAAAT TTATAAACTT AAAGAACATC AAAGATAAGC TAAAGACTTT	4260
ATGTGGTAAG GCTAAAGGCC ATCTTGGTAG CAATCTTTCT AGCGTTACTA TTGATGGGAT	4320
TACTAAAGAG AAGGTAGCTC AAGCTTATCT TATCATTTAA CTAATACACA AAACATTAAT	4380
TTATATGAAT GATGATAGTA AAGGTAGCCT TGCTACTATA CTTAATGACT TAGAAAAGGA	4440
TGCCAAATCA ATATAACTAG CACAACAATA TCTTCTTATT TTAAAAAAGC CTAAGTACTT	4500
GTATCTTAGG CTTTTTTAAA AATTATCTTG CCTCTTAGAC CATTCCTGAT CATAATAATA	4560
CTGTTAAGAA TAAATTAATG CTAAATGGA TAAGTACACT TACACTAATT ACTATTTTGT	4620
CAGTAAATAT AAAACATTC CCACTACTGA TGGAATAAAT ATTCTAATA TCCAATAAAA	4680
TGGATATATC AAGCTTTTTA TATGCGAGTT GTTCTCACTT CTTATTTCTT TAAACAACCC	4740
TATAAGCTCT TTATGATTG TATTTATTTT TTCATCTAAC TTGCCTATTC TTTCATCTAA	4800
CTTTACTATC TCACCCCTTA GCTCACTTCT TACTTTTTCT ATTCTTTCAT CTAACTTTAC	4860
TATCTACCCC TTAAGCTCAC TTCTTACTGT CTTTATCTCT GCAGAAAGCT CACTTCTTAC	4920
TTTTTCTACC TTTTCATCTA ACTTGCCTAT TCTTTCATCT AACTTCCCTA TTCCACTTCT	4980
AAACTCATCT CTAGCTTTAT TCATTTCTTT TTCTAGCATA CTCATGCTAC TTTCTAGGTT	5040
TTCATATACA TAATTTGAAC TACGAAGTAG CACATAATCA ACTACATCTT CTGGAAAATC	5100
CTTATCAAGA AATACCTGCT TTACATACTC ATATTGGGGT TTAGCTTCAC ATGCAAAAT	5160
ACTCATATAA CCCTCCTTTA CTGCAATTTA ACTACTTTTG TTATCTATAT TTAACATCCT	5220
TAATATCTAC TATTAATAGT AACACACATT TTAGCTAATA AGATAGGTTG TCAAAGCTAG	5280
TGACAAAATC AAAGTTCTTT CTAAGTCATC TTTTAGTATT AGTATTGCTT GTCTTAACAA	5340
GATTCATTAT CATTACTTCA CTTGTCTGCT TCTAACTACA AGATCAATAT TTATTGATAA	5400
ATTTCTATAT TTCCTAATTA CAAAATTATA CTTTACTAGT TCTCTGATAG CTCATAGCAA	5460
ACTAGACATA AGAACCCCTA AAAGTAGATT ATAGGATAAT CTAGACTAAG CTTCTGGCTT	5520
CTATTTTTAT AGAATAGAGA AGCTTGGCTT TAAAAAATAA CAATAAAGAA TAGCAGTTAA	5580
GAACTGCTAC TATTCATTCT ACAGGTCATA AATAAGTCGC TTGCATGCTT CTGTTATATC	5640

905

ACACACAAC TCTCTTATTA AGCTTAATGG CTTACTAAAC CGTTTTTCTT CACTCTTACC	5700
TTCTTGCAATC AACTCTTGAG CAACACCATC GCCATTTCCT TTAATATCGC CAAAAAGGCT	5760
TTCTACTTTT CCCATTAACC CAGTTACACA CTCCTTAACA ACTTCACCGT TTTTCTTAGC	5820
GCCTTCTACT TTAAGAGAAA ATGCTACAAG ACCACCTTCT TTTCTCTTC TAAATTCTTC	5880
TATTACCTTA TTTACCTTAT CACGCAAACC ATAATCATCA TCTTCATGCT TAAGGCCACT	5940
TTCTTTTGCC ATTTCTAATA TTTTATAGT AAGCATATGC TACTTATCCC TGTCTTAAGA	6000
TTATCTTTAA GTGCTCCTGC TACATTTATC CTGAAGATAT TAATGCAGAT ACACCTGCCT	6060
CTATCCTTCT AGCTGTTTCT TTAATTTGGC TTACAAGAGA AGGTACTTCA CTTATTGGTA	6120
TTTTGCTACT ACCGCCTTTT GTCATGCTAT CTAGTACCTT AACCTTAGTA TCACTAGCTA	6180
CATCCTTTAC CTCTTGCGC ATCTTTTCAA GCCCATCTTT GCCTAATGCC TTAATCTCTT	6240
ATTTAGACTA CTTACCTACA CCCTTTTCTT TAACAACAGC AAGATCAAAA GCAGGTTCCG	6300
CCTTACTAGT CTTTTATGCT TCTGCTGGCC CAGTTCCTAC ATTTGAATAA AATAACTTAC	6360
AAGAGGTCGC TAAAAGAACA CTACATAAAC ACAAATATAT CCTCATATTA AAATCCTCT	6420
CCTTAAAATT AAAAATTAC TTGGTTACTT AAGTAAGTCT AGTCCTTATT CTCTTTTTTA	6480
ACCAAGCCCA CTTACTTATT TACTTTTCTC TTAGCCTTAT AGCTTGTATC AAATAATACA	6540
AGCTATTTTT ACAAATGTGA TATATTCTTT AATGATAAGG TGTTAAGGGG CAAGAATACA	6600
GATAGAGCAA GATGCAGGCA GTATGCAAAG ATATGATTAA AGACATGCAA ACTAACATAC	6660
AAAATAATAA TAGTAGCCCT ACTCCTCAGC AAGTTAATAA CCAAGGGAGC GAAGCTAGAG	6720
ATATTAAGAG GGAAGTCGAC TCTTATGTAG AAGAGTTTAT TAGACTAGAT ACAGAACTAG	6780
ATGAAATAAA AGTAAGCCTT AGTAATATGG AATGCTTGCT TAGCACAGCT GCCTCTTATT	6840
TAAAAGAAGC TAGAACTACT CCTAGATCTA ATAAAGTTAA GTATTCCTTA TTGTATAACT	6900
TGCATAAAGC CATTAGCAAG GTTAAGAGTA GTTATGCTTC TCTTAATGTT TGCTATGTTG	6960
ATGCAACTTA TTCTTTAGAA AAAGCTTGTG TTATTTTATG AGATACAAAT AACAAAGGCTG	7020
ATGATGCTTT AGCAGAAGCT TTAAGAGAAA GCAAGGATAT TAGATACAAC ATGTTTTCAG	7080
CATTATTGCT TGACAAATCA CAACCTAATA CTAACAAGAA GGCTAATATT GTAGATAATA	7140
ATGAAATAGA AAATTTTTTG TTTATAAATC TCTTCTCCTT AGATTTTAAT AATTAAAAGT	7200
CACTTTACAA AAATTAATAA GCAATATAAA TAAATATACC TCGCGGGATA GATAGTAGGC	7260
TCTATTGCAA CAAGCATGAC TAATTTTATC TTTTATGTA ATAAACTAG TCCAAATTTA	7320
TATTTATTTT TTGCTTTAGC TATAGAAATT ATATTCTAAA TTAATCATTT TTTAAATATT	7380
TATTGGTTTT TATTTGTAA GCCAACTAG CTTTATTAT GGGTAAATAT TAGAAGTATA	7440

yCAAGATAAT ATAATTTATT ACTTAAATGA AAATCTTAAA AGAACTATAC AAATTACTCA	7500
GCATCTTCTT TTTTTTTAAC TTTTTTAGAA AGTCTAAAAA ACTTGTGCTA AAATAAAAAA	7560
ACACATATTA TGCTCGCAAT TTTCAAATAG TGTAATTAAG CTCTTGATAT TAATAATAAT	7620
CAAATACyTT TCTCTAAAGT ATAGTCAAAT AATAGCAACA CTAAAAAGTA GTAATATTCA	7680
TTAATGTGAA TCTCTAAATC TCTGGCATAC ATTTTAAATG TCATTCAACG TCTTATCTTC	7740
ACAGGATTGC TATTAATAGG AGAAAGTCTA ATGCACTCAA TTCTCCATTA TTGCTATCCA	7800
CTTAAAGAGA TGGGGGATTT GAAAACATAA AATAATTATC AAAAACATTA GCAAATCCCC	7860
CTTTATCTCT ATGATGCTCC TTCACATCTA TATGATTCTT ATCTTTACCT TCTACATTAA	7920
GCTGATTATC TCTACCATAT TTAATATAGC TAAGCGGCTT TTTAACTTTA CCCATATTTT	7980
TCAGTTTGAA TAAAAACCTT TTAACATACT CTTCTATTTG GGATACATCT CCTTTTCAAT	8040
AAAAATTAAA ATGCGCTGAT TTTATACATT TACGAAAAA GTTAATGTAT CGAGTTTTTC	8100
ATTACTAAAT CTAAGATTGC TTTTCTAACC TAGTTTTAAA TTAATACTTT CATAAGCTTT	8160
ACAAGCTTTA GTCGCTCCKC ATATAAAATC CAAAATTCAA TTGTTTTATA TAAGTAATA	8220
TCAAGTAAAT TTAAATTGGA TAGTAAAATA TTAAATAGGG GAAAAACAA GCTTAATATT	8280
GAGTGATAAA TAAATTTTTT TCTTATTAAA TAGTATAGTA ATGATATCCA AAGTATCAAG	8340
GGGCCATTAT TCTTCATTAG ATACCCTGCA CAATTTTTAA TATAGTCTT yAACCTTTTA	8400
GTTGTAACAG GCACAATATT TTTAACAATA TTAAGTAATC CTTTAACATA TTTGCGAATT	8460
TCTTTTGATG AATTCTTATT CACTTTTTTT GTTTCATTTG ATTCCAATCT TAATTTGAKT	8520
TGATAAAATG AAATTAAGAT TGAATmAG CTGACAATAC CATTTTGTAT GCAAGCTTAA	8580
TAGTAAAAGC TATTCTAAAT ACTTACTTTA AAACATGGCA ATCTACCAAT TCTGATATAA	8640
ATCAAAACAA TATTTTTGAC TTTTATCTAA ATCAGTTAAT ATACCTTTTG TAAATTGACG	8700
AAATCCATTT TCTTATCCAC AATACTTTTT TACAAC TAGA ACTTTAATTA TTTTACTTTA	8760
AACAAGCTAC ATATTTACAT ATTATGTAGC CTGTTTTAAA TTAAAAAAT TAATATTAGT	8820
ACCAAACGCC ATTCTTGTC AATGATACCTT GCACTTCTTT AAGAGAATCC CTCATTAATA	8880
AGATTGACGT TACTATTGCT TTATATGCTT CGTATAAATT AGATTGTTCT TTGATCTTTG	8940
CAATTAAAGT TTTTATTTCT GCTTCAATGT TCTCTAATTT CCTTTTGTGA TCGGTGTCAT	9000
TTATGTATAC AAAATTTGCT GCAGTCTTTA CACTTACTTG AATATAATTT AATAAGGTCT	9060
TGAAATTTTT TTCAAGGTCT TCTTTGTAA ACTTTCAGC TTCTTCTTTA GCTTTGGCTT	9120
TAGCAAAGTT GTCAAGGCGT GTAGAATACA TTTGGGTTAG CTTTGTGAA AATAATGTAT	9180

907

AAGTATTATA TATCTTAGTA ATTGTTTGAA TTGCTGAATC TACATTATAT TTAACACCTT	9240
CTAGATAAGA TTGATATCGA TTGCTTAATC TTATTTCCCTC TTCATCCTCT TCATCATATT	9300
CATCTAAATA ATACTGATCA TAATCCTCTT CCTCTATTTT ATCAGTGTAT GAAATAGAGT	9360
TTGATCCTGC AATGCCTTGT AAGGAACCTT TTGGCCTTAA ATCAGAATCT ATAGTAAGAT	9420
CAATTTTCATT ACTTTCAATA GGCTCCTCCA ATTCACCACT TTCACCGCTA AGGGAATTTA	9480
AACTTCCTTG AGTCATCCCT TTATATTCAT CTGTTGTTT TGTATTTTT TCTTTTCTAG	9540
TCTCAGATTG CTCTTTTAAT AATTCAGTTT TTAAACTTTC TTCCTCTAAA ATTACATTTT	9600
TTTGTAAGAA ATTGCTTTTA TTAGCAGAGT CCCTTTTTTAA ACTATGAATA TACGGTTCTT	9660
TTCTAGAAAC CTTGCTTTTG CCTTTCTTTC TAGCAATCTT ACCTTTACCT TTCTTATTCA	9720
TAGGCTTTTTT AATAGATTCC TCGCTAGTCT CTAAAATAGA GTTTCCCTTA TCAAATAAGC	9780
CAGGGGATTC CTCTTTCATT TCATATCTTA TGAATAAATC ACAACTTATA AAACCAAAAA	9840
GTAATCCCAA AGCCAAATAT TTAATTTTAA CTTTTTTCAT GCTTTCTCTC CTTTAAAGTT	9900
AATACTAACT TTAAATCATT TTAAGTCGGA TTCCAAAAAT TAATAAACTT TTCTTATCAA	9960
AAAGAGGCAA AATTATTACA ATTTTAATTG TAATAATACT AAATAATAT TTACTATTAT	10020
TTATCAATTC ATTGAATTC TCTTTCTTTT TAAAAATTTA AAATAAGTGC TATCAAGAGG	10080
GTGAACAAAG TACTTTTTAT TAAATTTTAT AAACAGATCT TAAAAAATAA CTTCTAAATA	10140
AAATTGAAAA AAGTTTAAAT GTAGCTACCA TCTTATCATA TGCTGATTTT ATTCTTAGAA	10200
TTCGAACTGT AATCAGACCT TTATATTCTT TATCAATTAT CATTGCCCTG AATCATAAAT	10260
TTTGCTTTAA AACTTGATGT GCAGGTTTTA GTATTACTAA GTTGAAATAT TGCAAATTTA	10320
AAAAGTGCTA CCACATCTTT AAATCTTTTT TGATTTTGAA ATTGATAAAT ATAGTTAAGT	10380
TTATAATTaG CAAATATATG CTTTCTTAAT GAACTAGAAT TTAGTGATAT TGCAGATATA	10440
ATCAGTTTAA TTGAAAATAT TTTGGGGAAT AAGCCTcTAG TGGGGATAAA GAAAAAATGA	10500
AGAAAATTAG AAAATTAAGT AGCTACTATA AAATTTTTC ACTATGGAAT TGAGTTTCCA	10560
GATGTTTcAGG AAGGATTGAT ATTGTAATTA GAAATCCACC AGGGAGAAAA CTAGTTTAAT	10620
GAATCAGAAT CTTCTCAAAA CATATTCCTA GCTACAGAAG ACTAAGCATA nAAGACCAAG	10680
TAAAAATAAGG CAGAAATACT AGTAAGACAT TATATTGAAT ACTGATACAA TGAGGAnAAA	10740
GGCGTATAG	10749

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10502 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

AATGAGCAAA GTTTGATGGA ACAAGAAAAG AACTCTCTAT ATGTATATGC GCATCAATAA	60
ATCCTGGCAG CACATATTCA TCCAATGTCG CATTAATTTT TTCTATGCTC GCAATATGAC	120
CGTTTGCAAT CGCTATACTA GCTGGATAAA TTTCTTTATT AAAGATGTCA ATATAATTAG	180
CTTCAATTTT AAATAAATCC ATTATTTATC CTCTCCTAAA AACTTTTTGT TCATAATATA	240
CTCTACCTTA AAATCTTTAA ACTTAAATTA TAGCGCAAAG TGCCAGTATA TTTAATTGCA	300
ACTGTATTTA GAAAAAATAA AAATCGTCGA TATTTGTTAT ATACGATAAA AATCGAAGAT	360
AATTTTTTGG GTAAAATAAA TAGAAAAAAT TTAAATAAAA AATAGCTAGC AATTCTAATT	420
TTGATACCAG CAAAGATTAT GTGGTAAAGT ATCAAACAAT TTTTAATTGA TTTTATAAAA	480
AAGGTTTTAC ATTAAATTTA AAATTAAATA ACAATAATAT TTCGAATCTC TTTTCTAGA	540
TTTATAGGAT TTTTATCCAT GCTTAAAACA ATATCTGAAA AAGCTTTATT TAAATAATCT	600
CCCAATTGTA TATTTTCAGA CTTGATGGAC TCTTTATTGC TGTTATAATC ATTTAATAAT	660
TGTTTAACAA GCTCTCTAAA GGTGTCTCTT AAAGATAAAA AATTTTCAAG ACAAATTTTA	720
ATCCTTTTAA GATCAGGAAT ATTTAATAAC ATTAGGTTGT TTTTTTTATC AAGTAACAGC	780
CTCATTATTG CCTCAAATCT AAATTGGAAT TCTATGCCCC CATTTTGCAT AATTTTATTA	840
GCAATCTTCT TAATGCTATG TAAATTTGAA TTTAAAATTA ATCCTAATTC TTTCAACTCG	900
CTTTCATTGT AATCTAAAAC CGCATACAAA CACCCTCTAG CCTTTTGA TTTCTCTACA	960
TTATCAGCAA GTGTTTTTCT TAGTGTATAC CAACTAACAT TTTTAAATGG AAGATTATAT	1020
TGATTAGATG GCTCACTTTT GAATTTTTC AAGAATTAT CTATGGCTTT ATTATTAAC	1080
TCTACAAAAT TATTTATCCA AGATAAAGT TCATCTTTTT CTCCCCGCAC ATATTTTTC	1140
CCAAGTTGTT TTTTATAATT ATGATTTTTG CTAGCCTTAT TTTTATTTAA ACCATCGTTT	1200
TGATATGAAA TAAATAAAAA AATATTGATT AATAATATTA ATTTTTTTTC ATAAATAAAG	1260
CCCTTAAAT GTTTTACAG AATATCTGCA AAGCCATAAT ACAAACCTAT AATAAATATT	1320
AAATAGTAAT CATTATAAAA TTAAATATAA TTTAAAATG ATTTTTTTC AATATTTTGA	1380
AATGTTAAAT AATTATGTGC TATTTCTAAA CACAAGATTA TAAATAACT TCTTGCTTTA	1440
ATATCATGAT GGCTTTTAAT TGCTTCAATT AACTTAAATT ATGCAGCTAT CTTGGCTTTT	1500
CTTTTTTATA AAACATTGTC TTTAGCAAGG TCATAAAATT ATGATCTACT AAAATGTATT	1560

CGGATTTATT	AATATTAAGC	AATATGTTAA	AATAAAATTTA	AATACAGTAA	TTTAATATAT	1620
TATTGCTTTT	AGGAGGTCAA	TCTATGTTTA	GAGGAAAAGA	AATATATTTT	TTGTTATTTT	1680
CGTTACTTTT	GTTTATATCA	TCAATTATAA	TTTCTCACGG	AATAAAAAAC	ATTGGCACCA	1740
AAAAAGAAAA	TTATATTACG	GTAAAGGGTC	TTAGCGAAAG	AGAAATTTTA	TCAACGTCTT	1800
CTAGTTGGGG	GCTTAGATAC	AGCTTAACCG	GTAACACTAT	AAATGATATT	AATAAAGCAA	1860
ATAATTTAAG	CTTATCGAAG	ATTAAAAGTT	TTTTTTTAAA	ACATGGATTT	AGCGAAGACC	1920
ATATAAAAAT	GGGATTTATG	GAATTTAATG	AAGAGACTTA	CAAAGAATCT	CTTTATAAGT	1980
ATAGAGCATA	TATATCTTTA	ACTGTTTATA	CAAAAAATAT	TGAGAAAATG	GAAGCAGCAG	2040
AAAAAAATAT	TGCTGAGCTT	TATAATCAAG	GTATATTAAT	TAGTAATAGT	GGGGGGCCAA	2100
GATATTACTT	TGACAAATAT	AATGATATAA	AGCCCGAAAT	GTTAGCAGAT	TCAATTAGAA	2160
ATGCGAAATT	AGCGGCTTTG	GAATTTGCAA	AACATTC'AAG	TTCAAAATTG	GGGAAAATTA	2220
AAAACGCAAA	TCAAGGATAT	TTTGAATTTT	TTCCAATTGA	TAGAAGCTTG	GGCGATCAAG	2280
AACGTTATCC	AAAAAAAATA	TTAAGAATCG	TTACAACCGT	TTCTTATTAT	TTGGATTGAT	2340
ATTTGGCGAA	CTATTTTTTT	TAAAAACCCA	TATAAATAGC	TTGCGGTTTC	ATACCATGAC	2400
GCGATCTACA	CACCTAATTG	AAGCATAGCT	ATATATATTT	ATTGCTGTAC	TCTTTATCTT	2460
GTTGGCTGCT	TAGCTTAAAG	TTGTCAATGT	TTTTTCGTAC	TCACCATCAT	TTTTGTTTTT	2520
AAGTTCGCTG	CATACACCTT	CAAAGTATGT	TTCTACATTT	TTCATAAGAG	TTTGAATACA	2580
TTTTTTAGTT	TCAATTTTAC	TGTTTGAATG	TTCTTTAAAA	GAAACGCTTA	CCGAATTTTC	2640
AGCATTA AAC	TTATTTTACAA	CGGTTTTAAG	TTCATTTGAT	TTTTGGGTAC	TTTTATCACC	2700
ATTGCTACTT	ACCGATATTT	TTAGCAACTC	ATCCAGTAAT	TTACCATCTT	TTAGTCCATT	2760
CTTCAAATTA	CTTTTGCTG	CATAGGTAGC	ATTATAACCT	ATATTAATTA	GTGTTTGAAA	2820
AACCGAATCA	ATTTTTTCTG	ATGAATTCCT	TATCAATTTG	ATTAAGCGAG	GAGTATCCCT	2880
TACTTCTATG	TTTTTACTTT	CCTTGGTATT	TTTTTGATCT	TCAATTTCTT	TTTTGGATTT	2940
TTCAGAGTCA	TCTTGAGCTT	CCTTTGCTAA	ATTTTCTAGC	TCTTCCGGAG	TTAATTTTGT	3000
GATTTTTTCC	GAACCTAGGC	CTGTGGCTTC	ACTTATCTCA	TCTAATACTT	GATCAATAGA	3060
TGTTAGTGCT	GATTTACTTT	CTACAGTTGC	TTCATCAATG	GTATTGTCTA	CATACCATTT	3120
ACATGAAATT	ATTAGCAGTA	TAGATATTGC	CAATATTAGT	TTACTCATTT	GTAAACTCCT	3180
TTAGGCGGTG	TAGTTATAGT	GCAAAATATTT	AGCTTAGACT	ATAAAAAATCC	TCAAAAGTGA	3240
AAGTCAGGGA	TAAGAAGATT	TTTGATTTAG	TTAACAATCT	CCTTTCGGCG	ATAAAGAATT	3300
GAAGATTCCC	TTATTGAAGA	GTAAACCTAG	CAGTAAATTT	AAAATCATTG	ATCCTAAAAG	3360

GATAATAGTA	ATCCTAAAAA	GTATACAAAA	TTATAAATTA	ATGAAATTTT	AATGCTACTA	3420
AAAGATAATG	TTGACAACAT	TAATTCGTAG	CAATCCAAAT	ATAAAGGCTT	AAAAACTTAT	3480
AAAAATGGGA	GAGCTTGTTA	TTCCCAGCAG	AAACAGTTTG	TGGAATTGGT	ACAAATGTAT	3540
AATCCAAAAA	TGATCTTGAA	AATTTTTTCTA	ATTTTACTTT	ATTTAGAACA	TTTTAAGCTT	3600
AGTAAAGCAA	AAATAAATAA	AATGCTAAAT	TTGAACTCCA	AAGACGAATT	CTTTAAAGAA	3660
AAAGAAAATA	ATTTTATTTG	AGCCGGTCTT	ATTTTTTAAC	TATAAAAGAA	TTTAAATCT	3720
TACTTAATGA	TTTTAACACA	TTAAAAAATA	AAAAAGGAGA	AAAATATTTT	CTTCTTTGG	3780
CAAAGGGTTC	TTGCAACTAT	TACTAAATG	TGCGCCCTAT	TTGTGAATTT	AAAAAATCT	3840
CATAAATGCC	TATTAATTA	AAATATCCAA	AAAATTGAGG	TAAATGGGG	CAAATATTGA	3900
AAAGTATATT	CCCAATATCC	CAATCATAGT	GCCAAAATCG	ATTACTAAAA	ATAAACCCAT	3960
GAAGTCTTT	ATAACAAAAA	AAATATTTTT	TCCAACATTG	CTTTCATAGA	TATATGGACT	4020
GCCAAATCT	CTTAAATTTG	AAATTATTTT	GTCAATTTCC	ATTTGTTTTT	GAATTGTATA	4080
CTTCAATAA	CTTTTAAGAA	CTTGATAATT	TCCAATTTTG	TTATTCATAA	ATTTCATAAG	4140
ATATTTAAAA	GTTAAAAATC	AAAATAGTTG	AGTGCTGATC	AAGACCGAAA	CACAGTCAAA	4200
ATAAGAAAAA	TTACATAAGA	TTTGAAAAAA	ATAAAAAAAT	TCTTAGAAAA	GCTCAAAAAA	4260
TATCTTGTA	ATCCAAAAAA	TTATAAAAAA	ATCAAAGAAG	GCGTAATGCC	TCTAAGAAAA	4320
AATTAGAATT	TCCCAAACCA	GAATTAAAAA	AATCTTTACC	CACAAGTTAA	TTGTAAAGAT	4380
TTTTGCAGTT	AAGGTAGAAA	TGAATTTTGA	GCTATAATTC	ACTAAATATA	TTAAATATTA	4440
CACTACAAGG	AGGTGTTTAC	AAATGAGTAA	ACTAATATTG	GCAATATCTA	TACTGCTAAT	4500
AATTTTCATGT	AAATGGCATG	TAGACAATCC	CATTGATGAA	GCAACTGCAG	AAAGTAAATC	4560
AGCACTAACA	TCTGTTGATC	AAGTATTAGA	TGAGATAAGT	GAAGCTACAG	GTCTAAGTTC	4620
GGAAAAAATC	ACAAAATTAA	CTCCGGAAGA	GCTAGAAAAT	TTAGCAAAGG	AAGCTCAAGA	4680
TGATTCTGAA	AAATCCAAAA	AAGAAATGA	AGATCAAAAA	AATACCAAGG	AAAGTAAAAA	4740
CATAGAAGTA	AAGGATACTC	CTCGCTTAAT	CAAATTGATT	AAGAATTCAT	CAGAAAAAAT	4800
TGATTTCGGTT	TTTCAAACAC	TAATTAATAT	AGGTTATAAT	GCTACCTATG	CAGCCAAAAG	4860
TAATTTGAAG	AATGGACTAA	AGATGGTGAA	ATTACTGGAT	GAGTTGCTAA	AAATATCGGT	4920
AAGTAGCAAT	GGTGATAAAA	GTACCCAAAA	ATACAATGAA	CTTAAAACCG	TTGTAAATAG	4980
GTTTAATGCT	GAAAATTCAG	CGATAAAGGT	ACCATTAGAA	AATGGTAGTA	AAATTGAAGC	5040
CAAAAAGTGC	ATAAAAACTC	TTATGACCAC	TGTGGAAACC	TATTTCAAGG	GCGTGAGCAC	5100

911

CGAACTCAAA	GATAAAAAAG	ACGACAAATA	TACTAAAAATA	TTGGCAGCTT	TGAGTGAGGC	5160
AGCCAATAAA	ATAGAGAATG	CAGCAATGGC	CATACATTTG	TGCTTTAATA	ATTAAACTG	5220
GGCATTTTGG	TTTACAATTC	TAATAAAAAG	AAAAATCTTA	AAAATTTCAA	CTAAAATCCC	5280
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AATATAATGA	ATAATCAAAA	ATTTCAAAAA	CCTCCTATAG	TAAACAATAT	CAAAAACCTA	5460
GCAAGTTTGT	TTGCAAAACA	AACCAGAGTC	TTTTTTTTTT	TAATGACAAA	TAGAACAAAC	5520
ACTAACTTTA	GAAGAGCCCA	AACCATCATA	TATACTATTT	TCCTTATGCA	TCTAAACAGT	5580
GAAAGCAAAA	TCAAAATATA	GATAACATAG	TGAATTTTCAT	TCCTTGATGAG	CTTTCAATAA	5640
ATAGCATTTT	AAATATTGTC	GAAACTTTTG	CAAAAAAGAA	TGAATTTTAA	AATATAAAAA	5700
CAATATTATT	AGATATTATC	GATACCGTGA	ATGGAATTGA	TCTGAAATTG	ACTTTCAAAA	5760
ATTTTTATGT	CACAAGTTCG	GGTTCATACT	CAAAGATTCT	TGTCTCAACT	TTTATTAAAA	5820
TTTTCTAATT	CAATATGATT	ATTTTTTTAG	AAAGACCAAA	GGTATTTGCC	ATGCTCCAGA	5880
CCGATTATCA	ATTTCAATTG	CAAAAATCTT	AACGAAATAT	TCAAAAAAAT	CAATCTTTAA	5940
AAGGGATCCT	CGACTATTGA	CAAAGTTGCC	GTTTTAAATT	TTATAATTAG	AACCGAAACC	6000
TTTCTATTAA	AAACTGTCAA	AATCACTTCA	AATCATTTCT	TAAAATCTCA	AAAAGTTACC	6060
ATAGAACACA	TACTAAAAAA	TGTCTGCGGA	TTTGAATATT	GGGATTAAAT	TTTGGAACCTA	6120
AAATTTATCA	TAAACTTAAT	TATTTTAAAT	TATTTGATTA	GATACAAAAA	ATCTTTTGAG	6180
TATGTCTATC	AGTCAATCTA	GTTTTAATGT	CTTTTTTTTT	AAACCTAGAT	CATTTTTTCA	6240
AATTTTTGAA	TAAATATAAG	AATTTTTATA	TTTATTATTA	CTTAATTTAT	CTTTGCTAAA	6300
TTTCCTTAGT	TTAGTTTAAA	TCAATTCAAT	CCCATTGAGT	ATTTTACACC	ATTTTATAAG	6360
TTATAAATGC	TATATAAAAA	CCTTTTTTCA	TCTTCTTTTC	AGAAGATTGG	CAATCGTTTC	6420
ATTAATATTG	CATGTCAAAT	AACGTTATTA	AAGCATTCCA	ATTTAAAAAA	ATCTTCTATG	6480
GAAATTCATT	TTATGTAACA	CTAATTTCCC	CAATTTAAGT	TTTATTTTGT	TTGGGGCACT	6540
ATAATAATAA	TTTTTATTAG	ATTAAAAATT	TTCTAGAATT	TAAAGATATA	TTTGGATTTA	6600
TTTTGTATTT	AGCTTAATAT	TGGTAATTAA	ATAATTATTC	ATGTTCTAAA	TCCATAAAAG	6660
ACATATAGTC	CTTTATAGAT	CAAAATATTC	TTTATTGGGC	CTATTATAGG	CCATAATACA	6720
CTAGGATAGA	TATTGGTTTA	CTACTATTCA	CCGCATTCTT	AAAAATGGAA	CTTATTTTAT	6780
TTATTCTGAA	GAAGAGCTTA	AAAACAAGAA	AGTAAACAAA	GTTGCTACCT	ATTATAAAGG	6840
CAATATTTAT	CTTGCATCTA	GATCTCTTGA	CAGAAAGAAA	AATGGAGCAT	ATTACACCCC	6900

AGAAGATTTG	ACGGAATTTA	TGTTGTGTC	TTCAATTGAA	GAACGGCTTA	AAACTAAATC	6960
CCCTTTAGAT	ATAAAAATCA	TTGATAATTC	TTGTGGATCG	GGAAATTTTT	TAATTTCTTG	7020
TCTAGATTAC	TTAACAGAAA	AAGTGTGGTA	CGAGCTAGAT	AAATTTGAAG	ATGTAAAAAA	7080
AAATTAGATA	TGGAGTATAG	AAATGTTAT	AATAAAGCTA	AAAAATATAA	TATTCAAGAC	7140
AGTATAAGCC	GGAAGACCGT	TCTTAAAAGA	ATGTTGCTTG	GAAAATGTAT	TTACGGAGTT	7200
GATATTGATC	ATATATCTGT	ACAAATCGCA	ATGTTAGGTT	TATGGATTAA	TACCTTTATT	7260
TTTTTGAAAC	GCCACTAAGC	TTGATTAAAC	ATCACATAAA	AGTAGGAAAT	GCCCTTTTAG	7320
GGTATACCAA	GGATGAATTT	TTGAATATTT	TGGATAACGA	ATTTAGAGGT	AACTGCTTGT	7380
CAGTTGTAAA	AAAGATTAA	GAAATTATGA	CTATTTTAGA	AGATATCCAT	CAAAAAATCA	7440
AAGGTATTAA	TTATACCATT	AAAGAAGATT	TAGAAAAATC	TAAAAAGATA	TACAAAGAAT	7500
ATCAGGAAAA	TGAAAATATA	AATAATTTAA	GAATAATATT	TTCTTTAATT	AACTTTTATT	7560
CGTTGTCTTT	TGATAAATCT	TTGAATATAA	AATTTAGTGA	TATTACAACC	GTAATTAATT	7620
TGATTGGAAA	TATTTTAGAC	AGTAAATTT	CTAGTGAAGA	TAAAGAAAAA	ATAGAAAAAA	7680
ATTAGAAAAT	TAAGTAGTTA	TTATAAATTT	TTTCACTATG	GAATTGAGTT	TCCAGATATT	7740
CAAGAAGGAT	TTGATATTGT	AATTGGAAAT	CCTCCATGGG	AGAAAACATA	GTTTGATGAA	7800
TCTGAATTTT	TATCAAAACA	TGTTCTTAAC	TACAGAAAAC	TAAGCATAAA	AGAACAAAAT	7860
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GAAAAGAACA	GTTTGAAAAC	TTTGAATAAT	ATGTATAGGT	TGGTGTTCAG	AGAATTTTCT	7980
AGTGGGGGGG	TCCGAATCTT	TTTAGATATT	TTACGGCTTT	CAATTTGAAG	CTAGTGAAGC	8040
CCGGCGGCAA	CTTAACCTAT	TTGACTCCTT	CCAGTTTGTG	GAGCGAATCC	GGCTCTAAAG	8100
CACTGAGGCA	GCATATATTT	TCAAATTACA	AGCTTAATTA	TATATACCAG	TTTGAAAATC	8160
AGAAAGGGTT	TAGGGCCATG	ACCCCTGGCT	TCAAATTTGC	AATATTTTCAG	ATCAGTAATA	8220
GTAAGAACC	CACAACGAAA	TTTAGAGTAA	AATTTGTTAT	CCAGAGTAGC	GATAATATCA	8280
TGAAAGAAAT	AACCAGTGAT	CTGAAAGAGG	GTAATGAAAA	TGCTTATAAG	GGAATCGAAT	8340
TGGATATAGC	TCAAATCAAA	AGGCTATCTC	CTATTCAAGA	GTCCATAATA	GAATTTAGAG	8400
ATAGCGCTGA	GTTACGCTT	GTTAATAAAA	TGTTTAGTCG	ATTTGATACT	CTTATTCAAG	8460
AGTATATTGA	TTTTAGAGAG	GGACTAAATT	TAACAAAGTA	TAAGGCACTG	TATAAAGAAT	8520
ATAATAATGA	AAAATTTATA	TTTCTGTATT	CTGGAGCCAA	TATTCACCAA	TTTAATTCAA	8580
GATTTTTTTGA	AGATAGAGCT	GCAAAAGAAA	GTTCTAAATT	ACTATGGATA	GATAAAAAAG	8640

ACTTAGAAAA AGTATTAATG AAAGACAGCC AATATCAAGC CGAAAGAGTA TTCTATAGGG	8700
TAATTGCAAG TAACACAAAT GAAAGAACGA TGATTAGCAC ACTTCTCCT AAAAATTGTT	8760
ATTGCGTGAA TTCAATATAT ATAAATTATG AGGAAATACC AATATCACTT TATAAAAAAT	8820
TATTTATTAT ATCAATTTTT AACTCATTTG TGTGTGACTT TATAATTAGA AGATTGTGTA	8880
ACTCAAATGT GCTAAATCA TGTTTATATC AATGCCCAAT GCCTCAACCC GAAGAGGATG	8940
AGATTTTAAA TAACTCTTTA TACTTAACTT TAGCTAAAAA CACTTCCTTG CTAATAGTTA	9000
AAAATGATCC CGATAACTTT AAATATTTGC TTTACTTAGA ATATTTTGAG TTTGGCAAAG	9060
AAGAAGTTGA CAAGATGTTA AATCTAGACC CCAAAGATGA ATTCTTTAAA GAAAAAGAAA	9120
ATGAAAATAA TTTCATTGTG GCCAGTCTTT ACTCGTTAAC CAAAGAAGAT TTTGTAACTT	9180
TGCTTAATGA TTTTAAGGTT TGCAAAAACA AAAAAGGAGA AGATTATATT TCATCTTTAA	9240
TAAAAGGATA TGAGAATTAT TTAAGAAGAA TGGATAAGCA TAATGCAGCG TAAATAGATT	9300
TGATGAGCCT CTGTTTGTGA AAGTCTGAGT TTGGTACACA CAGACACTGA AATTATTTAA	9360
TTTACTTTGT AAATTTATTT CCACCTAAAT TTCATAGAAA TTATAAGTGG AATATTCTTT	9420
GTTATTTTTT ATTGAGACTT TCTAAAACAG TTTTTCATG TTTAATAAGC TCTTTTATTT	9480
CTTCCTTCT CACCATTGGT TCAATCTTT TAGAGGCAAA AGATTCTAAA TTACTTAAAG	9540
CACTTCTTGC GTCACCTAAA GCCTGTCTAG ACAATTTTAA TGCATAAGAT CTATTATTTT	9600
TACTCTCTAA TCTTTTAATA ATGCTTCTT TTAACCTTTT CTGAGCGTTG TCAAAAAGA	9660
AAGCCGCAGA GCTTATTTCA TTTTCTGCCA TATCAATCAT ATTTATAAGC TGCTCAAGTT	9720
CACTATCTAT CTTTAAATTA TTTTGCAACA ATTGTGTTAA TTTATTTATC TTATCTCTAT	9780
TGTTCTTAGG ATCTCCATT AATGATGTTT TTTTATTGTT AATCTTTCCA ATTACATCAT	9840
ACAAATCAGC TTTTATTAAA GCATATTCAT CTTTAATTAC ACGTACTTCT CTAATTAATT	9900
CAGAAAATTT AGAGTTTTTA AGAATATTTT CTCTAAATA TTTAATTGCT GCATCAGCTT	9960
CCTTTCTTTC ATTAGTAGAA GGGATTAAAT TCTCCTTTTT TGTCTCTTTT TTTTCAGTAT	10020
GCGCAATTGA AATATTTGGT ATATTAGCCT TATCTTTTGG TGATTCTGAA GGTATTATAG	10080
GCTCTATAGG ATTAATTAAA TCCTCATATT TCCGTTCTCC AAAATTTTTA GTAAAGCTTT	10140
TTTGCTTTTC TTGATTATTA TATAAATCAT TAAGACCATC TTCTTGAACA CTATCCGAAA	10200
CTTCTTTTAC ATTATTGTTA TTTTTTTGTT CTTTGTACT AGATAATTG GAATCTAGAT	10260
TACAAGACAT CAATCCTCCC ATTAATAATG CATATAAAAA CAACTTTTT CTCATAAAAA	10320
TATTCTCCTT TTATCAATTA AGAATAATTA TTATAAATAA TAATTATTCT TAATTGATAT	10380
TATATATCAA TTTGTCTTAA TTACAATAAA TTGTAAATAA AAATATTTTT CAAAAGTATT	10440

TAGATATTTA AGATTTTTGT ATAACAAAAT GTTAAGTGAA AAGATTATAT AAATTAGTAG 10500
TT 10502

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9842 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

GAATTTAGTG ATATTGCAGA TATAATCAGT TTAATTGAAA ATATTTTGGG GAATAAGCCT 60
TCTAGTG GGGG ATAAAGAAAA AATGAAGAAA ATTAGAAAAT TAAGTAGCTA CTATAAAATT 120
TTTCCACTAT GGAATTGAGT TTCCAGATGT TCAGGAAGGA TTTGATATTG TAATTAGAAA 180
TCCACCATGG GAGAAAAC TAAGTTAATGA ATCAGAATTC TTCTCAAAAC ATATTCCTAG 240
CTACAGAAGA CTAAGCATAA AAGAACAAAA TAAAATAAAG CAAGAAATAC TTAGTAAAGA 300
CAATTATTAT TTGAATACTG AATACAATGA AGAAAAAGC AGTATAAGCG CTATTAATAA 360
ATATTTATAA AAGTGATTTT AAAGACTTTG CTAGTGGTGG GGATCCAAAT CTTTTTAGAT 420
ACTTTGTTGC ATTTAATTTG AACTAATAA AACCAGGGGG TAATTTAACT TATTGGTTTC 480
CTTAGGCTCT TTGGAGTGAG TCTAGTTCTC TATGTTTAAA GATTGTGCAA AAGATAATAA 540
ATAAAGTTTA ATTAAAGAAA ATATTATTCT TAAATTATCT ATATATTCAC TTTCTCATA 600
TTCTTTGTAT GTAAGTAGCA ACTTTGTTTA CTTTCTTGTT TGCAAGCTCT TCTTCGGTAC 660
GAATGAGATA AATCCCGTCT TAAATAATAC GATGAACAGT AGTATCTGCA ATTCTTAGGC 720
CATATTCAAG TAGCGTTTCG TATAATTCTC CAAAACTTTT GGGATCTAAC CTTGAATACT 780
CTACAAATTT TTCATCTTTA ATATTTTTTTT CTTCAAAGAA GAGTATTTTA ACAAGTATTT 840
CTTCAAGTTC ACTAATACTT AGCAAACTTT CATTATTCAA ATATTTAACC TTATCTTCTA 900
CAAATAATCC TCCATTAAAT ACGGGGAAC TTTATTGAATC ACTTCCCTTA TCAAGTAAAT 960
TAAAAATTGT TATTATTTTT TATATCCTAA TTTCTTTTTT GTATTTTAAT CATAAAAAAA 1020
TATCTAAAG ATATAGAAGA TCTGTATAGC TTGTTTCTT CTAAAATTTT CTTAAACTG 1080
TCGTTGTCTT AAATATATGC AATAAAAAAT ATTCTTAAAA TAAAAATAAT TGCCTCTTTA 1140
AGTATGCTAG CCAAATATA ACGAGTAAAT TCTTTGTCTG ATACTTTAAA TTCTTTGTCA 1200
TATATATTTT TTTTACAATT TTAAATACTA TAGAGTCATC AGGCTTCTCA TAAAGCATCT 1260

CTCTAAGAGT	TTTTTGAATT	ATATCTTTTT	CTTTAACTAT	TGCTCTTTT	TCAACTGCTA	1320
TTACATTACT	TGTTTTTAGG	TAGCTTTCCT	TTCTTATAAT	ATAGCTAAAT	AAAATAAACC	1380
ATTCTTGTTA	TTTGTATTCT	TTTTTGTCCT	CAATTTTAGA	AAAATCAAAT	TCAATATATC	1440
TTTTTCTCC	ATAAAGTCCT	AGATTTATCA	TATAAGCTCC	ATACCTTCC	ATTTGAAAGT	1500
ATTCCATAAT	GTTTTTGATA	TTGATTTAGA	CATCTATATA	GCTGATCTTC	TGCTTCTTTT	1560
ACCTTATCTT	TAGCATCAAA	ACTAAATACT	GGATGCTTAA	CTTCCGCTAT	AAGTAAGATA	1620
TCTTCAGTTG	AAAATATGGG	AATTATTTTT	TTAGCTTCTT	CTAATTTTTT	ATTAAAACT	1680
ACTTTGTCTT	TATCATTTTC	AAAAAGTAGT	ATATCTACTT	TGGATTTTAC	TCCTTCTATT	1740
TGCCCACCTT	TTTGTGTGTC	TACTGAATAA	TTTAGTTCCT	CGAAAATAGA	TTTGTAGTAA	1800
GACTCTATAT	TTGCTTCTGT	TGAATTATCA	TCTATTGAAG	AAAGTTTATT	TTTATAAAAA	1860
ATAAAAAAGT	CTTTTAAACT	ATTAATACTT	TCTTTTCTTA	TAAAGTCTCT	TTACAGTTCT	1920
TTATAAAGAG	ATACATTTGG	ATCATTGTGT	TTTATAATGT	AATCGGCTTT	CATTGTTTAT	1980
GTTTAAACCA	TCATGTTATT	TACAAATCCT	TTTGTAGCCT	TCTTGATACT	CACAATACTC	2040
TTCTCTAAGA	TTAGTTTTTT	TTAATTAAAA	AAACTAATCT	TAGAGCAAGT	CGACCAAAAC	2100
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TGATTAAAGA	GTATCTAAAA	AACACTTTTT	TCTTTAATCC	GAACCTTTCT	TAAACGCTCT	2280
CCAATTTGTG	AAGCATAAAC	AAAAAAATGT	TTTATCCTT	TTCAATTTTA	AAATTACAAT	2340
TATAGAGTCT	TTTGTTAATT	TCTTCTTTAA	AAGCATCTTG	CTCAGAACTA	TATAAGCAAC	2400
AAAGCTGTGA	AAAATTTTTA	AAAGAACTTA	TCAGTGCAAA	AACAACGCAA	GTAATAACCC	2460
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CAATTTTTTA	GCAAGTAGTG	AAAGTGAAAA	AACAAATCAT	CCTAAATATG	TAACAAAAAA	2580
TGAAAATAGG	CTTAATAAAT	ACCAAAGAAA	ATTATCAAAA	AACAAAAAGG	TTCTATTAAT	2640
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GAGCTTATTA	ATTACTCGGA	CATGCAACAG	GGATTTAAAG	TTAAAAAACC	TAGCATTCOA	2820
TGTCAAATTC	CAAATTTAG	ATTTAAAAAT	GAAAAAAACC	CTTTTCGGGG	CATCTTTTTCG	2880
ACATTAAACT	AGGCAAAACA	ACTTAAGCCT	ATTAGAAGTA	ATAGAGTATC	ATTAATTAAG	2940
CATTAAAGTC	AATAACCCTT	GAAAATTTAT	TTATTCCTTT	TCTTTTTAGA	ATTATCATAT	3000
TTAATTATAA	TCTCCGATAA	AATATCTTTT	TTATTTTTTA	AAATCTCCTT	TAAAACAAAA	3060

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CTAATTGGGA TATTTTCTTT GTTGTTTGTA TTAATATCTT CTTGATTTAT TTCTGATAAC	3180
CCTTGTTTTT GTATGGCGTG ATATATGCTA TTAAACCCCG CTTCTTAAT TTTATCAATA	3240
GAAATAACAC CTTCTAAAAC CTTTTCATAA ACTTTTAAAT ATGTATAAGC CTGGGTTTTT	3300
GCAATTATAA AAGATTTTAT AAATTGTTCA AAGCTTTTAA AACCATCATA TTTGTAAAGC	3360
TTTTTTTGT TAATTTTATA TAGAATTTTC ATTCTTTGAA TTTTATTGTC AATATCATCT	3420
TTTAAATTAA GCTTTAATTG GTCTTTTAGA TCATTATAAA TTATTAAATT TTCATCTTGA	3480
TTATTATTTA AATTTTGA CT TTTATCAATA AAATCTTCAA ATCTATCATT TAAAATGATC	3540
TCTTTTTTAT TTTTCTTTTT ACTTTCTTTC CCTATCATT TGCACCTCCTA TTGCTTTAAA	3600
AGCAGATATT TATATGTATT TAACATTAAC TTGCATTTAA AAAATAAGTT TAGACTAATA	3660
ACATGAGACA AAAACACATA ATAAATCTAA TATCACTAAT ATATGAATAA TTATTGACAC	3720
AAGTTAAAT TTGTGTCAAT AATTATTCAC AAATAAAATC GTTCGGTTCT GAACAATACA	3780
AGAGGATATT TCTAAATCAA AGATTATATA AATAGTGGTT AAAGAAAATC TATTTTTTTA	3840
GATTGTTTTG ATTATTTACA CCCTGGTTGT TATTTATTAT TCTATTCTTA ATTGAGCCTA	3900
TTAAAAGCT TCATTCTAGC TACTGCATAA TAGTAAATGC TTTTTTGTCA AAAAATCACC	3960
CCCTCTCCCA ATTAGCTTAA ATATTCTTAA AATGGTTTTT GGCTTTAATT TTAACAGAAG	4020
ATTGAAATTT ATTATTTTAT ATACTATAAT TTTTAACTGT AAATTAACAC ACATTAAGCT	4080
GAGGGACAAA AAATGAAAGC CGTTATACCT AGTTATAGCC ATCAAATTAA TACCAATAAA	4140
TCTAATAAAT TACTTTCAA AGACTGTAAA CTAAAAAAA TAATTTCCGT TATTATTTAC	4200
TTAAATAAAG AGTTTGAAAA AAAATATAAT GAATCAATAC ACAGAATTCA TTTTGACCTT	4260
GAAAACTAA AAGAAATTCG GGTTCATCAT CAAGGAGATA TACTTCGAGT GCTAACTCA	4320
AATATACATA GAGAGAATAA AAAAGAACT ACAATTAATA CTCTAAGAAT AGATTTAAGA	4380
TTTTTGTTA AGCTAAAAGC ATTGGAAAA AGAATGCTAA CATTTTCAA TAACTTCGGA	4440
GAATTTAGAG GAAAGCTCTG TATATATAAG GCATCCCCTA TTGCATATAA ATTGATCGAC	4500
ACATATTTTA GCAACACCAA ATCAGACTTA ATTAAAAAAG TAAAGAAAGA AAAAGATGTT	4560
TTAAGGGAAA AGAAAGAGCA TTGTAAACCT CAAAATATCA CTGAAAATAT CACTGTATAT	4620
AATAACAAT ATATAAATAT ATATAATAAG AATCTATAG AAACTCTTT TTTAAAAAA	4680
ATTAAATCCA TAGTTTCTAA TACAAAAAC CCAATTAAAA CACTAAAAA CACTTTATTA	4740
AACTATAAAG ATTTTAAAA TTATTAAAA TATGATTATG AGGTAAAAGA TATTAAAGAG	4800

917

TTTTTCTTGT	CCAAATTAAA	CATTTATAAG	CATAAAATCC	ACTTTATGAG	AAAAATTGCA	4860
CCCTATAAAA	CCGATTTTTA	TACTCTTGCA	GGAGAATTTA	AAGATATTTA	TACTACTAAA	4920
TGGAAAGCAG	ATAAAATAAC	TAGCTTTTCA	GGACATGCTG	GTACAATAGC	CAATAATATT	4980
TTATCTAAAA	TTTTGTCAAA	GGGATTGAAA	TTTGAGTAAT	TTGCTTGAAA	AACTCAGAAA	5040
CAAAAAAGT	GATATAGAAA	AAAGAATTAT	ATTCAATAGA	ATTGAAGAAA	TAGATAGTAG	5100
AAAAATATAC	TGTACAAAAA	TATTTAAACA	TTTAGTTAGT	TTTAAATTTA	CAAACAAAGG	5160
AAAAAGGCTA	AGACTTACTT	TTCAAGAATT	TAATAACAAT	GAAGATTTTC	TTTTCTTCAA	5220
TTTATTTCTT	TTAAGAGAAA	ATGATAAGTT	CCTAGAAAATA	AAATATAAGC	ATGATAAACT	5280
TGATAGACCC	TTTTTTCTTA	AAAAAGAAAA	TAATAAAACT	TATGCAATAA	AAAAGCTCTA	5340
TTATATAGAG	TTTGTCTTTA	AAAATGGCTC	TATTAAAGCC	TATGTTCAAT	CTTTAAGAAC	5400
ACTTTTAAGA	AAAAATAAAG	AAACTACCGA	GTATTATCAA	TTCAATTTAT	CACATTTGAA	5460
AAAAATGGAA	AAAAAAGTAT	ATGAATTTTA	TAATAAAAAA	CTAAAAGATG	GGGGGGTTAT	5520
AAATAAATGG	ATCAAAAAAA	ACCAATTGTA	ATTACACTTG	CAAGTTTAAA	AGGAGGAGTC	5580
GGCAAAAGTT	CACTTTCTAT	ACTTTTCTCT	TATGTTTTAA	AAGAATTGGG	GAAAAAAGTG	5640
CTACTGATTG	ATTTAGATCC	ACAAAATCTT	TTAACTTCTT	ATTTTAATAA	GTATATTTCA	5700
AGTATTAAAA	AGTATAACGT	TTATGAATTT	TTAAAAGGAA	ATACGTATTT	TGATAAATGT	5760
GAAAAATAAA	TTAATGAATT	TATTTCTATA	ATTCCTCTCT	ATCCTATTTT	AGAAAAATTT	5820
AACACGGATG	ATATAGATTA	TAAAGAAATT	ATTTTAGAAT	TTAGATTAAA	TAAGAGCACC	5880
AAAAGTTTTG	ATTTTGATTA	TATTATAATA	GATACTTCTC	CTAGTAGGAA	TTTCCTTTTA	5940
AAGAATGCTC	TAAATGTTAC	AGACCATATT	ATAATCCCAG	TTCAAGTAGA	AAGATGGTCA	6000
ATAGAAAGCT	TTTCTATTTT	AACAGAAACA	ATAAATAATA	TTCAGATCAT	TAAAAACAAA	6060
AGATATAATA	TTTCTATTAT	AGAAAACCAA	TTTATTAAAA	ATAGGAATAC	CTTAAAAGAG	6120
GTAGAAGAAG	TGCTTTATGA	AAAGTATGGC	AAATATATAA	AAGGTAAAAT	TCACTTTTCA	6180
AATAGTATAA	AAGTTTTTAT	AAATGACCTT	TTAGAGCCTT	CTTTGAAAGA	AATTTATTAT	6240
AGGGAAGCTG	AAAGCGCTTT	AAAAAATATA	CTGTAAATCG	CTATTC TGCT	AATTGCTGGA	6300
TTTTAGAAAT	AAAAATTATA	AAGAATTTTA	CCTAATTGGT	TTTGATGATC	TTAAAAATAT	6360
AAAATTAACC	ATAAATTAAT	TATTTTATT	GTACGAAGTT	GAATTTTAGC	ATCAAAAAAC	6420
TAATTGATTT	AAACTTATAA	AAAATTCTAA	ATATTTGAAT	TAGAAGCTTA	TCAATTGTAG	6480
TATTAAAAAT	ACAAATCTAA	AATTAAGTGA	TATTCTTTAG	ATTTACAGTG	GCTTTAGCAA	6540
GTTACATTTT	AATAAAATAA	AGAAGCCCTT	ATTTT TAGGG	GCTTCTTTAT	TTTATTGAAA	6600

TGTAGTATTT TAGTTTCAAT TGTTAGGTTT TTCTTTTCCA AATATTTCTT CTTCTAATTC	6660
TTCTGCTTCT TCGTCTCCAA AATCTTCTCT ATCTAACATC TCTTGCTCTT GTTCTGCCTC	6720
TAATTCTGCT TCTATTCTGC CATCAGGATC ATCTACAAAT TCTGCATCTC CGCCGCCCGG	6780
TATCGGACTT CCTAATAGTG GTTTTTTCTT GCTTTTTAGT AAATGTTTTT TAAGTTCAGA	6840
TAATCGAATT ATATATATCT TATTATCTTT AAATCTAAT AAAATATGAT CATTATGTTT	6900
TTTTATGGAA GTTAATTTTT TATTATTATT GCCAATATTT ATAACTTTTA AAGCTGTTTG	6960
AATTCCAAGA AGCATGGCTT TTTTAAAATC ATATCTTCTT TTAGATTTTA CTTTAAAAAG	7020
CTCTTGATTA TTAATACAAT CTTTAATTAT AATCTGCTA TCTTTTTCTT TTATGCAAAG	7080
TGTAGTGTTA GTACCTTTTT CAGTGTCTAT ATTTCTTTTA TTGATAGGAT TTGAAACCGA	7140
TTTAGCGGGT ACTTTAAAAT TGTATTTTTG GCGTGATCGA GAATCTTTTG AAAAAAGATT	7200
GCATGAAAGC AATAATAAAC ATAAACTTAA ATTGATAATA TATTTTTTCA ATTTATAACT	7260
CCTTAATTTA ATATTTACTT TATTTAAAAG TATATGTTTA ATTTTTTATT AACTATTTCC	7320
CAATAATATT GATATTATAA TTAATAAATA TCTTTTTTTA AAATAAAATT TTTATAGAGG	7380
TAATAAAAAA TATAAGTGCA AAAATATAAT CTCATAAGGA TGCTATTAAAGCGGAGCCG	7440
AAACAAAAAT GATTTTTTAT TGATTTATTT TTAGATGTAA TGAGATAAAA AAAATTTTAC	7500
TAGTTTTTAT ATAAGCTCGG GTTCTAAGGG AGCTAAAGAA TTAATTAATT TGTTCCTTAA	7560
GATTAAGACT TGGACAAACA ATAGTTTATT TTAACCGGGG GGTATAAATG TTATTTATTG	7620
AGAAGATGCA TCAATATTTA CACATATGGT TTCCATAAAT TAAATCAATA GTAACGTTTT	7680
GCGTTATTAC AGGATATTAT TTATGGTGCT TGTGCCTCCA AACAGCAATC AAAAATACT	7740
TTTTGCTTAA GGATTTAATG CATAAAATTT TTAATAAATA AAAGTCCAG ACACACAATT	7800
AATAATCCTT AATAGATAAT AACAGACAAA AAAGTTTTGA GTTCCTTCTA CAATTTTATC	7860
GCTTAATTTT TTAATCTTTT TTTGCCTTTT TATAATAATT TAAATTAAT AATCTACAAA	7920
ACAAAAAGAA TCAACATCAA ACAGTCCTTT ATCATTATATC TTAAATGGG GAACCACCGT	7980
TAAAGACATA AAAGACAAAG TCATTAGAGG ATCATCAAGC CGAGAGCCTA AAACATTTTT	8040
ACAAAAATCA TTTAATTTTA TATATTGTGA AGCTACTCTT TCGGCTGAAA GAGTACTCAT	8100
TAATCCAGAA ATAGGAAGTT CCATTATTAT AGTTTTTTCA TTGTTTAGTG CACATAAACC	8160
CCCCTTATTC TGGATGATTG TATTTGCCGC TTTACACAAA TATTCATCAT TGCTTCCAAC	8220
AAGTATGATG TTGTGAGAAT CATGAGCAAC TGTACTTCCT ATGGCGCCGT TTCTTATTC	8280
AAAATTTTTT ATAAATCCTA TAGAAATTTT ACTATTGTCT TTATATCGAT TTATTATAGC	8340

919

TATTTTAA	ATATCCTCGG	CAATATTAGA	TTGAAAATCT	GGGGCCAATA	AATTGCTATC	8400
AATCATAGTT	TTATGAGTAA	TAATTTGGTT	GCTGATGCAT	TTGATTACTG	GGATCATCTT	8460
ATTTTATAGTG	GAAAATTTAA	AATCCGAAAT	AGATTTTTTG	CTACAATTAA	AATTGTTTAT	8520
AGGAATTTCA	TTTATTAATG	GGATAAGTGA	AATTCCATCA	TTAAAAACCA	ATTTACCATT	8580
AATGTAGGTT	TTATTTATTT	TGAATGTTTT	GATATCTTTT	GTAATTATAA	AATCAGCAGG	8640
ATCTCCTATT	CTTAACAACC	CCACTGGGAT	TTTATAGTGT	AAAACCGGAT	TAATGCATGC	8700
TATTTTCAAA	ACATCAAAAA	AGTCGTGCCC	ATGCTTTTATT	GCACGAGCTA	CTATTAAATT	8760
AATATGTCCA	TTTAGAATGT	CATTTGGGTG	TGCATCATCA	AAACAAAACA	TTAAGGAATC	8820
ACAATATTTT	TTAGAACATT	CACTAATCAA	AGGATGCAAA	GATTCAAAAT	TTTTAGCGGC	8880
ACTTCCTTCT	CTAATTAGTA	TTTTCATGCC	CAAAGATAAT	TTATATCTTG	CATCTTCTAT	8940
TGTTAAACAT	TCATGATCAG	TGCTAATGCC	TGAAGATGCA	TACTTTAAAG	TTAAATTGGG	9000
GGACAAACCA	GGAGCATGCC	CATCAACAAC	CTTATTACGC	TTAATGCAG	AATTTATTTT	9060
ATTTATAATT	TCAATATCTT	TGTTAATCAC	GCCTTTAAAA	TCCATTACTT	CAGCCAAATA	9120
GTAAATATCA	TCTAATTTCA	TCAATTCATC	TATATCTTTA	TCATTTAATA	CATATCCTGA	9180
AGTTTCAAAT	TCTTGTGACA	ACGCTGGCAC	ACAAGAAGGA	GCTCCAAAAA	AAAATTTAAA	9240
CTCGGTTTTT	TTAGAATTAT	TTATCATAAA	ATTGATGCCA	TCAATACCAT	TAACATTGGC	9300
TATTTTCATGA	GGATCGCTTA	TTGTAGCCAC	AGTGCCGTGT	GCAACTACTA	AATGAGCAAA	9360
GTTTGATGGA	ACAAGAAAAG	AACTCTCTAT	ATGTATATGC	GCATCAATAA	ATCCTGGCAG	9420
CACATATTCA	TCCAATGTCG	CATTAATTTT	TTCTATGCTC	GCAATATGAC	CGTTTGCAAT	9480
CGCTATACTA	GCTGGATAAA	TTTCTTTATT	AAAGATGTCA	ATATAATTAG	CTTCAATTTT	9540
AAATAAATCC	ATTATTTATC	CTCTCCTAAA	AACTTTTTGT	TCATAATATA	CTCTACCTTA	9600
AAATCTTTAA	ACTTAAATTA	TAGCGCAAAG	TGCCAGTATA	TTAATTGCA	ACTGTATTTA	9660
GAAAAAATAA	AAATCGTCGA	TATTTGTTAT	ATACGATAAA	AATCGAAGAT	AATTTTTTGG	9720
GTAAAATAAA	TAGAAAAAAT	TTAAATAAAA	AATAGCTAGC	AATTCTAATT	TTGATACCAG	9780
CAAAGATTAT	GTGGTAAAGT	ATCAAAGGGG	ATCCTCTAGA	GTCGACCTGC	AGGCATGCAA	9840
GC						9842

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9542 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

TGAAAACCTT AAGGATGAAC TTGCCGGGGA TTGATAAAAA TCTTAAAGGT TATGGCTATA	60
AGTATCAGAA TTTCAACGAA ATAGCTAGAG AAATTAAAAA AGTTATTGAT AAGCACAATT	120
TATGCCTTGA TTTTAAGCAA TTTCGACTT TTACAGTTGT GGGGAGCAA CAAGTTCTAC	180
ATGTTGTTAG AACTACGTTT TATAGTACAA ACACTGGGTA TAAAGACTCC TTTGATACGC	240
CAATACTTAC AGAAAATTTA AAATGGAATA ATGAAAATGG GTCTAAAAAT GTTGTAATA	300
CAGTGCCACA ACTGGTAGGC TCATCAATTA CTTATTTTAA AAGATACGCA TTAGTAGCAT	360
ATCTTAACAT AGAAAGTGAA GTGGATACTG ATGCAGCTCC TATTTACAAT AACCACGAAA	420
ATGAAAATTC TATGCCTAGC AAACAAGCTG GTGTTAACCA AAATCAAGTA AAAAATTTTG	480
ATAAAAAGTT AAAAACCGGA AAGTATTATT GCTATGAACT TTTTAGAATT GCTTTATTTA	540
ACATAAAAAA CTGGGTAAAT GATGAAAAAG AAAAAAATAA TATAAATGCT CTTATTCGGG	600
CATTATGTTT TGAAAATGAG GCGGATTTAG ATGAAATTTT TAATGATAAT CCTGGGTTTA	660
AAAGCATACA ATATTGGGCA AATATTCTTT TAGAATATTT CAAGAAAACT AATAAATTAG	720
ATGAACATAA TAAGTTTGAA GACTTTATAA CTAATAATCA CGACGTTTAT GAAACAAGTG	780
TCTTGAAATT CTTTTGCATG TTAAAAAAG AAAGACAATT TGATTATATA TTTGCAGTGT	840
AATAATACAA ATAAATCCCC CTTAAAGGGG GAAATATTA ATCAATTATT AAGATATTTT	900
GGCTTTTCTA CTCGCTTTAT ATAATGCTAT CTATACGCCT CATAAGGTTA TAAATTATTT	960
CTTTTTAAGC TATTTTTTAA ACTTAATCTT TAGGCAAGTC TGCCAAAATT GTTTTTAATA	1020
TTTGTTTAAC TGCCGTTATT TTATCTTTCT TATAAGATTC TTCAAAATTC TCTCTAGCTT	1080
TTTCTCCATA TTTTTCGGCA TAATCAATTT TATCCGAATC TAATTGTATT AAATAATCGA	1140
AAATTGAATT TGGATAGCCC TTTATGAGAC TATTTATGTT CATTATAATA AAAGATAAGA	1200
AATCAGTTGT TATTTTGCTT TTTATAAAGC CCACAACATC AAGTGCCTCT AATAAACGC	1260
TATTTTCTTT AATTCCGATT TTTCTTAAAC TTCCCCTAAT TTCTGGAGCT TTAGCAAAAA	1320
AAAAGCTTTT ATCATATTCA CTTTCAAAAT CATAATTATC TAGTCTTTTG TTAAGTAAAT	1380
CATAATCTTC TTTAGAAAAA GCTTTTTTTAG CTTTCTCATA ATTTTTTTTT ATATCTTGAC	1440
TCATAAAGC ACTTAAATCA ATGCTTAACA TAAATAATAA AAATAACAAT AGGCTTATTT	1500
TTCTCATATC CTCTCCTAGG CTTTATTATA TACATTCTTA TTAGCAATAC TAATAAGAAT	1560
TAGAACAAGA CTAACAAATA GTCTTATTTG GTGTTGCGAA ATTAAGCATT GTTGATTAAG	1620

921

ATTTTGGTAA TTTTATTTTG CTAAACTTAA TAATTAAACCA AATAATAAGA CCAATTAACAA	1680
TAATAGAGAT AAAGGGGGTT ATTATTGTGA AAAGAAAAAC ACTCTTTCTA TGGTACGCAT	1740
TAAATTTTGG TAAACAAAAC GCTTTAGTTT TATAAAGATT TTTTGAATA TCTTTAATAT	1800
CTTTTCTAA ATTAAATATT TTAGTCTCTA AACCAGCAAT TTTCCATTTT AAGTTAGAAA	1860
AATTCCTTTG TGAAAGATTT TCATCATTAT TTATTTTAAA CTGTTATTA TCTACCATAA	1920
GAAAAATCCT TAAATTTTGT CTAAAGTACT AGCATTAATT TTCTAAAGTA TGAATTATTG	1980
TTTCTTGATG TTTATAACAT TGTTTACAAG AAATTAAGAA CATAATAAGA ATACAAAAAA	2040
TAAAAATTTT ATTTTGCATA GGGCCTCTCC AAAAGTTAAA AATAAAGCAA AATTATTTAA	2100
TTGTAAACA ACTAATTTCA AGATATATTA TTGAAAGTAA AACATAAAAA AAATCAAGA	2160
AATAGTTTAT ATATTTTGC AATAATTCAG AATGAATTTT TTAAGGATTT AAATATCTAA	2220
TTTGTTACAT TTTGCTATTA CATATTAACA AACTATAAAT ATAATAAAAA TGAAATTTTA	2280
GGAAGTCTT CATTATAGGA ATTAATCTTG TTAAATGGC TAATAAATGA CATATAGTAC	2340
AAATTTAGTA GTTTTTTATA TAAATAGTC GTAGTATATC ACATATTCAG TCTAATCCC	2400
TTGAAACTAC CACTTTTGTT TATTTAACT TCTCTATAGC CCTAATTTTG TATTTAATGT	2460
TAGCACTACT AGCTATTCTA GCCCTAATAT TTTTGTAA ATTTGACTT GTAATTTTAA	2520
CTATTTTTTT AACTTAAAGT TTACAACCTA GAACAAAATA GTTTTGTAA ACTCAATATA	2580
TTTATTTGTT TTAAATAAAA AAAATTAACA AAACTATTA AATAAAAAACA AAATCTTTTA	2640
ACTACTACTT TAGAGTAGCC AACTTGATAA AGTCTTTTAA TAATGAGCAT TATCACTTTA	2700
CAAGTTTAT TTATAAAGGG GGATTTATTA TGAACAATA TTTTAATGAT GATATACCAT	2760
GCAATCTTG CAATAGATTA ATTAGAAAAT ATGACCAAAC TTGTGTCGCT TGTGGGGCTA	2820
AAAATAACA AAATAAAAAA TCTTATTATG GATTAATAGC ATTTTATTT TGTCTATTTT	2880
TTGGCTATTT AGGATTTTCT AATTGTATT TAGGCAAAA CCCTAAAATA GGTTTACAT	2940
TTTATTTAT ATCTATTGTT TTTTGTAC TTGCAGTGCT GCTACATAAA TCAAACAAGA	3000
CTAATTATTT ATTAGTCTTG TTTGACTGT TAGTATACTT TTTTGTGTA AATAGATTTA	3060
AAATCTATAA ATTTTAAA AAAGTAACAA GAAAAATAAT TAGTCTCTAA GAAATTAGTA	3120
ACAAAATCCA TAAAAACATT TTCATAGTAG TTACAATTTT TAATGTCTAT AAAAATAAA	3180
CCAAAAATAT ATAAATATCA TATATATATC CTCTTAATCT TCAAGTTTGG GGGGTTTGG	3240
CATAAAGTCT ATGTTGCGTT TTTGTGGTCA CTTCAAATTT GCATTTTAC TTAATAAATT	3300
GCTCTAGTGC TCTAGCTCAA ATTTGCATA CAATTAAAGT TAGATAACTA TATTAAGTGT	3360
GTAGTAATAG ATATTTTATC TTTTAAGGCT AAATATTTGT TGTTCTTTAT TTAATCTTCT	3420

TCAAGATATT TTATTATACT GTCTATATGT GCTACTACGT CTTCAGATAG TTCTTTTATG	3480
TTAATAGCAT GGAGTGCAAT AGGACTGGTA TTTACTCCGG CTGATAGAGC TATTGAGCGT	3540
ATTTTGAGTT TGTTCTTTTC TAAATCATCA TTATCGTTTG CATTAATCT TTGGATATCT	3600
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AAATTTAAAA ATTTTTCTTC GAATTCCTTA GCATTAGTTG CATATTTTAA GTCTTCTTTT	3720
AATAAGCTTA TTTTTCTCT ACAATGTTTA AATGCAACTT CATCGGCCTC ATCATTAAGG	3780
CCTGAGACAC TCATAATAAG CCAATTTATT CTTTTTTTTT CTATTGTTGT TGTTCCTGTA	3840
ATTGTTGCTC TCCTTTTTAT TATAAATAGT TCACAAGATA TTACAAATAA TGAAAATATT	3900
AATATAAAAA TTAATTTAGC TATGTTTATT TTTTGCATTG ATTTTTCCTT TATTTAATAA	3960
TGAAAATTAA TACAATACAC AAATAATCTC AAAATTTTAG TGAATTTTTT GATATCATAG	4020
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TGATTTAAAA GTGGAGTTAA TTAATGGAAA TTGATAATTT TTTAGATTTA CAAAAATCA	4140
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TAAATGTGT CAAGACATTA AAACAAATTG ACCCAATAGC TGGATGGTTT GTACACCTAC	4380
TGGTAATAAG TGGGTGTAGG GGGGCCGAAC TGCAAAAAGT AAAAAAGCAA GATATTTCAA	4440
CTTTTTTAAG CAAAACCGGA AAAACTTTAT ACAACATAAA AGTAAATGTG GCAAAAAAAA	4500
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AAGTACACGA AATTTACTTC AAAAAGAAAA ATCTTAATAC TAGCCGCACT TATTTTTTTC	4620
AAAAAACCAA ACATAGGTTT AAAGATAATC GAATTAGCAT TGAATGTATT GCTAAAAAAT	4680
TCAAAAAGTT ACTTAGAAAA TGGGGTTTTG AAGCACGTAA ATCACTTCAT TTATGTAGAA	4740
ATTTGTTTAT TTTCAATTTA AAATCTAATG GCTACAACCT TTTTCAAATT AAAGAACTTA	4800
TGAAATATTC TTCAACATAT GAAATTGATA ATATTTATGG ACTATCTCAT GCAAGTAAAA	4860
TTCAAGCGTA TGAGTGCATA AAAAATAGTA TTGCCTTATA GCTTAACCAG TTAAGCTTAA	4920
ATGGTGAATA TCTTTATTTT TGACATATAC TCCTTTATAA TCCTTTACAT TTATTTATGT	4980
ATTTCTAATA ATCTTTATCA GTGTCCCAGT CAATAGGGGC ACTGATACTA TTTGTAAACG	5040
CTATATTGCT AAGAAAGAAT ACTTACTACT TATTGGCAAA AACCCCGTAA ATCTATCTGA	5100
TATTGCTCTT TTATTCGGAT CATAATTAAA CACAAATCT CTAAATTTAT AATTCACATT	5160

923

ATTAATTAGT	GGATATTTAT	GCATAATCTC	ATTAATTTTT	ATTTTGAGCA	GTTC'TTTTAT	5220
AGGATTTTCT	TTTTTTTTGT	TTTCAATTTG	AATTTTATTT	AAC'TCTAATT	TTAGATTTTC	5280
AATCTCAAAA	ATAGAACACT	CAAGATTTAT	AGCGGCCTCA	TCAGTTCTAA	TTTCAAGGTC	5340
TACACAATCA	ACATATTCTA	CAAATTCATT	TATCCAGTCA	AACTCAATCC	CAT'TTTTATA	5400
AAAATCACTA	TTTATTACTA	AATCTTGAAC	AAGATTTATA	AAAGTATCAT	TAT'TCCCATT	5460
ATGAGATATT	AATAAATTGA	CCGCCTCATT	TTTAAAAATT	TTATTTCTTA	AAT'TGGAAAC	5520
TTCAAATTCA	CATTTATTAA	CAAATTCAAA	CAC'TTTTGTT	ATCAAAAAGAT	TAT'TTCTTTT	5580
AAT'TCTACAA	TTAATAGGTT	TATTACCTAT	TAAAAAGAAC	AAATTACAAT	ACTCAAGCCC	5640
AGTGCACGCT	AGCTGCACTT	GTGCTTGTA	ATAATATTTG	AAAAAATATT	TACTACTTAA	5700
AAAATTGCCA	TTTTTATTGT	ACTCAGCAAT	AGCACTACTC	ATATAATTAG	AGTCGCTACT	5760
TTTAATCTCT	AATAGTTCTA	AATCGCCATT	ATTATTAATA	AACCAGCCAT	CAAT'TGTTGA	5820
GCCCACTAAA	GTTTGTGAAC	TACCCATTTT	TTTGAAATAG	TTATACTTAT	CAACACCGTT	5880
AGCATATTTG	TTTTTATACA	AAATATCAAT	ATTATCTCCG	TGTGCTTTAA	TAAAT'TCTCT	5940
AAATCCTAAA	TTCTCTAACT	CTTGCCCTT	GAGCATATAT	AAAT'TCTCTT	CATAAGGCAT	6000
ACTTATACCA	AAATATTTAA	GCAGTCTATT	CATCATTAAT	TCTTTTAACC	CTACACCACC	6060
AGTTAGAATA	TTGCCACTTT	CACTAGCACC	GTATTTATTA	AGTTTGT'TTC	TTTGCACACT	6120
AAAATCAATA	TTTCGATTAA	ATCTAAAACA	TTCTTGACTG	CTTATTCCGG	GTAAT'TTCTT	6180
ACCTATCTTA	CTTAATTTAC	TTTTTTCTTT	AGTTTGATTA	ACTTGATAAT	CAAGTTCTAT	6240
AAAATTTTCA	AAACCAATAA	AATTAGTTTG	CTTATTTATT	TGATTAATTT	TTTGTGGATT	6300
ATTGTTTAAG	TTTTTCATTT	TTTACTCCG	CAAGTTATAA	TTTCTTATA	TATAAATATA	6360
TAGCAAAAAC	TATTTTGGCC	AACTTTTTTA	CAAAAAATTT	TTTATTAAAA	CAC'TTAGGGC	6420
TTTACTAAAT	TCTCTTTTAA	AAGAACTTAG	AAAAGCCCTA	TGGATTTAAG	AACTGATTAT	6480
ACTTACGTAG	TAAAAATACT	ACAGATATTA	ATAGTATAGG	CTATGTTAAA	ACTATAATCA	6540
ATTTATATTT	ATATAATCTT	GTAGCTTGAA	AAAAATATAA	AAACATTTTT	TTGTATTTTT	6600
TTTATAAAAC	ATTAAC'TTTT	AAATCAAAAA	TATGTTATAT	ATTTATATAT	AAGAAAATTA	6660
TGACTTGCGG	AGTAAAAAAT	GGAAAATTCT	AAAAAAAATA	CCCTTTGCCA	AAATAAGACA	6720
CAACATAAAT	CAATAGTTCT	TATCTCAACA	CTAGAGTATA	TAAACAAAAC	ACATAATAAA	6780
TACACACAAA	AAAACATACT	CTATTACTTT	AATGAAAATC	TTAAAAGAAA	TGGTCAACTA	6840
CCCGTTAAAA	TAAAAACACT	GCAAAATTAT	CTTTACAAAT	TAGAAAAAGA	AATTAAAGTA	6900
ACAAC'TAATT	ATCACAAACA	CTTAGGAGTA	AATTGCGGCA	CCGAAATATA	CTATCAACTT	6960

AATTTTTC	AAAAGAATG	TTACCAAAAA	ATCTATAAAT	ACTTTCAAGA	AAAAAAGAT	7020
TTAAGATTTC	AAAATAGAGC	TACAAGGGGC	CTTAAAGATA	GATTTACTAA	AAATGGGAGT	7080
GTAGATTTAA	AGGAGTGTTT	AAATAATAAA	AATAATATAA	AAGAAGAAAG	AAAGATTAAT	7140
GAAATAGAAA	AGTATCAAGT	AAGAAATTAC	TTCAATAAAT	GTAACTTTTT	ATGTAAAAAA	7200
ATTCCTTCAA	TTTTCTTAC	AATTTTATTC	AATTTAGATA	TTGATAAAGA	TAATATAATC	7260
AAAATACTTA	AAATCATAAA	ATAATAGAA	ATTAAATTGC	TAAAAAATAA	AAATATACAT	7320
TTTACTAAAT	CTTGCATGAA	AGAAAAACAA	GAAAAATTAA	AGAAAATTCT	ATGCAACACT	7380
CAAAAAGAAT	TTGAAAAAAA	TGAATATAAT	CCTAAACAAT	TAGAAATAAG	TTTCCAAAAA	7440
ATATACGAAA	ATTACAAATT	TAAGCCTCAT	TTTATTATTG	AAAGTCATAA	ATATAGCGAT	7500
TTAAACAATA	TAAAGCGTAA	ATTAGAGAAG	TCAATTGAAA	GAAAAAAGA	AAATTCTCAA	7560
CAAAATTATC	AAGATTTAAA	AACAAACaTT	TTCAATATCC	TTATTGAACA	ACTAAAAAAA	7620
GAAGTAAATA	TTGAACCTCT	AAAGCCAATT	ATAAAAGAAT	ATTTGAATAA	CCAAAAGAAA	7680
ATAGAATACA	ATAAAGTGTT	TTGCACATAT	TATTGCGAAT	TATTAGAACT	AATAAAAAAC	7740
CAAAAAGTT	TATTGAATTT	AAAAGAATTA	GATAGAAAGG	CTATATAAGG	ATTTAATATG	7800
GAAAATTCAC	TAAAAGTTGG	GCAAACATAT	AAAGAAATAA	TTGATATAAA	AAGAAAAAAA	7860
CGATTTATTA	AAATTGAAAA	AAAAATAAT	AAAACGTGT	ATCACACTAA	GATAATGATG	7920
GATATTCATA	AATTAGGAAT	TGTTAATGTT	AAAAAAAATC	AATTTCTGTG	GTCATTTAGA	7980
GAATTATATA	ATCAAATGGA	AATTCAAGAA	ATTCGCCAT	ATCCTATAAG	GAAAAAAGAT	8040
AAATTTTATG	GAATTTTFTA	TGGCTATAGA	AAACCAGTAA	AAAATGTTTT	TGTAAGATAT	8100
ACAATGGATG	GAGTTAAAA	AGTATATTCA	TTTTCAAAAA	CGTATTACAT	AGAGTTTAGA	8160
TTTAAAGCTG	GTAGTGTTTT	TTGTTATTTA	AAGGGTATGA	GGCGTTTAAC	AAAGAAAGAA	8220
AAGATAGATA	CACCCTATAA	TAAAGCACTT	TTTGATAAAT	TGATAGATTT	AGAAAAACAT	8280
GTATATGAAT	TTTACAATAA	AAAATACCCA	GAACAAGGAT	TAATTCCTAA	GTGGATATTA	8340
AAAAATCTAA	AATAGTAACA	ATAATATTAA	TTAAGGAAAA	TGTTGACAAA	AATAAAGGAA	8400
AATTTTATG	GAAAAAAAAC	GTGTTGTTAA	AGTTTTAACA	AAAAAGATAG	ATACTTATGT	8460
TGAACAAAAT	TTAATGATTA	ATGAAAGTAA	AATTTCTTAT	TACAAGACAC	TAAAGGAAAA	8520
GTTGAATGAC	AATTTCAAAA	AAGAAATATT	CCACAGGGTG	GAAAATATTA	AAATTTTAAA	8580
AGAAATAAAA	GATAATCAAT	ATTATAAATT	TGATGGTTAT	AAAACTTTTC	TTGATTTTAT	8640
AAAAGACTTT	GATGTAGCAA	AACTCAAGC	GTATAAGTAT	TTAAGATTAG	CAACTGCACT	8700

925

GCAAGAAGGG CTTATAAAAG AAGATTATTT AATAGAAAAT GGTATTAAAA ATTCTTATAA	8760
TTTTATAAAA GATAAAGAAA GTCCGGCGTT AAAAAAATCT AGGCAAAATC CAATAAAACC	8820
ATTAAGATTT CAACTTAAAA CTCAAGAAAG TTATGATTTT TACAAAAAAA ATGCTAAATT	8880
TACAGCGTTT ATTTTGGAAG AACTTCTTAA AAATCAAAAA GATTTTCTTA AAAAAGTTTT	8940
AAGGAAATAT GAAGAACTAA AAATCTAATT TTAGAATTTT GTAAATAATT TAGAGAATAG	9000
GTTTTTATAA GTTCTTTTAA AATAAGATTT TATAAAAGCT TTATATTTTT GTATTTTTAT	9060
AGACCGCAGT GTAATAATAT TAATTGATTT TAATTTAAGG TTGAACTAAA CTAAATATAG	9120
TTTTGTAGGA AATAATTTTT CATTATTTCC TACTTGAATA TTGGATCGTA AAAATATTAG	9180
GGCTTTACTA AGTTCTTTTA AAAGAGAATT TAGCAAAGCC CTAAGTCTTT TAACAAAAAT	9240
TTTTATTAAA AAAAGTTGAC AAAAATAGTT TTTGCTATAT ATTTATATAT AAGAAAATTA	9300
TAACTTACGG AGTAAAAAAA TGAAAAACCG CAAAAACAAT AATCCACAAG AAATTAATCA	9360
AGCAGAAATT GACTTTTAA GAGATATGAA AACCTAAGG ATGAACTTGC CGGGGATTGA	9420
TAAAAATCTT AAAGGTTATG GCTATAAGTA TCAGAATTC AACGAAATAG CTAGAGAAAT	9480
TAAAAAGTT ATTGATAAGC ACAATTTATG CCTTGATTTT AAGCAATTC CGACTTTTAC	9540
AG	9542

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

TTATTACATT CTTTAATAA AGATTACGA TTCTTAATGC TTGGATCTAA GCCTTTTTTA	60
AAATCAATAT ATCCTTCACC AAGAGCACTA AATTGCTAA ACATTTTATT AATAAGAGTA	120
AATTCTTCAT TGTCTTGAA TTCTATTATT GATTCTTGAA TAGGAGATAG CTTCTTAATT	180
TGATTATAT TTAATCAAT TCCTTTATAA GCATCGTCTT TACTATCTTT CAAATCCCTA	240
GTTATTTCTT TTAAAAATAT ATCACTACTC TGAATCATGA ATTTTGCTTT AAAGCTCGAT	300
GTAGATTCTT TAATATTACT AAGTGAAAT ATTGCAAAT TAAAGCTGA ATGCACATCT	360
TTAAATCTTT TTTTGTTTTT AAATGATAA ATATAGTTAA GTTTATAGCG AGCAAATATA	420
TGTTTTCTTA GTATTCTAGA ACTAGATTCA TTCCAAATAG CTGAAGGAAC TAAATAAGTT	480
AAATTACCTT TTTCTTTTAT TAATTTTAAA TTAAATGTAA CAAAGTATCT AAAAAGATTT	540

GGGTCTCCAC CACTAGTAAA GCATTTAAAA TCAAATTTAT AAATATTATT AATGGCAATT	600
ATACTATTTT TTTCTTCATT GTATTCAATA CTCAAAGGAT GATTATCTTT ACTAAGTATT	660
TCTTGTTTTA TGATATTTTG TTCTTTTATG CCTAGTTTTT TGTAGTTAGG AATATGTTTT	720
GAAAAAACT CTGTTTCATT AAATTTAGTT TTCTCCCATG GAGGATTTCC AATTACAATA	780
TCAAATCCTT CTTGAATATC TGGAAATTCA ATTCCATAGT GAAAAATTT ATAGTAGCTA	840
CTTAATTTTC TAATTTTTTC TATTTTTCT TATCTTCAC TAGAAGTTTT ATTGCCCAA	900
ATATTTTCAA TTAAACTAAT TACAGACGCA ATATCACTAA ATTCCATATT TAAAGATTTA	960
TCAAAAGATA ATGAATAAAG TTTAATTAAA GAAAATATTA TTCTTAAATT ATCTATATCT	1020
TTACTTTCTT CATATTCTTT GTATATCTTT TTAGATTTTT CTATATCTTC TTTAGTAGTA	1080
TCATTAATAC CTTTAATTTT TTGATAAATA TCTTCTAAAA TAGTTATAAT TTCTTTAATT	1140
CTTTTTTTTAA ACAAAGAAAA TCCACTTTCA AATTCTTTTT TTACAATATC AAAGAATTCA	1200
TCTTTGGTAT ATCCTAGCAG GGCATTTCTT GCTTTTATAT GATGTTCAAT AAAGCTTAGT	1260
GGTGTTCCAA AAATAAAAGT ATTAATCCAC AAACCTAGCA TAGTAATTTT AACTGAAATG	1320
GGATTAATAT CAACACCATA AATACACTTC TTTAGTAACA TCCTTTTAAG TACTAATTCT	1380
TTACTTATAC TATCTTGAAC ATCATACTCT TCACTTCTT CAATAATAAC CCTATATTCT	1440
TCATCAAGTT CTTTTTTTAC ATCTTCAAAT TTATCTAGCT CGTACCATAC CTTTCTGT	1500
AAGTAATCTA GACAAGAAAT TAAAAAATGC CCTGATCCAC AAGAATTATC AATTATCTTT	1560
ATATCTAAAG GGGATTTGGT TTTAAGCTGC TCTTCAATTG ATGATATGAC CATAAAATCA	1620
GTCAAGTCAT CTGGAGTATA ATATGCCCCA CTTTCTTTT TATCAAGTGA TCTAGATGTA	1680
AGATAAATAT TACCTTTAAG ATATGTAGCA ATTTTGTTTA CTTTCTTATT TTCAAGCTCT	1740
TCTTCAGTAC GAATAAGGTA AACTCCGTCT TCAATAATAC GATGAACAGT GGTATCTGCA	1800
ATTCTTAGGT CATATTCAAG TAGAGTTTCG TATAATTCTC CAAAACTTT AGGATCTAAC	1860
CTTGAATACT TTACAAATTT TTCATCTTTA ATATTTTTTT CTTCAAAGAA AAGCATTTTA	1920
ACTAGTATTT CTTCAATCTC GCTAATACTG AGCAAACCTT CATTAATTTAA ATATTTAACC	1980
TTATCTTCTG AAAATAACCC TCCATTAAAT ACAGGAACT TTATTGCATC ACTTCCTTTA	2040
TCAAGTAAAT TGAAAAATGT TATTATTTTT TTATATTCTA ATTTCTTTTT TGTATTTTCA	2100
TCATAAAAAA AATATCTAAA AGATATAGAA GATCTGTATA GCTTATTTTC TTGTAATATT	2160
TTCTTAAAAA TGTCGTTATC TTCAATATAT GCAATAAAAA ATATCTTTAA AATAAAAAATA	2220
ATTGATTCTT CAAGAATGCT AGCTAAAATA TGCTGAGTAA TTTCTTTGCC TGATAATTTA	2280

AATTCCTTGT	CATATATATT	TTTTGCAATT	TTAAATACTA	TAGAGTCGTC	GGGTCTCTCA	2340
TAAAGTATCT	CTTTTAGAGT	TTTTTGAATT	ATCTCTTTTT	CTTTAGCTAT	TTGTTCTTTT	2400
TCAACCTCTA	TTACATTACT	TGTCTTTAGA	TATCTTTCTT	TTCTTATAAG	GTAGATGAAT	2460
AAAACAAACC	ATTCTTGTTT	CTTATATTCT	TCTTTTTCTT	CAATTTTAGA	AAAATTGAAT	2520
TCAATATATC	TTTTTTCCTC	ATAAAGTACT	TTGATTTTGT	CATATAATCT	CCATACCTTT	2580
CCATTTGAAA	GATATCCATA	ATGTTTTTGA	TATTGATTTA	GATATCTATA	TAGCTGATCT	2640
TCTGATTCTT	TTAATTTATC	TTTAGCATCA	AAACTAAATG	TTGGGCGCTT	AACCTCTGCT	2700
ATAATCAAGA	TATCTTCGAT	AGGAATAGGT	TCATTATTTT	TTTTAGCTTC	TTTTAATTTA	2760
TTATTAAAGG	ATGCTTTGTC	TTTGTGCTTT	TCAAAAAGCA	GTATATCTAC	TCTAGACTCC	2820
ACTCCTTCTA	TTTGACCGGC	TTTTTGTTGT	TCTACTGAAT	AATTTAGTTC	TTCAAAATATA	2880
TACTTTAGCA	AAGACTCTAT	ATTTGCTTCT	GTGGAATTAT	CATCTATTGA	AAAAAGTTTA	2940
TTTTTTATAA	GAATAAAAAA	GTCTTTTAGC	TTATTAATAT	TTTCCTTTTT	TATAAAGTCT	3000
TTTGATAATT	GTTTATAAAG	AGATATATTA	GGATTATTTG	TTTTTACGAT	ATCATTAGTT	3060
TTCAATTATCT	ATGCTTTTAA	AAACCTTTTA	TATTATTTAC	AAATCTTTTC	CATATATTAT	3120
TAATATTAAC	AATATATTTT	AAAAAAATTA	AGTTTTTAAT	TAAAAACTTA	ATTTTLAGAT	3180
AAATAGGTTG	ATAGAATAAC	TTTCAATGAA	TTCAACCACA	ACAAAAATCA	TATTCATTTA	3240
TCACTAGAGT	TTGCTCCCAA	TATACACCTT	CTAAATTTAT	TAATAATCTA	AAAAAAGTAT	3300
CTTTAAGATT	TATAAGAAAA	AAATATTTTA	CTTATTTAGA	CAAGTATTAC	CGGAAGCCTT	3360
ATTTGGTCTA	GAAATTATTG	TCTTCTCTTT	ACTAGAGATG	ATTCTATTGA	TATCATCAAA	3420
AAGTATATTC	AAAAACAAAA	CAAACTATT	TATTGGCAAA	TCATATCCA	CCAAAATTTT	3480
ATAGAAATTA	TAGATGGAAA	ATTCTTTGTT	ATTTTTTGGC	AAATTATTTA	ATAATATTA	3540
AATTATTTGA	TTTTTATTAT	TAAATTGTAA	TATTATTATT	TTGAATTAAA	ATTATATTTA	3600
TTAGTCTAAA	TTTGTAAGGA	GAATATTTTG	AAAAACCCCA	AATCAAATAA	ATCTAAGCTT	3660
AACATTATTA	CAGCAATATT	AGCTTCAATT	TACATATCAT	GTGCACCTAT	TGGAAAGGTC	3720
AATACAAAGC	CAAATAGTGA	TACCAATCCA	GAAAATAACC	AAAATTAGAA	TTAGAGAAG	3780
CTTTTCGTAT	AAATTTTTTA	TAATTTTCAG	GATTATACTC	ACTGGCAACT	ATGTTCAATA	3840
TTCTCAAAT	GGCTATAATA	AAGGAATATT	GAAATTATAG	GCTATGTAAG	CTGCCGATGC	3900
ACTTTCATA	TCTATTATAA	TTGTATTTTC	AAATCTTCA	AAAATATTTT	AGATATATTG	3960
ATTTTCATAA	TTAATAGATC	AGTCTTCCAA	CAATTATTAA	CCCTAAATGT	GATATTGTCC	4020
TGCCTATCTT	GATTTAGAAG	CCTTTATTGC	AAATGTTTAT	TTGATATAAA	TTTTTTAGAA	4080

TGTTCTGGAG CCTGTCCTAT TTAATACTTA GAGGAATTTA AAAACATAT ACAAAGCTAA	4140
AAATTATCTA AAAAGCAATT TTTCATACTA CATGTTCCAG ATGGTATAAA AATAAAAAAT	4200
GATTTAAGGA ACTATAAAGT TTATCTTTTA AAGTTCCTTA AATCCACAAA AGCTTTGCTA	4260
TAAGCTCTGA TATAAATTAT AGAATATGGG GAAGGAAGTA CCAATAGTTA AAATTATAGC	4320
TTTTAAGTCA ACTAAAGGGG TTGAAGAAAA ATATAAAGTT AAAAGCCCAA AGTTAATTTT	4380
TGAAGTATTG AATATTGATT TTTATCAATA TAAAATTAGT ATTGCTCTAA TTAGGTAAAG	4440
GGGCTTCAAG AAAGCCCGGG CGCATTAAAT CATATAATTT TTAGGGGTTT AAATGACTAT	4500
TTAAAAAGC ATTTGTTAAA TTTCTCTACA AGGAAAGCAA ATATAATTAT ATACTTGCGC	4560
ATCTTACTAT ACAAGATAAA CAAAATAATA GGGATAAAAC CTATAAAAT GCATTGGGTC	4620
TAAAATTATT TCATTATGGT TGTTAGCCCG GATGTTTAAA GTTTTTTGAG ATTTTTTAAAT	4680
ATCATTAAAA GCTTGAATT TTTTGTAAAT AGCTGTAATG ATATTTTAC TAAAAAGGG	4740
ACACTTTCTA ATCTAAAATT GAGTGCGGTT GAACGTGTA TTTTAGATGA CATGGAAATA	4800
GTGATAATGA ATTAAAAAAT AATTATTTG AAAGTTATGA TGAAAAACT TGGACGAGTT	4860
TTTTATGAGC TTGGGATCTA ACCTTTTTTA TACAATTTTT TAGCTTGAT TGTAAATAT	4920
ACAACTTTTT AAACCTTCT TACATAATTT CAATTTATTA ATTGAAATTA TGTTCATACA	4980
TATTATATAA ATCTTAAAAG TTCTTAAATC TAATACTGAA TATTACGATT TATTTTTAGT	5040
TATCATATAA TTTTAAAAAA AAAATATTAT ATTCAACCTT ATTAACCTCT TTATTTAAAA	5100
TATCCGTATG GCCCAATAAC TATAAAATAG ACATTAAACG TATGTGCAAC ATGCCCTATT	5160
ACGACACCTT CCATCTCAAT AACTATTACA TCTTTAAAGT TTTTATAAT TTTGTTTATA	5220
TATTTTAGAT CAATAAATG ATCTCCTGAA ACTATTATC CCAATATGC ATTAATAATCT	5280
ATAATTTTTG ATTTAACAAC CTCTATAGCT TTACTAGCCC AATATTAAAA ACATATACAA	5340
AAATTCAAAT TTTTACCACT TTTTTTAAAT TTCTTGCAA AATATTGAAA AAGGGATTTG	5400
ATCGTATTAA CTGCATTAAAT AAAAACCTA AATACATTAA ATTTAAAATT TTATTTGCCC	5460
GCGCTATAAA ACAAATTTG ATAAGCATAA AAATACCTT GCTTCTTTTT CTAAATACTC	5520
TTTCACTCTT TTTAAGCCTT TATCATTTGC ATAATTGTTG CAAGAACTTA TCAACACAAA	5580
AATAATAAAA CAATAAACAT TTTTTTGCAT ATTGCTCTAT AGAGTAAAC AAAATACAAT	5640
ACTATATAAA TTATATTTAC AATATTTTCT ACAAATCTA AAAAGTTAAC AGGTCAATTG	5700
ATATTGATCC ACAGAATTTT TTGTCTTTTG CTTAATCTT TTTGTGATAT AATGAAAAA	5760
TATTTTATAA ATTCTTGACT TTGATCAAGG TAATAGGAGA AATTTTATGC AAAAAGACAT	5820

ATATATTTTCG AATATATTTT TATATATACC ATTATTTTAT TCGTGTTTTT TGACGCCACC	5880
AAAATCTTTA AAAATCAACA GTATCAAAAC TGAAGTTTTT GATTTTAAGA TAATTGAAGA	5940
GGGGGATATT ACAAATATA ATAAAAACCC CATTAAAGAG AGTAACAATA ATATTTGTCT	6000
TACTTTTAAG GAACCCGAAT TAAATGAAAT AAAAGAAGGA GAGGTGTTTG AAATACTTGC	6060
AAATGGTTAT GTTACATGGG CAAATCTGG TGATTTAAAT GATATAAAG ATAAAAATAA	6120
YAATTTAATT GAATATCTTA GAGAGCTTAA GTATTCCTAT ATTTTTTCAC CCATCCGATT	6180
CAAACTTAT TCATTGCTTA CCTTTAGCTA TACTTAATTA TAGCATTAAAT GACAATAACT	6240
ATAAAAATATT CGGTCAAGAA GTACCTATAG CTAAGATAAT AGCATTTGAA TCAACTGAAG	6300
AGTTTGAAAA CAAATATGAA ATCAAAAGTT TAAACTTAAA TTCTGAAGAG TCGAATATTG	6360
ATTTTGAACA AAATAGAACT GGTTTTGCCA AAATCAATTT AAAAGAACT TCAAGGGAAC	6420
CTCAATACAT TTATTCATAT AATTTTGGGG TTTTGTACAA TTCCTTAGTA GATTATTTTA	6480
AGCTCTTTTA CAAGAAAAGT AAATGCAACT ATATGCCTGC ATATCTTACT ATAAAAGATA	6540
AACAAACAAA TAAAGATAAA ACCTACGAAA TCATATTAAA TCTAAAGCTA TTTAATAATA	6600
CTATTAGATT AATATTTAAT AAGTATTCAA ATTTATCAA AGAAAAATTA AAACCTTTTA	6660
CTGATGAATG ATAAAAATTG AATAAGAAAA GCAAAGACAA AAATTTATCA ATTAATGTAA	6720
ATAAATACAA TTCAAATTG ATAAAGTTGT GTGACATATT CGGCATCTCA ACTTGTGAT	6780
TTAAAGTAT TGATAATAAA AACCAATTTT AGCCCTTTTT CAAAGATGTT ATTTAATTAA	6840
TCGGTTTTAC TTATTAAGGC TAATATTAAA TATTTAGAAT ATTTAAATTT TCAAGACCGC	6900
AAGTATCAAA TATTTATTTT TCAATGGACC GGATTATATT ATTATTAAAA TAATTAACT	6960
TGTTAAAAAT CAATCAAGGA TATATAAAC AGATTTTTTA AAATATTATA AAACCTTTGA	7020
TAATAAAAGT ATCCTTGTAT TATATATAAT AATATTTTTA ATTAAATAGA TAAATATAT	7080
TATTGATATT GAATTTGATT AAATAATTAA GCATACTAAA TACAGAGCCA TTCAAGGAGA	7140
GTATTTATGA AATACTATAT ATGTGTGTGT GTTTTTTTGC TTTTGAATGC TTGCAATTCA	7200
GATTTTAGCA CTAATCAAGA AGATATTAAA TATCCATCTG ATAAAGAGAA ATCAAAATCC	7260
AACATGGAAG CAAGCTCTAA AGAAGAAGAT CCAAATAAAA AAATAAAAAA TACACTGCTT	7320
AATGATTTAA TAAATTTGAT AGAAATAGCT AATGAGCATA AAGAAAAATA TGAAAAAGA	7380
ATGCAAGAAG AACCTTCAGA TCAATACGGA ATATTGGCTT TCCAGGAATT AGACTTGTCC	7440
GTTGGAAAAA TATCTGAAGA CACCCGCAA TCTAAAAAT TTAGAAAAA CACCTATTCT	7500
CCCTTAAGCG CTATTGATGT CAATAAATTA AAAGATCTTT CAGAGATTAT AAGAAATTCG	7560
GGCCAAATAC AAGGTTTATT TAATATTTTC AACAGATTCG GAGGCATTTT TGACGACTCA	7620

CTTAATCACG TATATTCTAA AAAAGATATC CTAGGGGGAC TAGAAATTTT GGATTTAGAT	7680
AAACTAAAAA ATTCGTTTGA AAAATTACTA TCTATAAAAG AAACCTTCTC AAAAATGCTA	7740
AATCAACTTT TATTAGATTA TAAAAATGAT AAAGATCATA TACGAACAGA GACAAATAAA	7800
CTTAAATCTC ATACAACTGC ACTTTTCGAA CAACTTGATA AAAAAGAAGA CGAAGCATAT	7860
GAACCTAAAA ATCAGATATT TTCAATAAGT AACCTTTAAA AAAAGATTCA ACTCCATATA	7920
TAAAATTTAA AAATTGTGCT AACATTCATT TATAAAAAC TAATTATTAG GAGGTAATAT	7980
TAATATGAAA AAATTTTCAC ATTAATATTA ATTTTATAGT TAACAATGCA AATCTTTGCA	8040
CAAGAGAAAC TTGAAAAAGG TGTGGAGAT ATTGCAACCG TAATGAAATA TGAAAGTAAA	8100
AAAGCAACCA TATTAGCACC ATTACTTTTG AACATCTTTT TATCTTTAGG AATAGGATCC	8160
TTTGTTCAGG GAGATTATAT TGGTGGTGGT GCACTACTTG GCTCTCAAGT GCTTGGAGGA	8220
ATACTTATAA TGGCTGGATA CATGACCGGG GATATTGGAT TCGTTACAGA AAGCACAGCA	8280
ACAGTAATAA CCGGAGGAGT ATTATCAGGA ATAGGAGGGC TCACAATTGC AGCATCCTAC	8340
ATCACTGGAA TTATCATTCC ATTTAAATTT GCTAATAGAT ACAACGCAGA CCTTAAAAAA	8400
AGACTCGGCA TTGCACTTGC GGGGCTTGAA CCCAATTTTG ACATTGGAAT AAACGGGGAT	8460
TCCAACATATC GTTTAAAAAA TCCTATTGAA TATCAATTTA CCTGGGGTTA AGAGAGATTA	8520
TTAATGCAAA TAATCTCTCT TCAAAGCCTA CTAAAAAAT TCATTGATAC TATTTGAAA	8580
TCAAGAATTA CATAAATAAC TTTTGTCTC AATTCACAAA AGTTTTTTAA ATTTACAAG	8640
ATTTACCTAA ACTAAAGTAG TAATAAAAAT GAAAAAGTC CCCCCAAAA GGGACGCTTT	8700
GATTGCGACG ATAATTGTGG AAGGACAAAC GACATCATCC AGCCTAAAAT AACAATAGCA	8760
CCATATATGA TAAAAATCAA GTATTTGTTT TTATCTTTT TTTTCTTTT ATATTTTCA	8820
TATTCATTAA TTAGATCTGA TAAGACTTCT TTTTAGTAA AAAAAAGTCT TTCAAGAATA	8880
TAACACGCTC TTTTAGTATC TTCTTACAA AACGTATAAA ACTCTTTATT CTTCATAAAA	8940
AACCTGATAG ACATTTTTTT ATTATTTACT TCGGACAAAT TTTCTTTTTT TACGTTTAAT	9000
AAATTCTCTT TCAATTGTCT TTGCAAGCCT CTAAATCCTG TTTCTTTAAT ATTATCTATA	9060
GAGATAGCTC CTTCTAAAAC CTTTTCATAA ACTTTTAAAT ACAAATACGC TTGTGTTTTT	9120
GCAATTACAA AATGTTTTAT AAATTGCTCA AAAC TAGAAA AATTATCATA TTTGTAAAGT	9180
TCTTTTTTTT TAATTTGTA TAAAATTTT ATTCTTTCAA TTTTATTATC AATATCATCT	9240
TTTAAATTAT ATTTTAATTT CTCCTTAAA TTATTGTAAT TAATCAAATC CTTATCTTGC	9300
ATGTTATCTA TATTTGTCAA CTCTTTATTC ATATGACTGA AAGTCCTACT ATTTAAGACT	9360

931

AGCTCTTTTT TGTGTATTT TTTCCCATC TTATCATCC

9399

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9360 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

GGGGTACAAC AGAACGTAGA AGTTGAGGCT GGTGGTGGGG ATGACTTGTA CGGAATATGC	60
ACTGATATAG ATGAGTTTAC TGGCATGGCA ACTGTAGTTC CAATTACAAA TAAC TTCACA	120
GGGTATTTAA CATTTAAGAA AAATGGACAA AATGGTGTGA ATCCGGGTGA TAAGCTGCAT	180
TTTAATGCAC AAGGAGAGCT TGAAAAGAAT GGGGGAAATG ATAAATCTGT TAATGCTATA	240
GCACTTTCAA AAGTACATAA ATTAAGTAA GAGTTATCTA TAGTGCTTGC TAGTGTTTTT	300
GGGAATAGAG CTTTAAAAGG TAATTAAATT ATGGCTTTAA AAGGCAAAGG GCAAGCTAAA	360
TCTCCTAATG TTGATGATAA TCCACAATTA GGGTTAGAAT CAGAAATTCC AGCTGCTCCT	420
AGATCTAAAC GTCAAACAAG ACAGGCTGAA GAAGTACAAG CAAAAGATCC TTATTTAGAT	480
TCAGTTAAAG AACTTGACGA TGTCTTTTAA AAATTTAAAA AATATTCAAA ATCAATGAGT	540
TCGATTGAAA ATAGGGTTTT TAGTAGTTTC GGTGGTTGTT TTAAATTAAA GAATGAGCGA	600
GTTAATGCTT ATCTTTTAC ATGTTCAAGC TTTGCAGACA AAATAGAAGA ATACCTTTAT	660
GATCCAGCAA ATAGTTTTC ATATAAGCGT GGGGTTAAAC TTGTTCCAAA AGAGAACTCT	720
ATATATGTTG AAGTTGGTGC TGATACTGAT ATGTATGGGA TATGTGTAGA TGTATGTGAG	780
TTTAGTAGTA CTGCGTATGT ATTACCAATT ACGAATAACT TTGAAGGTA TCTTGTTACA	840
AGAAATCCGA GTATAAAAAT GGGAGAAATA TTGGATAAAA GTGCATTTTT TAGAGTTTTT	900
TCTGGAGATT GTGTACATGC TACGATTTTT TTTATCTTTT CAAAAGAGA ATTTCTTGAA	960
TTCTTATTAT TATTTTTTAT TAATTTTTTA TTATATACAG TGACATTTTT AGACTTTAAT	1020
TTTTCTTTAT TTGATTTTAT TTTTTTGGAT AACTCAAGCT TGATACTAGA AAAATAAGTA	1080
TCAATTATTG AGTATGAAAT TCTAGAAGTT TGGTATATAC AAAGCTTGCC TTTAAATTGT	1140
CCTATGTTAT TTGAAAATGT TAGAATTTTT TTATTAATTG CTTTAATTTT AATTAAAAAT	1200
CTTAAATCTT CTCGTAATGT ACGAATTGTA GTTGGCTTAT ACCCTTCTTT GATTATAAAT	1260
GAATTTAGTA TATTTAATAT GTCTTGTTGG TGGTGATAAA GAATACAAAG TGCAGTATTT	1320
GTAATATCTT CTTTATGAAG ATTAATATTA CAATTTCTTT CGAACTTTTT ATTTAGAAAA	1380

TTTATTATGC	TGATTATTTT	TTTAAGCCTA	AGGTTTTTTG	ATAATAACCT	TTTAGTTTTA	1440
TAACAATAAT	TATTGTTATA	GAGATATAAC	TGATATCATA	TTGAATCTCC	AATTTATCGT	1500
TTATTCAAAC	TTTTTTATTA	ATCCTTATTA	ATAAACTAT	TATAGTTTAA	ATGGTGCATA	1560
ATTTTCAACA	TTTTGGCTCG	AAGATTTTTT	AAAAAAGTGT	TGTGATTTTC	CTAGTAGAGT	1620
AAAAGACCAT	TAGCTTTTGC	TAATGGTCTT	TTACAAGGTA	TTGATAGTTC	ATAATTTATF	1680
ATGTAACAT	CAATACAAAT	GTTATATGCT	AAAAAATATA	AAATATCAAG	AAATATGAAA	1740
AAAATTTTCA	TATTTCTCTA	TTCTGCCATT	CTAAATGTCA	TTAAATGTTT	TTTTGATTTT	1800
AGCATTCTAA	CTAATTTTTT	AGCATCAAGC	ACATCTCCAT	AAAAGTTGTA	GTAAAAATTA	1860
TTTACAACCT	TACTGCTTTG	GGTCTTTTGT	AATTTAGTAA	TTTCTTCTGA	AATAATTTTA	1920
GCTTCAAGTT	TGCATAAATT	TGCATCTATT	GGTGCAGGAG	TTATTCTTAC	CAATTCGGGT	1980
TGCCCAAAC	CACTAGACAT	TACACCTAAG	TTTGGTATAT	ATGTCGGTTT	ATTTGAAACA	2040
AATCGTTCAC	AACCATGAGC	AAGTGTATAT	TCTTCAATAG	ATCCAGCTGA	TTTTACTGTT	2100
GCAATTCCTT	TTAGTATTTT	GTCTAAAATT	TTTTGCATCT	TTCTTAACCT	ATCGGCCTTG	2160
CCCAAATTC	ACCAATTTTT	ATCATTTACC	TTATCAACTT	CGGCCTGTGC	TTTTATTCTG	2220
TCGGGCTCTG	GTTTAGAAAG	TTTGTTTTTG	CGTTCTACTT	CTAGGTTTTT	AGTCTCTTCG	2280
GTCTTAGTAA	GTTGGGTGGT	TTCTATATCT	TTTTTTGTGT	TATATTGTGT	TTGTACATCG	2340
TGTAATCTTT	TTTGAAATTA	TTCAACGAGT	ATTTGTCCCT	TACTTTGAGC	CTGTTTGAGA	2400
AATTTTATTT	CTTTAGTGTA	TACATCATCT	AATTCGCTCA	ATTTTTCTTT	TTTCATTTTG	2460
ATTTCTGCAT	CAAAACGATC	TTCAAGCTTT	TGAAGTTAAA	CTTCACTTAG	TTTTTTAAGT	2520
TCCTCCAAAT	CTTAGTCCCG	TTTTTTTTCAA	CTGCTTTAAT	TCTCGCTTTT	TCATGCCCTT	2580
TGAAAATTC	CCAAATAAAA	TCGGTCAATG	CTGTTATAAG	TTCTGCAACA	GCTTCTCCCC	2640
AAGGTCCAAG	AATTTTTTCA	GCGGCTTTTA	ACCCACTTTT	CCAAGTTTCG	TACATTTGTT	2700
TTGACATTTT	TTCCAAAAC	TCACCCCAAT	GCCCATCATG	AATTGCTTCT	CCAATACTTT	2760
CTCCCATATC	CTGATTCAAA	AAATTACAGC	TGACCGATAG	ATCTTTCATA	AAGGCCTTTA	2820
GGCgTCTAAC	ATGCGGTCAT	ATAAGCTTTT	TGACGTATCT	TTAGCTTTCT	CAGCCATTTG	2880
TTTTAGAGAG	TTTCTGATGG	TTTCATTTAG	CTTTTCGAAT	TGCGATTTGT	GCTCATTCAC	2940
GAATTTTTTG	TACATTAATT	GAATGTCGGA	TGCCATCTTT	TCTTCAGCAC	TTGCTCTTTC	3000
TTTTGCTGGA	AGTAACATTG	TTTTCTACTC	TAAGTCGGTT	ATTTCTTTTT	TGCAGAGCTT	3060
TTTGAGCCTC	GACAAAAGAT	CGATCTAAAG	AGGTTTTTTC	AAATTCCTTA	ACCTGATTTT	3120

933

CAAGTGCAT	TACAACTG	CTGTTAGACT	CGTTCAGAGT	TTCGAAACTT	TTTCCATATT	3180
TTTCTACGAA	CGCTTTGTTC	TTTTCATTGA	TTTCATCATT	CAGTTTCTGT	AAAGCACTTT	3240
CTTCATCTAT	ATGGGGTAGG	GTTAATCGTA	TTTTTCTTTC	ACGACTTTCT	TTTTCTTTTA	3300
GATAGATACT	AGTCTATTTT	TATCTAGATT	TACCCCCCA	AAAAAAGCAA	ATTTACTTTT	3360
GTATTTTGT	GCTTTTGTAT	TGTTAATAAT	TTGACCTGTA	CATCGATTTC	TTTTATTTAC	3420
CATTTGCTTG	TACGCTGTAA	GTTCTTGTAC	TAGAAAACG	ATATTGTCTA	TTTGCGAATC	3480
AAGGTCTCCT	TCCTAGTCAA	TTTTGAACTT	AATGTTGTAC	TTTTTTTCAT	TGCATCCAAA	3540
AATGCAAGCT	TAGCGTCTTT	TACACTCAGA	ATATTGCAA	AAGGTGGAGC	AATTTTCATAC	3600
TGCTCACAAG	CTTCTCATAA	ATTTGACAAA	ATTTTGGAAAT	CTTTGAAAGC	ATTAACCTCG	3660
GTTTGCCCTT	CGGCTTGTTC	TCAAGCTTTC	GTAAAGTTAC	TCTCAGCCTC	AGCAAGTCGT	3720
TTTTCAAAAT	CTTCTCGTGA	TATCATGTCT	GGCAATTTTT	TTTCATCAGCC	ACTAACCGTT	3780
CATATTCTTC	TGAAGATATT	GTTACAAGTT	CTTTGTCAAT	TTTTGGCAAA	GATTCAGGAA	3840
TTGTAACAGT	TTCTTCATTT	ATTTGTTCTT	GCATATTGCC	CTCCTTAAAA	TTAAATTTTC	3900
TAAATTTGCA	AGTACTGATT	CATTTTCATCT	TGTATTTTTA	AATACAAACT	ATCATTTCCC	3960
ATTTCTTTTG	CTTTACTTAA	AAGCTCCACA	TAAGTTGCTA	AGGTTTTTGC	ATGTTTTTCA	4020
TCAATTTTGG	CTTGTTCTTT	TTGACTAATT	GGTTTTACTG	GTTTGTAACA	CCAATTAGAG	4080
CTCAATCCAA	ATTTTGAAAG	TACCGCATTA	ATGAATGGCG	GTACCATTAG	TTTGCATATC	4140
TGTTAAATGT	TTAGATATGA	TAAATAAATC	AAGTGATAAA	TATATGTTTT	TCTTTGCCAA	4200
TAAAGTATTA	GACGCGCTTA	AAATAGAACG	AATGAAAGTA	TCTATAAAGA	CAATAGAATG	4260
TATTTTCTAG	AACCTTCACA	AAGTATTAAT	CTTATAGAAA	AGAAAGAAAG	TACAAAAAAA	4320
GAAAATAGAA	TTATAATATC	ACTTGGCGTG	TAGTGATATT	ATAATTCTAT	TTATATTTAT	4380
TCATTAAATT	CTTTAAGATT	TTGTATTATT	TCGTCAATTT	CTTTTGTAC	ATTAATTGTA	4440
TAGCTAAGCA	CTTTTATAAC	TTTCTCAAGA	TGTTCAATTT	CGTCTTCATT	TTCATTAATA	4500
ATAAGTTCTT	TCCCTTTTCT	GTACTTTAAG	TAACTTTTAA	GCACTTGATA	ACTTCCAATT	4560
TTGTATTCAT	ATACTTCTTT	AGCTACATTA	GTAAAACAAC	ATGTTGAATT	ATAGTAAAGT	4620
TCTTTTGTGT	CTTCTTTATA	AGTAATTTTC	TCTACAATAC	GATTATAGTC	TCCAGTGTGA	4680
TTACCAATAC	TATTGTTGAG	CTTTAAATTA	TCTTTTAATA	AATGAGAATT	AATGAGTTTA	4740
GTTCCAAGCT	TACTAAGCTC	TAAAAATGCA	TCTACATTAT	TTACAAAAAT	AATCTTAGGA	4800
TAGTCTATTT	TTAAAAATTC	GTAGAATTTT	TCTCTATAAG	TATTTGAGTA	TAGCACTGCA	4860
TAGATATAAC	CAAATATTTT	TTCTGGAGTA	AATATTTTAC	TGTATTTAGT	ATTAATAAAT	4920

TCTCTAAAAA	TATCTTTATT	GTCCTTTTCA	TCCTTCTTAA	AGTTTTCCTT	TTTATATTTT	4980
TTAAATACAC	CTTGATTTTC	TTTTATATAA	AGTGGAAGAA	GATAGCATGA	TTCACTACCT	5040
TTATTTGAAA	CAAAACATTT	ATCCGAAATT	TCAGAAGTAA	CCAAAGCATG	TTTAAACTA	5100
TTTGTTGATA	AAAGCCTTGT	TGTAACAAGT	CCTATATTGC	CTTCAATTTT	TAAAATATGT	5160
TTCAATTGTTT	TATATCTTGG	CTCTACTACA	ACCCCTTTAT	TTTTAGAATA	ATAAGTAAAT	5220
CTATTATCAA	ATGGTCTATA	TGATATTTCT	TTAACATAAC	TTTTATTAAA	ATTGGTATTT	5280
TTTAAAAATT	TTTGAATTTT	TGATAACTTC	CAAAACATAG	AATCTTTTTT	TATATCATAT	5340
TTGTTCCCTG	CATCTTGTTT	TGGTAAATAT	GCAAAATCCC	TAAGTTTATC	CATAAGGTTA	5400
TCTTTTGTAT	AATCAATCGC	TATTTTGTCT	TTTCTAGTTA	CTATTCCAAC	ATTAAATTCA	5460
TTAAAAATAT	CTATTAAAGA	TTTTCCTTTA	TTATAAATAT	CTTCATTTGA	TAAATCTTTT	5520
TTAAGAAAAA	AATAATTAGG	CTCTTTATAG	TCAAGTTTTT	CAAAATTAAG	ATCATAAATA	5580
TGATTTTTAT	TTAAAAATC	ATATTTATGA	TCTCTTTTTT	CTTTTATACT	GCTGTAGTAT	5640
ACATTAGCCA	GTTCAATTCT	TTTTTCTTTT	TCTTTATATT	TAGCAAAAAT	AGCAATTGCA	5700
ACCCCAAGTT	GAATGTCAAA	TACATTTTCA	TCTATACTAC	CATCGTCAGT	TTTTTCTTTT	5760
TTACGCGAAC	TACCATGTAG	ATTAAGGATG	TAGATTTTCAT	CAAAAGTGCT	TAGCAAATGA	5820
TGTCTCATGC	CTCTGAATGT	GATGTTATCA	AGGTATCCAT	TGTTTGTAT	AATCCAAGA	5880
AGTCCTTCTT	CACTGCCTTT	AATAGTTAAC	AATCCTTCTT	TTTTATTGCT	CTCTAATTTA	5940
TTCTCTGCAA	ATCTAATAAA	CTTAACATAA	TCATCATTA	GTGTTTFACT	ATTTCTTTCA	6000
TTTATAGGAC	TATTTTTTAT	TTTTTTATAA	TCATTAACTA	AATTCAATAT	ATATTGATTA	6060
TTATTTTTTG	ACTCTGCACT	ATAAGGAGGA	TTTCCAAGTA	TTACTAGTAT	TGGATTACGT	6120
TTAATTTTCAT	TTGGCTTCTT	TCGTCTCTTT	TGCAATATCT	TTAAAAAAG	AAAAAGAAAA	6180
GAATTTCTGA	TCTGTAAATTT	CTTTTAAGTC	AAGAGTGTTA	GTAAAGTACA	CTTTGAGCTT	6240
TGAATCCTTA	TTAAAGTCAA	CTTTGCAAAC	TTCTTTTAAA	TACTGACTTA	ATTTAAGGTG	6300
TGTTACAGCA	TAAGGTGCCA	TTAAATATTC	AAAACCATAT	AAGTTTTTAA	GTATATGTAG	6360
ATTAATATAG	TCTTTTGTTC	TACCAGATTC	CTCTGGGATT	TCCTTTAGTA	TTATAGTACG	6420
AATAACTTCA	AGTAAAAATG	TACCTGTTC	TGTTGCAAAG	TCCAGTACTG	TAACTTTTTC	6480
TTTATTTGCA	AGGCCATGAT	TTAACTTAAA	TTCTTTTTTA	AGCATTTTCAT	TTAAACTACT	6540
AACAATAAAA	CTAACAATAG	GGCTAGGGGT	GTAGTAAACT	CCTTTTGCCT	TCCTTAAGGA	6600
TACATCGTAT	TTAGCAAGAA	AATCTTCATA	AAAATAAAGA	TAGGGATCCT	TTAAATTTAA	6660

GCTAGAATTA	GTAAATGAAA	ATTCATTAAA	AATAAGTTTT	GTATCAATAT	TATTTACTAT	6720
GCTTATAATA	CTTTCTAAAA	TCCATCTTAA	GTAATTAAAT	TCACATCTTT	TATGGATATC	6780
TTTAATTAGT	TTTATAATGT	TTTGTATAAG	TGAAAAATTA	GTAGGTATAA	AGTTTTCAAT	6840
ATTTTTAAAA	TTAATTTCTA	TATTTTCTTT	ACTATTAAGA	CGAGCAATAA	AAAGTCCATA	6900
TGTAATAGTT	TGAGCGATTG	AATCTGAAAA	TTCTGAAATA	TTAAAATCAT	CGCTATAAAT	6960
ACTTTTTTTA	AGTATTCTAC	AAGTTGAAAC	TAAAACATTT	AGCTCACCTA	GTTCTGATTC	7020
ATCAATATCT	AAATTTAGTT	TTTCTTTATT	TTCTTTTAAG	TTTACTTCAA	TCTCTTCTTT	7080
TAAAGATTTA	GTTTTACTTG	CAAGTAGGCT	AGCTAAAGCT	TCAATACTTT	TTATTTTTTTC	7140
AAAATGAGAG	TTAAAGAACT	CAAATAAAAT	ATTTATAATT	TTGGTTAATT	TATTTTTTATC	7200
GAGTTTGGA	TCTTCACTAT	ATAGCTCTTC	TTTAGTTAGT	AAAGACCCTC	TTAGTTTAAT	7260
CTCTTTGTCT	TTAATCCATA	TAAACTCAAT	ATAATTTGTA	AGAAGTATAC	TGCGTGTTAT	7320
ATTTTTGTAT	TTTTCAATTT	GGGAACTTT	TAGTATTTTCG	TCTAAGTTTT	GCTCAACTTT	7380
TTTAACTTCA	ATACACCCTA	TAGTACCCTG	GGTTATATTA	TGTCTAACAA	TATAGTCGGG	7440
TGATCCAAAT	CCTTCTTTGC	TTCTGCTTGG	CTCATGCTGA	ATAGCAATGC	TTGAATTTTG	7500
ATTAATTTTA	TTAAAATCAT	TAAGTAAATT	TTCTAAATGA	GTTCTGTTAG	AATACTCTGT	7560
TTTTTCTTCT	AATTTTGTA	TTTTTAGATT	AGCTATATAT	TCTTTTGCCT	TTTTAAATAG	7620
AGATTCATTA	TTATTCATTT	TTATAAATAT	AAAAGATATA	TAGTTTAATA	TCAACTAAAC	7680
TATATATTTG	AAAAAACTAT	TTTTGTCTTT	AGCATATAAC	AAAAATAAAA	CTTCTAAGT	7740
TTGATATAT	TGCTTTCATG	TCAGAATTTA	ATTTTTTCAA	TGTTTTTAA	TTTTCAGTTT	7800
TAATATTATT	GCTATTGCTA	CTATTTATAG	TAAATTCCTT	ATTATTTTTT	TATTGTCTAA	7860
TAACACGATT	TTTTTCATTAA	ACATACTAAA	AGAGTTTTTA	ATAATATTCT	TAAATATTTT	7920
ATCTGAATTT	TTCTGATCAA	AGTTAATTTT	AGTTTTTAAA	AATTTAAGAA	ACTCATCGCT	7980
TGTATTCTTA	ATCTCTTTTT	TAAATAAACT	AAAAATTTGT	CTGTATATTT	TTTCTCTAAT	8040
GTAAAAGATC	TAGCTTCTTC	AATATTTTAA	GAATTTCTAG	AAAATTTTTT	AAGATATTCA	8100
AAATCTTCAG	ATGTTAATTT	CTCTAAATTA	ATAATCATAA	AAGGCTCATT	GTCTAGTGAA	8160
TTATCTTTAT	CCAAATGGCA	TAGAATATAG	ATTCTATGCC	ATTTGGTAAT	ATGCCCAATT	8220
TAATTGCATA	TTTAGAAAGA	AGATTATAAA	AATAATCTGA	TAATTGACTA	AAATGATTTT	8280
CAAGATTTTC	TTTATGATGC	TTAACTTCTA	AAAAATAGTA	GGATTTTTAT	CCTTAGAATA	8340
AAGAACATAG	ATCGCTTTTA	TTTCATTTTT	TCTAGTAACA	ATAATTGAAA	CTTCAACTTA	8400
AACACATGAA	GGATTAGTAT	GACAATAACT	CATTGCATCT	AAAAATGGGT	CAATAAAAAA	8460

CGGTCTTTTT TTTAGCTTCT ATTTTAAGAC CATCCTTATG AGTTTGTATT TTTTFACTTA	8520
CAATACATTG ATATAAAAAT TTACCTAATT TCATTATTAA TATATTTAGT AGCGTTTTTA	8580
ATTACAATTT TTTATATACC TAATGATAAA AATACAGATC ATAATCATAG TAAAGAAGAT	8640
TTAAGTTTAT ATATTATGAA GTTTAAAAAA ATTGTAACAA CATTATTACA ATCTAAAGAA	8700
CTTTTAGAAT TATTTATTTT AATTGGCTTT ATTCAATTTT TTTATCAACC TTTTATTTTA	8760
AATTGGCAAG CAATTTTTAT TGACAAAACC ATATCTATTA GTATATTTGG AATTATCTAT	8820
GTGCTATTTA GTTTATCAGA TATTGTGGGG GCATGGGTAT TTAGAAGAAT TAAACATACA	8880
AAATATGATA TTTATATCAT ATTAACCATA ATATTGTTGT TATAAGCTTT AATAAAAATA	8940
GTTCACATA TTTATATATT TATTGCTGTA ATCACATTTT TAGTAATTTT AATTGCTATT	9000
TATTCTAACA ATTTAGAATA TTTTTTAAGG AAAAATATAG ATTCAAAGGT TTTAGGAACC	9060
ATAACTTCTA TTAATAGTGT AATATCCCGC ATATTTTCAT TTTTAGCATT GGCTATATGT	9120
TTGAATTTAA CTAATTTTAT AAGCGCTATA AATACATTTG TTTTATTAAT ACTTATTTTT	9180
TGTACATTAT CTATTATTGT GGTGATTGCG CAACTATAA TTTAATTTTT AAAAATATTT	9240
AACCTATAGC TTAATATGAC GTTAGATGGA TTTAATTTAA TTAAATTCGA GTTAAATGTG	9300
CTTTTTATTA TCCCCGTGAA AACCCTTTCA GCAGAAATAA TACAAGAATT TTTAAGCCAG	9360

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8905 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

AGTCTGAnGT GGGCCCTTnA ATATAAATAA AAAGGTTGAT AAAAAAATCG AATAGCGTCC	60
ATTAAAATAA ATAATTCTAA AAGTTCTTTA GATTTTACTA ATATTTTTTTT AAACTTTATG	120
GGATATAAAG TTAAATTTTA TTTATTATGC TTATGATCTA TATTCTTATC ATTTGGTATG	180
AAAAAATTGT AATTAAAGAG GATATTAAAT ATTAAATATT AAAATATATT AATAATAAAA	240
TTAAGTAAAT TTTTATATCA ATGGTAGTAT TTTACAATTT ATTTTGAAT TTCATTCAAT	300
ATGGGCTACT AAAAATACTC GAGACAGCAT AATCTTAAAT AAAAAGAATA CGGCTTCTAA	360
AAGAAAAGTG AAAAGTAAAA GAAGTTCTAA AGAGAAAAAT CAAAATTATT TATACACTAA	420
ATAAATAGTT CAAGGTTTAG AAGAATCTTT AAATAATAAT AAGTCAAATG GAACTAATAG	480

937

TGGATCGGGC TCTGCGTTGC TTGAAAATTT AAAAAAAGTA AAAAAAAGGT TGTATATAGA	540
TAGTTGAAAA ATCACAAAGT TTGTTGCATA TAAATCATGC AAATGAAGCA TTTAAGGAGA	600
TCAGTTCTGC AAAAGATAAA ATTGACAGTT CCGATATAGG TAAAGGAATT GTTGATGTTT	660
AAAAACGCA TAATAGATTA CATGATTTAT TGCGAGACAT AAAGACTGAA TTTTATAGCC	720
AAAAGAATTC ATTTTAAAT GGTGTTAGAG CTGAGAAAAG TAAGAAAAAG AATCAAATAC	780
TATTTAGATC TACTTCCTCT ATAAATGGAA AAATTAGAAA TGCAAATTAT ATACTTTAAC	840
ATCCTCTTTA AAAATTTTCT AACTTGGTTG TAGAAGCCGT GCAATTGCTA TTTGAGAGCA	900
TACCATTTTG ATTTTAAATA GCAACTCACT AATGATTTAT AGTGCTTTAT TTATTGTATT	960
CAATTCAAAA AAATACTAGA TCACCGGGTT TTGGTGCTGG GAATATGGAA GAAAGCAGAA	1020
AATTATGTTG ACAAGTTTGA TGAACCTATA ATTGTCAAGA ATAAAGAATT ATTTGTTATT	1080
TAAATTGAAA GATATGATTC TAATAGAAAA TATTATCCTT TAATTAGATT TGCAAATTTA	1140
ATTGAATTTG AAATTTTAA AATTTAATTG CAGAAAACT TTTTACTGAC AATCAAGTTT	1200
TAAACAATTT CAACAAACAA GCAAGCTTTG ATTAAGCCCG TTTGTAACAA AACATCTGAA	1260
TTTTTAAACA GCAATGCACT AAGTGAGAGT TCTTTTTTTA TTGAATTATA TCTGTTAATT	1320
TAAAGCCCGT TTATTGGTTT TGATATGTAG AAGCTTTGAG AAGCTTGAAT AATTGTTTG	1380
ATGTGAAATA TATTTTTATA ATAAAAATC CAGCTATTAT AAACAAAGAT TATTAACTT	1440
TAATTTACAT TAAAGGGAAA GAACAATACT ATTTTATAAT TTTTCTTTTT AGAGAATTTT	1500
TTAATTAAAA AAGTTAATTA TACATACATA TTTATATAAA TATGTATTGA TTCTAATTTA	1560
ATTATATTTT AATTATCTCT TGAGTTAATT AAAATATAAT GACAATAATA TACTTAAAAA	1620
GTTTGCAGGT TTAATGTTAG GTGTTGTCAA GGGTATCTTT GTTGCATCTT AAATCTCTAG	1680
ATAAATGTTT TTTCTCTATG TAATATAACC TTTCTCCTAA ATGTCGTATC TATAAAAAACA	1740
TAAGCCCCAG GTGTTTTTAA GTTTTGTAA CTTATGTATC AAAAAAATA TACATAATAT	1800
TGGTTCATTG CGGCGTGTTC ATACTAATTT TGTTTATGAT TATGCATTTT GGTGTCAAA	1860
AATAGCTGAA GATTATTTTC CAGATGCAAA GGATATAGTA TGTATAAGAG GTATTAAGAA	1920
AAAGCCTTAT ATATAACAGT CCTACTGCAG GGTATAACGA TCATTACTAT GCCTGGATAA	1980
ATAATGTTAA AGTCGTAATA AAGCGGGCTA AAAATATGCT TAAGATGTTA AGCATAAACA	2040
AAAAATACTT AACGACAAGA TAGATCAAGC AAAATTAGAC TTTGATAAAT TAAAAAGGAT	2100
ATATGATACT TTTAAATTT TAGACCCTAG ACCCTAGACC CTAGACCCTA GACCCTAGAC	2160
CCTAGGTAGC AAAATAAAGG CGTAAAAAAA TAATAGCTCC CTTTGTAAG TTTATTATAA	2220
GAGAACATTT ATTGCATTTT TATTTTGTGA ACAGATATAA AAACAATCCT ATTACTGCGG	2280

GAATAAATAT TCCTAATATC CAGTAAATG GAAATATTAA ACCTTTGACT TGTTTACTAA	2340
GTTCACTTCT TACGTCTGTT ATTTTGTAG AAAGTTCAAT TCTTGCTCTT TCTATCTTTT	2400
CATCTAATTT TCTTATTCCA TTTTAAAT CATCTCTAGC TCCCAATCAT TTGCTTTTCA	2460
AGCATACTTA TTCTGGTTTC TAGATTTTCAT TAATTAGAAT TTAAATTGCT AAGTAACATG	2520
TGCTCTACAA CATCTTCTGG AAAATCTTTA TCAAGATGGC GATATTTTAA AAAAAATTAC	2580
AATTCTTTTT AGTTTGCTCT TGATATTGCT TATCTCAATA CTTATTAAGT CAATATCCG	2640
TAATAAGTTT CTATGCTTTT TGAATACAAG ATAATAGTAA GTATTATATA CAAATAAAAA	2700
CACTATTATT AATTTCTTTT TATTACAAAA ATAAAAACAG AGTTAAATGT ATATTATCCT	2760
GTAGATTTCA TTTTAAATTA AAGATTTAAT AGAAAAGGAA GGATAAGCCA GCACAAAATT	2820
ATTCTTCCTT CCTTACTTCC ATCTTTTATT TATTTAAGTA TTTAACAAGG CCACAACTTC	2880
TTGTACTATT TCCTTTGCAT TCTTAGCTAT TTGTAATACT AACTCTGCTG CTTCTTTTAT	2940
ATCTGCAAGC TTTGTATTGT TCGTAGTTTC TGTCTTTATT TTATCCAATG TCTCTTTGAC	3000
TGTATTTTCT ACATCAATTA ACTTATCTTT TGCTTCTACT GTAGCTTTCC AAGCTATTTT	3060
TACGGCCTCT TTAGCTTGTT TTATTTTCAGC AGAATCAGAA TAGTCAGATT CTGATTCTGA	3120
TTCTGATATT TTTTGTGCT CTTTATACAG TTTTGCATG TTTTGTCTG CTGCTTTAGT	3180
AAGGCTATAT GCTTCTTTTG CAAGATTAGA TGCAATATT GCTTTATCAC TAGAGTTCTT	3240
TATTTTTTCT AAATCTATTT CTGCCATTTG AGCTAAATCA TGCATATTTT TTGTTGCACT	3300
TTTTACTTGA TCTGCAGCAG ATGAAATTAA ATTAAGTCA TTTATAACCG CTTCTACAAC	3360
TTTATTTGCC TCATTTGATG CATTTAAATT ATCTGTTGTA TTTTGGCTT CTTTGTAGTA	3420
ATTTGTAGTT TGCTTTAATA ACTGATTTAA CTCACTTAAT ATGCTCTGTT TTTTGTATC	3480
GTAATTTGAA TTTGCGCTT CATTATCTAA ATATCCTTTT TGATTATTTA AATTAGATTT	3540
TGATGATAAT TCTTGTTTAT CATGAACACA AGATATTGAG AGCAATAAAA ATAACTTAA	3600
CAGTAGTATT TTTATTAATT TTTTCATATT TATACTCCTT AAATATAATG TCTTAAATTA	3660
TATTTTAATA TCAATTATAT TTCAATATCA ATTATATTTT AATATCAATT ATATTTAAT	3720
ATCAATTATA TTTAATATC AATTATATTT TAATATCAAT TATATTTTAA TATCAATTGC	3780
CTACTAATTT CTATTTAGCT TGGCTAGCTT AAGGCTAAGA AAACAATAGT GAGTATTGAA	3840
AGGATGTTTA ATGATGCTAA AAACAAGCAA AAAAATTAAC TTTTATAGAG AATTGTCTTT	3900
AATTTGCGGT GTTATCTATA AACTATGTGA AAAGCTATTA TATAGCTAGC AAGCTTTATC	3960
TAATAATAAG TCTTTGAAAA ATGATAGTAA AAGTATGGAT TCTCCTAATA ATTTAGATAA	4020

CGGTATTTTA	AATAATGCAG	GAAATACAGT	AGAGACGTAA	GGCTAGAAGT	ATGATTATTT	4080
TTATAATGTT	GATGAGCAAA	TTAATAAAAA	AGAATATATC	TTAGTATAAT	TCCATGCTTG	4140
ATTACTAATA	TAAGAGAGCC	TTCTTTTAAA	GAAGGCTCTA	ATTTAAATAT	ATTAATATTT	4200
AAATATTTTC	TTATTCATTT	TAAGATTTAC	TTAAAACAGT	CTTTGCATTT	TCAATAAGTT	4260
CTTTTATAAT	TCTCCTTCTT	CCCATGGCCA	AACCTCTTTT	AGAAGAAGAA	GCTTCTAAGC	4320
TCTTTAAAGC	ATCTTCTACT	TTATTTAAAG	CCTGTCTAGC	TAATTGTGAT	GCCACTTTAT	4380
TTTCACTTTC	CAATCTTTTA	ATAATGCCTT	CTTTTAAAAAT	TTCTTAGCT	TCATTAAAAA	4440
AGAAAGCCGC	AGATCTTATC	TCTTGTCTTG	CAATATCAAT	GTGAACCATA	ATTTTCATCAA	4500
GTTTCATCCAC	TATCTTTAAA	TTATTTTGCA	ATTGTGTTAG	TTCTTTTATT	TTATCTCTAT	4560
TGTTACGACC	ATTTTTTATT	AATGATGTTT	TTTTGTTCCT	AATTTTAGTT	ATCACATCAT	4620
AGAAATTATT	TCTTATTAAA	GTATATTCAT	GTTTAAGTGA	ATACATACTC	TCAATTAACT	4680
CGGGAAATCC	AGAGTCTCTA	ATAAGATTCT	CTATATCTTT	AATTGCTTTA	TCTGCTTTCT	4740
TTTCTTCCTT	AGTAGAAGGG	GAAAGATCTT	CTTTTTTTAT	CTCTTTTTTT	TGATTGTGCT	4800
TAATTGAAAT	GGTTGGTATA	CTAACCTTAT	TAGCAGATGT	CTCTAAAGAC	ACTACATGCC	4860
CTACAGGGAG	GACTGCCGAC	TCTATATTGC	CTACAGTAGT	GGGTCTTGTTG	GATGCTAAGG	4920
ATTTTGCGAG	AGCAATTAAA	CTCTCGTCTT	TCAATTCCCTC	AAAATTTTTTA	AAATCCTTTT	4980
TTTCTTCTTG	ATTCCCATAT	AAATTATTAA	GAGCATTTTC	TTGAACACTA	CTACCCAAAG	5040
TTTCTTTTAT	ATCATTTGTTA	TTTTTTTGCT	CTTTATTAGG	CAATTTAGAA	TCTAGATTAC	5100
AAGATATCAA	TCCTATCGTT	AACAATGTAT	ATAAAAACAA	ATTTTTTTTG	CATAAAAATA	5160
TCCCCCTTTC	CTCTTTACTG	AGAATATATA	TTATAAATAA	TAATAATTCT	TAATTAATAT	5220
TATATATCAT	TTTGTTTGAA	TTACAATAAA	ATATAAATAA	AAATTTATAT	TTATACTTTT	5280
TTATTTATTA	ATCATTTGCA	GAATATTTGA	TAAGCTTTGA	ACTACTATTT	CACTTCAGAA	5340
AGAAATTAAC	AAGTTGTTTA	ACTAAAAGTA	ACAAAGAATT	CTTCACCTAT	AATTTCTATG	5400
AAATTTAGGT	GGAGATGAAT	TTGCTAATAA	ATAGGTTTAT	TTTTATTTTG	AATATATTTT	5460
TTGATGATAT	CAATAGAGGC	GTTCCCTCTC	TCTATAGAGA	TAAGGCAATA	GCTTCTAGAC	5520
CAAAAATAAG	GTTTTCAGCA	ATACTTATCT	AAATAAGTAT	AATATTTTTT	CTTATAAATA	5580
AGCCTTGAAT	ATTCTGTTTT	TAGATTGTCG	ATGAATTTAG	AAGGCTAAAT	ATTGAGGGTA	5640
AATTCTAGTA	ATAAATGAAT	ATGATCTTTA	TCATGGTTGA	ATTCATTAAG	GGTTCTTTTC	5700
CATAAAGAGC	ATATTATATT	AAGTATTATT	TAGTAAAGGG	AAGATGAAAA	CCTATCATTT	5760
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TAAATTTTTA TTTT TAGCTA AAGCAGGCAA TAGCTAAAA TAAAAAACT ATTTATCTCT	7140
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AATGTAGGTT TCATTTGCTT CTTCTTTATA AAAAACTTT TTCTATGATT GGGTTTTGTT	7380
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TTTTTTAGTA AATAGGAATT AATCAGCTCT GTTCCGAGTT TACTGAGTTT TTAAATATTA	7500
AAGTATTTTT TACAAAAATG ATTTTAGGAA AGTCTATTTG TAAGTGCTCG TAGAATATAT	7560

941

TCCGATAAAT	AMTTGAGTAA	AGAATCTCGA	AAATATAACC	GAAGCAAGGA	GCCATTTCTT	7620
TAATTTTTGA	TTTCTAAATG	GTATTAATGT	TTTTTATTTT	CATTGATAAG	CTTAAGAAGA	7680
GGGTATTAAT	ACTAACATGC	TCTTCCTAGG	TAAATTGATT	TTTAATAACT	TTTTTTAAAC	7740
GACAGCTGTA	ATCCGTTTAT	TCTAATGTCA	AAATTGGATT	TAAAACCTAC	AAGCCCAATG	7800
CCGAGTCTTT	TTTTAAGTTT	TCATTGTATC	TGTTTGCAAA	TTTAAAGGGA	ATAATAATTC	7860
TAGTTGTGTA	GGATGCTGTA	ATCGTGAGTT	CTCCTTCCTA	TTCCTAATGA	TTCTATTCCG	7920
ATTGCTTCTG	TTGGTGTTTT	TGACGGGATG	CTTCTGATAA	TGTATCCAAG	TTATCTCAAG	7980
TATATTTCCC	CGAGTACCTG	AGATCTAAGC	AATTCACCGT	GCTGCCAATA	TAATCCTCTT	8040
GGCCAAAAAA	AAGATCCTAT	TCCTAAAGTC	AAAGAGACAT	TTAAAAAGTT	ATAGTAATAA	8100
TACGGGTGCT	TTTTCGCTTT	CATATTTTCAT	TACGGCTGCA	ATATACTCAA	CACCTTTTTTC	8160
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ACTATTTCTA	TAATCTTTGA	TTATAGAAAT	AGTAGTTCAC	TATTAAGCCT	ATCCTTTTTA	8460
TAAAGGATAG	GCTTTTACAT	GATATCAATT	TCAATAACAT	AACTTTAAAG	GTTGCTTATT	8520
GATAATATGT	TATTTTTTCAG	CTCTGTTGTT	TGGAAGCTTT	TTTTTACAAT	TTGCTTGTA	8580
AGTTCCGTTA	AATGAGATTC	AAGCTTAGCA	ATATCTGTTT	TTGTAGAATT	TATATAATCT	8640
TTATAATCTA	ATAAAAGCTG	TTCTAACATT	TTTGAGATAT	CTGTTTTTAT	AGATAATAAT	8700
TTTTCAAACG	AATTTTTTAAG	CTTTTTTAAA	TCTGAAACGG	TCAGTGATC	TAGAGTCTCT	8760
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GTGCCAAATA	GGAGGGTTTT	TTGTTTTGAT	CGAATTAAAA	TCTTCGAAAG	ATTCGCTAAT	8880
TTATTGGTAT	TAATAGAATT	TAAAG				8905

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

CTCTACCTAG GACTTTAATT AAAAAATTG GATTGTnATT CCCAATGCTT TTTCTATCTT 60

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TTCAAATAAT AGGGCAAGTT GCTTTAYATA TACTCTTTAT TTTTTTTGAT TTTTGTATTT	180
AAGTGTGAT ATTATTAGTA ATATTTTAAA CTTTACTCTT AACTAAAAGC TTGTTTTATT	240
GTAAAAATA AAACACAAAC AATACCCTAT AAATAGTTTA ATATTGCAAT ATTATTTAAA	300
CTATAAAAAT ATGTAAATAA TAATTTATAA ATTAATAAAA AACATATAAG GGAGCTTTCT	360
TAATGAAAAT CAAAAATATA GCAAACATAT TAATATTTTT TTTATCTATA GTTTTAAATA	420
GCTGGGGAAA TGAGTCAAAA ATAAATACCC CAAATGAAAA TTCTCAAAGT AATATTTTAA	480
TAATCTCAGC TACAAAAGCA GAAATAGAAG AGATAAACAA GATTATTCAA AACAAAAAAT	540
ATATTTCAAT AGAAGAGCAT AGAAGAAAAA AAAAGATTGC CATGGGAAA TTAATGGATC	600
ATAATATAAT TACCATAGCT ACAGGAGTTG GAAAAATAAA TACGGCCCTT TGGACAAGCT	660
ATATTATATC AAAATATAAA ATTAGTCACA TAATCAATGC TGGAGTTGCT AGTGAATTT	720
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GTTATGATTT TGATCTGCAT AGATTTGGAT ATGAAATTGG ACATGTTCCA GAACACCCTA	840
AAAAATTTAA AGCAAACACT GCTCTTATAA GGAAAAC TTC TAAAAATAAA ATAAACAATA	900
TAACCTCATA TATGGGCTTA ATAATTACTG GAGACCAATT CATTGATCAT CAACTTTTC	960
AAGAAATTCC AGAAGAATTT GAAAACGCAA TCGCAATAGA CATGGAAAGC GCCGCAATGG	1020
CTCAAGTAGC ATACGGCTTT AAAATTCCTT TTATAATCAT CCGGGGAATA TCTGATATAG	1080
TCAATAATGA GAATAATTAC GATGATTATA AAAAATTTTT AAAAAAGCT TCTTCTAGCT	1140
CAGCAAAAAT AGTAGAAAAC TTAATTAAGT TAATGTAACT TAATTAAGTT TTTAATTAGA	1200
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ATAATAATTA TTAGAGCTCC TTATTAAAAT CAATATCTT CAATGAATAC TATTTTATAA	1380
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GATACAAAAA GCTCAATTTA ATAATTTATT TTCTTTTAT AAAACATTA AATACTCAAG	1560
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ATTCTCAAAA GAAAAGCAAA AACAATAGTA AAAATATAGA AGTAAAAGAT ACTCTTGGGC	1680
TAGTTAAAGC AATTAAAAAG TCATTATAAA AGATTGATTT GGCTTTTAAA GCATTAATTG	1740
GGTCGGGCTA TGACGCCTCA TCAACAGCTA AAAGTAAATT TAGAAAATGG CTTAAAGATG	1800

943

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AATTCAGCAA TAGCCATACA TGTTTGTTTT AATATAGATT AATTTTAAAT GCTTTTATA	2160
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CATTCCAGCA AGATATCAAT ATAAAAACAC CCAATATGAA AATATGCTAT TTAGAAAGAG	2340
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CCGTGCTATA TCCCTGTAAT TTTGACAAAA TCGTTAAAAT ACTGTAAAAG TATTTGTACT	2580
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CTACGAGTCA CAAAATTCAA AAAATAAAAG AATCAAACCTG CTATAATAAT TTAAACAGT	2940
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CATAAAGGTT TAAAAAGATA TTTAAAAAAT AAAGAATTTT TTATAAGGGA ATAATTTGAA	3540
CAATAAAATG GTAAATATTC TGACAATAAT AAGGGATAAT ATATCATACC GTATGTCAGC	3600

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ATAATGTAAA	TTTAATCCTA	TCAACACAAG	ATGAGGATAT	TATTTTTTTAT	ACAAATTATA	3900
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CAAAAATTCT	CTTAAACAAT	TATTCTCTAT	AAGGAAATTT	TTTCAACAA	GCATAAAACA	4500
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AAATACTATG	TATTTAATTA	AATTAAATAT	TTGCTTATAA	TAAATATAAA	TAAATAAATA	4980
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CGCCTACTGA	AAAATCAAGG	CCCAAACTG	AAAGCTCTAA	GCAAAAAGAA	TCAAAGCCTA	5160
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GTGATCACCT ATATTTCAAA AAAGACAATC TAGACAAACT AGATATTGCA GATTTAGAAA	5700
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CAAAAACCAC TATAATTTAA AATATGCATT CGAGAACTCA AATGTAATCA AGTTTACTAA	7140

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AGAAAATATA AAAAGCTCTA AAGAGCACAA AAAAGCTGCT CTATTGGTTA AATAAAAAAT 7200
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TAATCATTAT TAATAGATAT TAAATATCAT GTCCAATATT ATATTAAGAC ATGCAACTAA 7560
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AAATATAAAA GATATACCCA AAGTAATATA CTTTATTA 8318

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(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7624 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

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nTTCGCTTTA AATTAGTTT AAAAnAATAA TAGCTATATT TTCAAATTAT AAATAGTAAAT 60
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GAGTGTA CTC TCATTTATTT TGCCATATCC TCTTTAACAG ATATTTATCA AGAAACCAAA 180

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947

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ATCCAAAAAA AATTGAAAAT TGGTTTAAGA TTTTAATAGA GATTTTAGTA ATTTAAAATA	600
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GAAAAATTAA TATTTATTAA TCAGTAACTT TTATTGAATT TTAAAAATTA AAAACATTTG	1440
CTTATAAATA TTCTCTTTAA AGTTTAAATA AAGTTTAAAT GTTGAATTAT TTAAATATGA	1500
TAGACCGTTT GTTTTTTAAA AGTATGGTTG TTTTGTATT GGGTTAAGAT CAAATTTCAA	1560
AAATGAGTGT ACAGTATTGA ATTTATTTTT TTTATTATTT TTTCAAAAAA ATTAGAATTT	1620
ATTAAGTACT GAACTAAAGT TTGAATGGGG TAATTTATGAG AGAAATTAGT TGTTGTTTTT	1680
TATTATTAAC TTTTAGTGTT GTTTGTGTAT ATTCATTTGA TGTTTCAAGT AGAAAATTTT	1740
ATGGCATATT GGAAGGTTAT TATTCGGGCA AAATTGAGGA ATTGTCAAAA AAAAATGATG	1800
AAGATGTCTA TATATATAGG TTTGGTAAAT TTAAAGAAAC ATTGAGCGAA ATGAGCTCCG	1860
GCATCAAGTC ATATTTTTTT AATCTTGTG ATTACCAAAT TGCCAGACTT CTTCAGAATA	1920
AAGAAGGAAG AAGGAATTCT TCTAAAAGTT ATTCTGTTTT AAAATCCACT CAAAAATCTC	1980

TTTTAGAGCT CATTCATCA ACAGATTTTA AAGGTTTGA AAAAACCATT CAAAGCGATA	2040
TTTGCAGGAT CTTGGGAGAT GTTAATTTAA TGCTTTTGAG GTATGCGGGA GGTGCAGCTT	2100
TAAGCAAGCT TGCAAATGAG GCTAGAAAAT ATTTTGAAAA GTCCTTAAAA ATTAATAGTA	2160
AAAACTCATT TGCCAACACT TCTCTTGCAA GTTGGTATTT ATATGCTCCA AGGATTGCGG	2220
GGGGAGATCC AAATAAAACT TTGTCATTTG CTCAATTAGG ATTTAAATAT GGTCAAACAG	2280
ATGTGGAAAA ATATTTTGCA AATATATGGA TAAGTCAAGC TCATTTCCCTT CTTAAAAATG	2340
AAAAAGAAAG CCTTAAATAT ATACTCAAAG CTGGTGAAAT ATTTCCCAAC GGAGCTTTTC	2400
ACAAGATAGT TCTAGAACAA AACAAGGCTG GAAATTTGTT TATGGATTTT CCTATAAAAA	2460
ATTAGTTGAA TAAGAAGTTA ATATAACTCA TTTAAGATTT ATGAGTTATG AGATAATTTT	2520
TATATGTTAA GGGCATTGTT AATTTTMTTA GTAAATATTA GCCTATTTTC TTTTGAAAAA	2580
GAGGTCAAAG TATATATAGA TAAAATAGAA AGCGTTCATA CTAAATATTG TTCTGGTAAT	2640
TTTGAGTTTG ATTTTMTTTC ACCCGATAAA ATTTTACAA ATGAGCTTCA AAACATAGAA	2700
AATGTTATTT TAATGAAATA TAGAAGGGAA AGTATTCAAT ATAATTACTT AAATTTACTT	2760
ATGCTTTTGG TTTTGTGTGA CGTTCTTAC TTAATTAATG ATCCACATAA ATACAATGAT	2820
TTGATTCAAA AACTAATTCG CAATTATAAT TGTGCTTTGA AAATTTCTTT AGAAGATGAT	2880
AATGTTCCAG CGGATTATTT TAGGGCATTG GGAGAGCTTG CTATAAATTT AATACCGCAC	2940
AATAGGAAAG GATTGTATTC TTATTTTGTT AATGCCAAGA GGCATTTAGA AACAGCTTTA	3000
AAAATAGATG GTGATAACGT TAAAGCTTTT ATTCCCTGT CTATTTTATA TACAGTTAGA	3060
GTGTCAAATA GAGATTTTTA TAAGATTCTA TTTGCAAAAA GCTATATTGA TAGAGCAGAA	3120
GACAGCAATC TTAATGATAG GCAAAAATAT TTGAAAGAAT TAGTGAAAAG TTCTTTTMTA	3180
ATTCGCACTA ATAGAAGATT GGAAGCAATT GAATGTTTAA AAAAGCCAC AGCCATATTC	3240
CCTAATGGGA ATATGGCTGT GTTGGCAATT GAAAAATTAA AAGAGGGCAA TTCTTTCTAC	3300
TACTAGAAAA TTATTTAGAA TTTAATTTCA ATGAAGATTG AAGGTATTCA TGAAAAAGTT	3360
TTTATTTTTA ATATTGCCCT GTTTTGGGGT GTTTGCAAAT GAGTTAAATG ATGAGCTAGG	3420
TGATTTTGTA ATACGCGGAG TGGATTTTGA ATTTCTCTT GATTATCTTA GTGTTCCAAA	3480
TAATTTTGAA AATAATTTTG ATTTTATTTT AAACATTAAG GAAAATGATT CAAAAATCTC	3540
ACCTTTTMTT AGATTAGGAA CCGATTATTC TAAATGTTT TTATTTGGCA CTGGGCTTGC	3600
TTATGATTTT AGGAAATTTT TTTCTAAGGT ATTTTATGAA ATTAGGGTTC CGTTTATTTT	3660
TGATTCTAAA AATATTGAAC ATATTGGTAA TTTTGAGGTT GGTATAATT TTGATTATTT	3720

AAGACTTGAA AATAGATTTA GATCGGGATT GATGAATCAT TTAATCAAGG AAACAGAAGC	3780
TAATGTTGGT GGATCATATC ATAATGCTTT AACCGTGGAA AACACGGTTG CCATTTTACT	3840
TCCAATTTAT TACTCAGAAT TTCAGCGAGC AGATATTAGA ACGTCTTTCT TATATAAGTA	3900
TTTATCAGAT AATAATGAAC AGTTTATAG AGTACATTGG AATTTAAAAT ATCTTGTTTC	3960
TATTCCTTTT GGAGAATTGG GATTTAAGGC CGATCTTGA GTGGCAGGCG ATTTTAAAAA	4020
GTCTTCGTCT TCTATTTTTG AAACCGGATT TGATTATAAT GCTTTAAATT TTTATGCTTT	4080
GACTATTCCC AAAATGGGTC AAGACAGTCT TTATTTTAAT GTTGTTCTA ATTTTGGATT	4140
AGAGTATAGA TTATTTTTCC TTGAATCATT AAAAACTT GCTTCTGATT TATTTTTAGT	4200
ATTGTCCGCA GATATTGGAT ATGGGATAAA AGAGGATTG CTTTLAGATA AAGGAAAGTT	4260
TCTTTATATT TTGGGTTTTG GAATGGGTTA TAAATTATTT AAGGAAGTTC CTTTTGTTTT	4320
CAAGGTTGGC ATTAATCAGG ATAAAAAATT ATCATTGGA TTTTATTAA GTTCAATAAT	4380
TTTTGAGTGA TATTTTTTTG GTAAAGCTTT TTAATTTTA TGGTTGAATT TGAAATATAG	4440
GAGGTTTTGT GGGGAATGTT AATTAGATT TAAATTGGT TAATAAAAAA TACAAAATTG	4500
GACAAGAAAT TATTCATGCA AATAAGGATA TTTCACTTAA TTTAAATCA AGGGACATGG	4560
TTTGGAATTC AGGGCCTACG GGGAGCGGCA AGACAACCTT AATGAATTG CTTTCTGGAA	4620
TAGATTCTCT TGATACAGGG GAGATCCGCT TCAACTCAAC TCTTTTAAGT TCAATGAATG	4680
AAAAGGATAG AACTTTGTTT AGAAGGTATA ACGTAGGGTT AATCTTTCAG CATTTTGAGC	4740
TTATCCCAAG TCTTACAGGT TTTGACAATA TTTCACTACC TCTAAGATTC TCAAGAGAAA	4800
GTGCTAAGCG ATTAAAGTCT AAAGCGGAAG AATTGATAGA ATTTTTCAAA CTTTCAAAGT	4860
TTGTGAATAA AAAACCTAGA TATATGTCTG GAGGACAAAG GCAAAGGATA GGAATAGCAA	4920
GAGCCTTTGT TTATGATCCC AAATTAATAA TTGGAGATGA AATAACTAGT CATTTGGACA	4980
AAGAAACAGC TATTTTTGTT TATACTTCAA TACAAAAGTA TCTTAAAGAG AAGAATGCAA	5040
TTGGGATTTT TGTTTCTCAT GATTATAATT TAAAAAATT GGCTAATAAA CTTTATAGAA	5100
TAGAAGATGG AGTGCTGTCT TTAGTGGGGG GTGAGTGTGT TTAAATTGGC TTTTACAAT	5160
ATCTTTAGAG ATTTAAGGCG TACAATCATA TTATCTTAC TTCTAGCAAG TTCTGTGGTA	5220
TTTTTATTGG TTTTGTGTTG ATATATGAAC TTTAGTAGAG AGGGGATGGA AAAGAGCTTT	5280
GTTAGTTCAA GTGGCCATAT TCAAATTGCG AAAGAAAATT ATTTTAATCC TAAATTTAGC	5340
AACCTTAAGA ATGGGCCTTT ACTTGAAGAA AAGGATATTA ATTTGATACG GAATGAAATA	5400
GATAGTTATG ATGAATTACA ATCTACCAAT TTAATAGTTA ATTTTGATGG ACTTCTAGGC	5460
AATCTTCGA CAAGTAACCC AGTTTTTGCA TTGCTTATG AAGATCCAGA TATAATTACA	5520

AGCAGCCTAT CTTTATTAGA GGGTGAGCCC ATTTTCCACG ATTCTAATGC AGGTGAGTTT 5580
TTGCTTGGTA GTAATTTGGC CTCTTCGTTT GGTATAGAAA AAATAACAGA AACCAATTCT 5640
GATCTTACAT TAATGACAAA TTTGCTCGGG AGAGGTTTGA ATTTCCAAAA TATTAAAGTT 5700
GCTGGAATTA TAAAATTTCC ATTTTCAACA GCAGATAATA TTTTGAAT TACTACTATT 5760
AAGACTTTAA AAGACTTGTT TGCATTTGAG GGTGGAGCAC ATGTGATCCA AGTATTTTTA 5820
AAGGATAGTT CTACCTTAGA GACTTTTTAA AAGAAATTAG ATAATTTTAA AAAAAATAAG 5880
GGGATTTTCAT TTGATTATAA TGACTGGTTT GAGATTAATC CTTACTTTAA ATCTGTTTTA 5940
GGGATGACTA GAACAACATT TATGTTTATA TTGGTCTTAA TATCTCTTCT TATATTTATT 6000
GCATTTTTCC AGATAATGAC CGCATTAGC ATTGAGCGCA CTAGAGAGCT TGGTACATTA 6060
AGAGCAATTG GTTTAACCAA ATTGGAAGTT TTTTACTCTC TATTTTTAGA AATTGTTATT 6120
ATTTCTGTTG TCAATATTGT TGTAGGAGTA ATATTGGCTT ATTTTGCTAA ACTTTTTATT 6180
CAGTTTCAAA AAATTAGCTT TACTCCTCCA GGCTATTCAG AAACATACTA CATCAACATA 6240
TTTTATTATG CTAGTGATAT AATATATGTT TCAATTTTCA TGTTAATTCT TGCTATTTTT 6300
TCTTCTATTT TGCCATTTAG CAAAGCAAGT AAGAAATCGG TAGTAGAGGT AATGAATGAT 6360
GCTTAAGATT TTGTAAATG TTTTCAATTT TTGTGTTTTA AATTGTTAA ATGCTGGAGA 6420
TGGGAAAAGT TTAATAAAAG AATTTGAAAA TCTATATTAT CCCCATTAA AAAATGGAAT 6480
TTATGCTTTC AAAATGAATT TTAAAATTAA CGTAAAAAAT AATTTAGAAG AAAGCGTAGG 6540
GCTAAGAATT ATTAATGTTG ATAATAAGGA TGTGCGTTTA ATTTATATGT CAGGATCAAA 6600
AACGGATTTT GCCTTTTTAT CTATTAGGAA TAAAGGGCAT TTTATGCTAG GAAGACAAGC 6660
CAAGATTCCA ATTAAGGTAA GCTCATCCTA TAAAGTTAAG GGCGCATCTG AGCTTAAAGA 6720
TATTTTGGGT TTAAGTTTCA ATACAGATTT CGTTTTATTA AAATCCGAAG ACAATAGGGT 6780
TGAATTTCAA TCAAAAGAAA AATCAATATA TCCATTGTGA GATTTATTAA AAATTAATAA 6840
AAATGATTTT AAAACTTTAC ACAAAGACAA GAAATTAAAA ATCTAAAAG AAGTAATTTA 6900
TAGAAAGGGA AATATTAAAG GAATTGATGC TTTTGTTTAT TTTGAAATG AAGATAAAGC 6960
TTTTAACGAT TCTAGTACCA AAATTTATGT GGAAAATATT ATTAGTACTA ATCTGAATAA 7020
CTCTATTTTT AGCTTAAAAG GATTTAATAG AATATTTGAT TTATATTCAA GGTATATAAA 7080
TTAAGAGCGT AGAGGGATAG TTAATATTGG TATTTTTTAA AAAATTTTGT TTAATCTTTT 7140
TTTTGGCTTT ACCTGGTTTT TTGTTTGGCG AATCCTCTTT GTTTTTAAAG GAGCATTTAG 7200
GATTCAAAAC AAAATCTCTT TTATTGTTGC CCGATGAAGA TAAAAAGAT TTTTTTGGTA 7260

951

CAGGAGCTTT ACAATTTGAC AATGAAGCTT ATTTAGGATT TTTATTAAAC TATAAGATAT	7320
TAGAATTTGG CATTGCACCT TCTTTTATTG TGCAAAATAA TGATCAATAT TTTAGTTTTA	7380
ATAAATTATT CTTCAAATTA AGCTTTAATG ATTTTATTTT TAAATTAGGT AGGCAAAATT	7440
ATTATTTAGG AAATGGATTA ATTGAAAATA TTGTTTTAAA AAGGACCACA ATAGAACCAG	7500
AATGGTTTTT TGAGTTTTAT TATTTTATTT CTAATTATTC TGTCTCTTG GGTCTATGT	7560
TAGACAAArA AAgCTTArAT AAATTTTCAT CTCCCAAATA TTTATCCCCT TGGCTTTATT	7620
TTCA	7624

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7074 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

ATTGAGGCTT ACAATAAAAA TTCTGATAAC ATTAAATAG ATAATAAAGC GCTAGAAACC	60
ACATGGAAAA AAAATACTCC CATCCTCTTT ATCTACTAGA TCAAGCTGAT TAATTTAAAC	120
AAAAATTAAT AAGTTACACT TAATATTTTT TAAAGAGAA GTTAATTCCT CTCTTTTTTT	180
ATTyGTACAA TCTAAATCCA CGCTAAAAAC ATGCAATAGA AATTAAATTT TCAATATCAA	240
ATAAGTTTAA TATTACAATT TGATAWTAWT ATCAAATTGT AATATTATAA ATTTGAACTA	300
AAATTAATAA ATATTAATTC AAATTTATAA GGAGAATATT TTGAAAACT TTAAATTAA	360
TACTATTAAG CTTAACGTTA TTACAGCAAT ATTAACTTTA ATTTGCATAT CATGTGCACC	420
TTTTGGCAAT GTTAATCCAA ACAAGCTAAA AAATCCTATC ACCTCTAAAA ACCTAAAAAA	480
AmCAAAGCGA AGCAACCATT CTAGAAATCT AAAAAAACA AACAGTCACA CCAATTCAGA	540
AAATTCAGCA GAAAATAACC AAAATCTTGA AAATGAATCT CAAAATTCAA AATCTTCAAA	600
TCAAAATCCT CAAGAAGAAA CTGCAATCTC AAAATTAGAA AAAATTGGTA AGGACCTGGA	660
AGCTCAAAAA AAGGAAAAAG ATACACAAAT AGAAAAAATT AGTAGTGATG CTCAATATGA	720
TTTTCTAGAG AATTTTAAAC TTCACAAC TAATTATTTT ATGCATAATA CAAAAATGAC	780
ATTAAAAAA ATAATTTACT CATCCCTAAA TTACGAAAAA GAAAAAATAT TGACATTAA	840
AGAAATTCCT GAAAACTTG ATACAGAAGA TAATAACCGA AGAATAGCTG GTCAATTTTT	900
AGAAACATCA AGGGATATTC AACTTCAACA AGAAGATTTG ATTTTAAAAA AAATACAAGA	960
TACATTACAA ACTCTAAGCA AAGAAAAAGC TGAAGAATTA CTACAACACG CAGAACGCGA	1020

TTTAAAGATA	AAACAAAAC	TTGTAAAAGC	TTTAAACGCA	ACTATTGAGG	CTTACAATAA	1080
AAATTCTGAT	AACATTAAAA	CAGATGTTGA	AGCGCTAGCA	AACCACATGG	AAAAAAAATA	1140
CTCCCATCCT	CTTTATCTAC	TAGATCAAGC	TGATTAAATT	AAACAAAAAT	TAATAAGTTA	1200
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TCCACGCTAA	AAACATGCAA	TAGAAATTAA	ATTTTCAATA	TCAAATAATT	TTAATATTAT	1320
TTTAAGCTTA	ACGTTATTAA	TGAAAAATAAT	TATGATGATT	ATAAAAAATT	TATAAGAAAA	1380
GCTTCTATAA	ATTCTACAAA	AACAGCAGAA	AAATTGATTA	AATTAATGTG	ATTATATAAA	1440
GATCGTACAT	AAATAAGGAC	TAGGGATAGA	CAAAGAAAA	ATACTATTAG	CAGAGGCCAA	1500
TAACAAAAAA	TATAAAATGT	CAAGCGATTT	AAAAAAAAGA	AAGAAATGCT	CAGTTGCAAG	1560
ATGTATTTCA	TTAATTATTT	TTACCAATTC	TTTTAGTTTT	GATATAACCA	GTATTTTATT	1620
AATCTTATTA	ATAAAATACT	GGTTATTTAA	TTATTTTAAC	AATATAGTTA	TAATAAGAA	1680
AGATTAAATC	ATATTCAAGG	AGAGTATTTA	TGAAACACTA	TATAATTGTG	CATATATTTG	1740
TTTTTCTATT	TTTAAATGCT	TGTTATCCAG	TTGCATCTAA	TAAAATAGAA	TTAAAACCTA	1800
AAACAGAAAC	AAGCTTAAAT	CAAGAAGAAG	TCCCAAATCA	AGAAGCAAAC	TACAAAGAAG	1860
AAAAAGAAGC	AAAAGAAGAA	GGCATTAATA	AAAAACAGA	AAACACGCTG	CTTAATGATT	1920
TAAGAAATTT	AATAGAAACA	GCTAAAAAAG	ATAATGATAA	ATATACACAA	AAGTTAAAAG	1980
AAGAATCCTC	AAGCCAATAC	GGAATACTGG	CTTTCAAAGA	TTTGTTCCTG	CTAGATGGAA	2040
CAAATGAACA	ATTGTCCGCA	AATACCGAAA	GATCTAAAGC	CTATAGAAAA	CGAGCTTATA	2100
GCATCTTAAA	TACTATTAAT	GACGCTTCCT	TAAAGAATTT	TTCAGAAATT	GTAATGGCAT	2160
CAGGACAAAC	ACAGGGCATA	TTTAATACCC	TTAACTCACT	TGGGGGTAAT	TTTGAAAAGA	2220
TAGTTAATTG	TTTGTATCCC	AAAAAAGACA	ATTTGGAAAA	ATTAGAGACT	TCAGTTTTAA	2280
AAAAGCTTAA	AGATTCTTTG	GAAAATTTTT	TAGAGATAAA	AAAAATCGCC	TCAGAAATGA	2340
TGCACAAGCT	CTTATTAGAC	TATCAAAATA	ATACAAATCG	TATACAAACA	GATAAAAATG	2400
AACTTAAGTC	TTATGCAGAC	ACACTTTTCA	ATCAAATGAC	AAAAAAACCC	GAAGAAGCAC	2460
TAAAGCTAAA	AAATACCATA	TGCTCAATAG	AGGACCTTTA	ATTTATATAT	TGAAATTGTC	2520
ATAATATAAA	GACCTATCTT	TTCTTAAAAG	ATAGGTCTAA	AGTTGTTAAA	TACTATTTCT	2580
AAAAAAAAGA	TTATAAATAG	CTTCTTTATT	TATTCGCGC	TAGCTTTTCA	GCTCTACAAG	2640
AACGGTCGCC	CATCAGAGAA	TAATCACACA	GGCTTTATTT	CAGACAATTC	TTGCCTTAGT	2700
TTTTATTTCT	TTATAAGAAT	ACGCCTTAGG	ATTTAGAGTT	GCATTTATAT	CTCTATCATA	2760

CAAAGTGATA CAACCGCTAC AAATCCACAA TAGTGTGCGCT TAATTTTAGA GTTATATTTT	2820
TAATATCTCA TACTCAATAT ATGTACAGCC CAATATTAAA ATCTTGCGAA TTTATAAATA	2880
ATCTAAAAAC AGTATCTTCA AGACTTATAA AAAATATTTT ATTTATTTGG AGAGGTATTA	2940
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GATATCATCA AAAAGTATAT TTAAAATCAA AATAAACCTA TTTATTAACA AACTCATCTT	3060
AACCCAAATT TCATAGAAAT TATAGTTTAA GTATTCTTTG GGGGTTTTTG ATAAATTGCA	3120
TTAATATTTA ATTATTAAAA TTTATTGGGA GGTAATATCA ATATGAAAAA AATTTTAACA	3180
TTGATATTAA TTTTGTAGCTT AACAAATACAA ATCTTTGCAA CACAAGATAA GCTTGAAAAA	3240
AGTGTGGGAA GTATTGAAAC CATTATGAAA TATAAAGCG AAAAAGCAAC TATACTAGCA	3300
CCATTCCCTT TGAATTTATT TTAACTTTA GGAATAGGAT CCTTTGTCCA AGGAGATTAT	3360
ATTGGTGGTG GCGCAGTGCT TGGATCTCAG TTATTAGGAG GAATACTTTG CATAGCTGGA	3420
AATATTCTTG GCCATACAGA TGATGAAACA AGAGCAACAA CTGGGCATAT AATAACAACG	3480
ATAGGAGTAG GCACGATTAT AGCATCCAC ATAGCCTCAC TTATTATTCC ATTTACATTT	3540
GCAAATAAAC ACAATGCAAA TCTTAAAAAA AGACTCGGCA TTGATATTGC GGGTTTTGAA	3600
CCCAATTTTG ATATTGGAAT AAGCGGATTC CAACTATCGT TTAAAAAAG ATACTAAATA	3660
AAATATCAAA GCTATAAAAA TTAGTTACAA AAACTACTG TAGTGATATA AATAATAAAA	3720
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CTTGAGAAGC TCATCATAAA AAGAAGATAA ACAGTGTTAA CGTTTATTAG TATAAATAAA	3840
TCAAAATAAT ATAAATTTAA TCCTAGCAaT AAAAaTGGGA TCTtGTTTTT AGATAGGGTT	3900
TTTAAAGAC TTTAAAAAAA TATTAAAACT TAGAAAATAT TAAAAAGACT ATAACAATGC	3960
ACTTTTATTG TCAAAAATTA CTTATTTAAT CTAATAAAAA TATCTTATTA TTCTGTCAAT	4020
CTTATTGTGT TGTATGTTCT CTAATATAAT AATACAATTA ATCTATACTA ATTGAGGAGA	4080
ATATTTTTAT GAAAAACAAC ATAATTTTAT GCATGTGTGT TTTTTTACTT TTAAATAGCT	4140
GCACCGCTAA CCATGAAGCT GAAGCGAAAA TAAAAAACA TGTTGATAAA ACAAAAAACG	4200
AATATATTAA TGAAATAAAA AATTTAATAG CAACAACCAA AGAAATCATC GAAAAACGAA	4260
AATTGCTACA AGCTAAACCA GTAGATCAAA ACCCCGTAGA TGATACAAAC AATAAGAAAG	4320
TTTTCGAGAT AGATAAAGA GCTTTCGATT TTATAAATAG TTTTTTAACA GATGATGAAT	4380
TTAATAAATT TGTAACAATA TTTCATAAAC CAACACTAAA ATCACCCGGA AAAGTATTAA	4440
ATAGCATAGC AATTCTAGAG CTAAACATAG AGCAGGTAAT TAATCACCTA GACTCAAAAA	4500
ATGAGACCTT AAATAAAGCA AGCTCTTTAG ATTTGGAAAA GATCAAAAAT TCCCTTGAAC	4560

AGCTGTTCTC	TATAAGGAAT	TTTTTTTCAA	CAATCATAAA	AAGGGTCTTA	TTAGATCATC	4620
AAAACAATGA	AAATTCTATA	AAACCAGATG	ATTCTAAATC	AGGAACCTAT	TTCGATACGA	4680
TATACGATCA	GTTTAATGAA	AAAAATAAAG	AGGTTAGAAA	TCTGAAAAAA	ACCATATTAT	4740
CACTGCCGAA	TTAATATGGG	GGTTTAAGTA	AATTAAACCT	TTAAATATAA	AAGTCTAATA	4800
AAAGTTTATT	ATTTACCATT	AATATGCTT	TAATTAAACG	TGCAGAAATT	TAATTACACA	4860
AACAGAAAAA	TAAATTATAA	TTGAAATTAA	TCAATAAATA	GCAAACAATT	GAACCTTTAA	4920
GAAGTAAAAA	TTGCAAAAAC	AATTATTTTA	ATATTAAAAC	AAACATAATA	AGAGATTTAC	4980
TTATAATAGA	AACTTTTACT	ATTAATTTCA	GAAAGGTTAA	ATCGACATTA	AGAGATAAAT	5040
TTAAATAAAT	GATGTTGATC	GGCCCGAAAG	CATTCTGAAA	ACTGTCAAAA	TTAAAATCGA	5100
AAATTTAAAT	AACTGGGGG	GCTTTTAGAA	AAAATGAAAA	ATGTCTTAAG	AATCTAAAGA	5160
ACAGTGGGCC	TTGTTTATT	AAAATAAGCA	AGTATGTCCA	AATTGTTGAA	CCAGTATTAC	5220
TAAATTAGTA	TATTAATTTA	TAAAAATTAA	TCAAGGATAT	ATAAAATAAA	TTTAAAAAAA	5280
GTTTAAATTG	TAATAAAAAA	TTTAATTTTA	TTAACTAAAT	AGCTAATATT	TAATCAAATT	5340
AAATGTTTAA	TTATAATAAG	TATAAATAAA	TATGGAATGA	TATAAAGGAG	AGTATTAATG	5400
AAATGCCATA	TAATTGCAAC	TATATTTGTT	TTTCTATTTT	TAGCTTGCAG	TACAGATTTT	5460
AATACTGATC	AAAAAGGCAT	TAAATACCCG	CCTACCGAAA	AATCAAAGCC	CAAAACTGAA	5520
GACTCTAAGC	AAAAAGAATT	AAAGCCTAAA	ACAGAAAAAG	AACTAAAGAA	AAAACAACAA	5580
CTAAAAAATA	AACTACTTAA	TGATTTAAAA	AATTCAATAG	AAACAGCTAA	TAAGCATAAA	5640
GAAAAGTATA	AAAAAGAAT	GAAAGAAGAA	CCCGAAGATC	AATACGGGGT	ACAGGCTTTC	5700
AAAGGATCGA	ATTGGGGGCC	GGGGACTGAA	GATGTATCTG	CCAACACCGA	AAGATCTATA	5760
AGATTTAGAA	GACATACTTA	TACTATTTTA	AGCACGCTGA	GTCTTCATGA	ATTAAAGGAA	5820
TTCTCAAATA	TTGTTACAAA	TGAAAATAAA	CTGGTGCCAG	TAGTAGATAT	GTTTAATTTT	5880
TTTAGCTCTA	TTGGGACAGC	TCTTGATATA	ACAACCGATA	GCTTATATCC	CAAAAAGACA	5940
ATCTGGACAA	ACCAGATCTG	TCGGATTTAG	AAACGCTTAA	AAATTCATTT	GAAGCAATAT	6000
TGTCTGCAAA	AGAAAAAGTC	GCAAGCGGGG	TAATGCAACT	TGTAAGAGAT	TATAAAAATC	6060
TAAAAACAGA	TATTAATAAG	CTTAAATCTT	ATTTAAATGA	CCTTTACAAT	GAATCTGAAG	6120
AACAAGCTAC	AAAAGCAGAA	AATCTGGAAG	AGTTTATAGT	GTCAAAATAT	AACTTTAAT	6180
GTTTCGCTTT	TAAAATTTAT	TAACAATTTA	AAAATGTATA	TTTAAGCTTT	TGTGGAAAAA	6240
TATTTTATCT	ATTTAAGTAG	GGATCACTAT	TGATATTAAT	TTTGGCTTAG	AAATTCCTGT	6300

955

ATTATTTCTA CTGAAAAAGT TTTTACAGAT ATCATAAAAA GCATATTCAG AATCAAAAATA	6360
AATCTATTTA ACAAATTTAT CTACACTTAT AATCCCTGTG AAATTTGGAT GAAAAATCAT	6420
TTGTTATTTT TTATTAAACT TTAGTTTTAA GTGTATTATA AATTTAATAG TCTAAAAATG	6480
TGTGAACATT TGATTTTTGC TATTTAAATT GATTTTAATT TTATCTTTTA ATTTTATACT	6540
TTTTAGACAC GCTATATATT CTTTGGCCCT CTTTAAATAA AGAATCTTTT ATCATTCAAT	6600
GAGATAAATG ATAAAAGATA TACTGTTTAA TATTAAGCAA ACTATAATTC GATCTTTAAA	6660
AAAGATTTAA CCCAAAATAG ATAAGTTATA AAGCCTTCTA ATATCTTTTA TTTAAAAAAT	6720
ATGTTAATAG TATTCTATTT TCTAGCTTCT TCTATTATTT CTAAATTTAT ACACCACAAT	6780
AATAGATAAT GTACAAAAAA TCAATATTAA TAAAACAAAT GTATTTATAG CACTTATAAA	6840
ATTAGTTAAA ACCGAACATA TAGCTAATGT TAAAAATGAA AATATACGAG ATATTATGCT	6900
ATTAATAGAA GTTATAGTCC CTAAACTTTT TGAATCTATA TTTTTCTTA AAAAATATTC	6960
TAAATTATTA GAATAAATAG CAATTAAAAT TACTAAAAAT GTGATTACAG CAATAAATAT	7020
GTAAATATGT GAACTATTTT TTATTAGAAC TGACAATAAA GATATTATGG nTAA	7074

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6810 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

AATAAAAAAA CACATATTAT GCTCGCAATT TTCAAATAGT GTAATTAAGC TCTTGTATTT	60
AATAATAATC AAATACCTTT CTCTAAAGTA TAGTCAAATA ATAGCAACAC TAAAAAGTAG	120
TAATATTCAT TAATGTGAAT CTCTAAATCT CTGGCATACA TTTTAAATGT CATTCAACGC	180
CTTATCTTCA CAGGATTGCT ATTAATAGGA GAAAGTCTAA TGCACTCAAT TCTCCATTAT	240
TGCTATCCAC TTAAAGAGAT GGGGGATTTG AAAACATAAA CATAACTAAA CCATAATAAT	300
GATAAAGTTT TCAATCGAAT GGGTGAAAAA GTATAAGAAT ATTTAAGCTC TTCGAGATTT	360
TTAATTAAAT TATTATATTT GTCTTTTATA GGCCTTAAAT TACAAGATTT TACCTATGTA	420
ACATAGCCTC CTACAAACAA TTTCCAAACT TCTCCTTCTT TTATTTTCGTT TAACCTAGAT	480
TCTTCATCAA CATAACAAGT ATTGTTATTA TCTTCTTTAA TATTTTCTT ATTATTTTTT	540
ATAATTGACC CAATATTTAA AAAACCATTT ATTTCTGCGA TCTTACCTTC TTTGTCCCTA	600
TACTTATCTT TACACTCTCT TAACTTTTTT GATGAAATCA AAACCCCTCC TTATATTTTT	660

TTATATATAA AAGATAAAAC AAGAAAATAA ATAAACCAAA TATAGTCTTT TTGGCTTGTA	720
AAATTTTATT GGAATTTTAC TTAATATTTT TTTTATAAAT TAAATAAAAA CATTGATTTT	780
TGCACAAGCA AGGGTAAAAT AAATTCAGT CTTAATTAAA GATTCTTTTT TTAATAAAAT	840
CTTTAATCAA GACTTGAAGT CTTTACAATT CACCACAATA ATAACCTGGAA GATCTAAACA	900
AATAGAACCA CCATTTATAA GTAATATACA TCAAATTTCA AATAAGATCA ACCCTTATTC	960
ACAAATTTTT TATTTCTATT ACTAACTACT ATTTTTTAAA TCAAAGATTA TAAAAATAGT	1020
AGTTTATATC TTATGTTTTA TATACCAAAT TATTCATAAG TGCTCAACTT TTAAATCTTT	1080
CCATAAACTT TTCTAGCAAA TCTTTTTTCT CTATAAAAAC TCTATCTAAA AAGTAACCAG	1140
TAAATTTGGC GTTTTTGCCA TAAAAATCAT AACTTTCTCG ATTTTCAAGC TGCAATCTTA	1200
ATATCCTTAT TGATTTCTCT TTTGCAATGC CCTTATCTAT GTTAAACCTC TTAATCCTAC	1260
TATAAGTCTC TGCAAACTCT AGTTGCTTAA TTTCATCTAT TTTTAAATCG CCCGATAGTA	1320
CATGCTTGTA AAGCCTTAAA TATAAGAATG CTTGACTCCT TGCTATGACA AATTTTTTAA	1380
GAAAATCATC AAATTTTTTG TATCCATCAA ATTTATAAAG TTTTTTAGTC CTTATTTTAT	1440
ATAAAATTTT CATTAATTCA ATCTATTGT CTATTTGCT TGTGGCAATT CTTCTTATTT	1500
GATTTTTATA GCTTTCGTAT TCTATTTTAT CATCTTTATC ACAATTATTT TTTAATTGAT	1560
TAATACTGGT TTTTCTATCA TTTAAATGA TTTCCTTTCG CTCCTTTTTA GACATTAAAC	1620
CTCCTTTTCT TTTAACAGTA AAAAAGTACG TTCAGCGTAC TTTTACTATT TTCTCCAAAG	1680
CTTCTTGAGC CTCTTTGTAA TACACCGCAC TAACATCGGG TTCTTTTAAAC TCATTAATTA	1740
AGACTTTAAC GCTGTTAAAG CTATGAATTT TTCCCTTGAT TAATATACTA TATTTTTTTA	1800
ACACTTGCTT TTCTACATCT ATAAATGTAT TTCTATTTTT AATAAACTGA TTTTCCACTA	1860
TTGAAATATC AATCTTTTTA TCTTTAAAAA GATTGACTTC TTCTATCGCA TCCATTAACA	1920
TAGGAAATGC TTCTACAGAC CATCTTTCAA GCTGAACAGG TATTATAACC TTATTTGTAA	1980
TATTTAAAGC ATTATACAAC AGAGGACCCA AACTAGGAGG TGTATCAATC AATATGTAAT	2040
CAAAATTATT ATTAATTAAA ATTTTTTTTA CACAATACTC TAATAATTGT TCTTTATATC	2100
TTTTGTCTTC TTGTTCAAAT TTACATAGAA TTGGATGAGA AGGAACAATA TACATATTAT	2160
TATTTATTTT GTTTAAATAT TTGTTTGAT CAAAATCCTG ATAATCTTTA AACATGTAGT	2220
AAACATTAAT TCCTTCAATA CTCTTAATAT GCCTAATGAA GTAGCTAGTT AAACATTTTT	2280
GAGGATCTAA ATCAACCAGT AAAACTTTTT TATTAAAATT CTTAAGAATG TAACTAAAAA	2340
TAATTGCTAA TGCACTTTTA CCAACTCCCC CCTTAACCTG TGCAATTGTT ATTATTTCTG	2400

957

TTTTTTTTCT ATCCATTTTT TTATAAATCC TCCATTAGGC AACTTTTTAT TGTAAAATTT	2460
ATATATTTCT CTTTCTAACT TAATTATTAA TTTAAGTAAA AATTGATTAT ACTGTGTTTC	2520
TGCTTTTTCT TTTTAAATAA AACGAGACAT TCCCCTGATA TAACAATATA CACTTCCTCT	2580
TTTAAATCTA AATTCAATAT AATGAATTTT TGAAAATGCA TATGACTTTG TTGTATTGTT	2640
TTCTTGATAT TTTACTATAA TGTTTTGTAC TGGCCTTCTG TATCCATAAT ATATACCCAA	2700
GAATTCATCA TTTTCCTTTA AGGGAAATAA ATTAAATTCA CTAATTTTTT CTTTATTAAA	2760
TAGTCCTCTA AATGAAACAA AAAATTTATT TTGCTGATT TTATTAACAC CAAATACATA	2820
TAAATCACTC ATTATCCTTG TATGATATAT TTTTCTGTTA TTTTATCTT CCACTTTGGC	2880
AAAGATAAGT TTTTTTCGTG TTTTTTTTTAT TTCTGATTTT TTGATTTTGA GACGCTTTAA	2940
TAAACTTTCC ATAACTAATC CTTAATTAAC AATTTATTTA CATGCCTCTA ATGTGAACA	3000
CCATTTATTA GGCTCTACTG TCTCTAAGAT CTCGTAATAG TAATAATTGC TAAAGACCTT	3060
GCTATATTCT AATCTTTTTT GCTTATCCAA ATAATCTTTT AAAATCGGTA TTAAAATTTT	3120
AATCTTTATT TTATGTCTTA ATTGTTCAAT AAGTATATTA AAGATATTAT TTCTAATATT	3180
TGTGTCAATT TCTTTTATAT TTATTTTTTC TTGTTTAAAC TTATTTTAA GTTTTTCTGT	3240
TATCTTCTCT AAATCTTCGT ACTTATTTTT TTCTATGATA AAATGTGGTT TATCTTATA	3300
TTGCTCATAT ATATCTTTTA TTTCTATTTT TAATTGCTCG CTTTTATAAT TTTCGTTTTT	3360
TAATTTAATT TTTACTTCTT TTAGTATTCT TTCAATTTTT TGTGCTTGT TTTTAAGCTT	3420
ATTTACTTCT ATTACCTTGA CAACGTTTAA TTTTCAAAA ATGTTTTTTT CAATTAAATT	3480
TTCTGCCTTT TTTATCAATT TACATACTTC AATTGTAGCA TCTTTTTTTA ATCCCAAATT	3540
TAAAATAAGA GAGAATATAT TTGATTTAAA ATTGCATTTT TCAATGTATT TTCTGATTTG	3600
TAACTTTTCT ATGGATTTAC GGCTGTTTCT TTTTCTTCT TTATTATTAG ATATATTATA	3660
AAAACACTCC CTATTTTTTA CACTACTATT TTCAATGCAA TTCTTATTAA AATATGAATC	3720
AACACGGCTT TTATATTTTT TCTTTTTTAT CTCTTTAAAA TGTTTATTAA TTAAATGGTA	3780
ACATACTTTT TTGGGATATT TTAGTTTGTA ATGAACTTCG GTCCCATGT TAATACCTAA	3840
ATGTCTGTGG TAGTTACTAG TTTCTTTAAA TACCTTTTCT AATTGTAAA GATAGTTTTG	3900
TAGTGTTTTT AGCTTAACTT CTTTTTGACA ATTTCTTCTT ATATTATTAT TAAAGTAATA	3960
AAGTATGTCA TTTTGAGTGT ATTGTTCAAG ATTTGAATTT ACATAATTCA GTGTGATAT	4020
TAGAATGATT AATTGTGTT GGTATTTATT TGTAGAGGTT TTTATACTTT TCAITTTCTA	4080
CCTTCCATTA TTGATTGTGG TTTATATCAA GGAATATAAT AACTCAATAA GCAATGAAAA	4140
GTAAACTATT TTTTAAAAAA AATATTGATT TTTATATGGC CAAACTCAGG CACAATGTCT	4200

AGCATTGTC TATAAACTTC CTATCTAGCG TGTGATATA TAAGCTTTAA ACAAAAAAAG	4260
GTCGCTATCT TTTGTTAACA ATAATTTTAA CTTCAAGTTT GCGCAAATTT TCGTCTATTG	4320
GCATAGGGGT TATTCTTACT AACTCAGACT GCACAACTCA CTAGAGGACT CAAAATTTCTA	4380
TCCAAATATA ATAATCTTTA GAATTTTTTAA GTCTCGGTGA AAAATTGGGT TTTTTGAAAC	4440
AAATCTTGCA TCACTAGAAG AAAGTTAAT CTCTTCAGTA GATCTGGCTG ATTTTACTAA	4500
TACAATTCTT TTAAGTATTT TATCTAAAAT TTTCTGTGTC TTTTTCAAAT CACTTGCTAT	4560
TCATCATCTA ATTCACTTAA TTTTCTTTTT CTCATTTTGA TTTTGGCGTC AAAACTCTCT	4620
TCAAGTCTGG GAGTTGCATG GTCCTTCAA ATAATCAACG CCCACCCCTC CATGACTAAA	4680
ATCTCTACAC ATATCGGTTA TTTTATCTTG CATAGACTTG TGGACTTCAA CAAAAGATTG	4740
ATCTAGAGCC ATTTATCAAA TTCATTAACT TAAATCAATA AATTTAAAGT TTATGTAAAA	4800
CATGCTAATT ACTATTTCTA AATCAAAAAGT CATAATTTTT TATGACAGCT TTTTAAGAGT	4860
AGTCATCATT AAACAACTTT ATTATTAGAG CTTAATTAAG CATTTACACG AGGCAAAGAC	4920
TTAATTAAGC TCTAATGGCG GTCACAAATT AAGGTAAATT TTAAATGAAA AACTTATCCT	4980
TTACTTAGAA GGATACACCA ATTTAAAAAT AAAAGCAATA AATCAACAAT TCAACAATCA	5040
TATTAATAAA CTATTTAAAT TTTTCTTTA AATTCTCTTA TAATTTGTTT AACCCAATCT	5100
TTTTTATCGA AAAAATTTG TCTAAAAATA ACTCTGTAAA TTTACAGTTT TTTATAAAAT	5160
AAATAACTTT CTGATTTTTT AAGCTTAAAGT CTTTATATC CATCGAGTTT ATAATAAAT	5220
TTATTTTTGG TTCCATTAA ATATATATGG CCTCTATCTT ATTATAGATG TTCCCTTTTA	5280
CATTATCTTT TAATTTATTT TTTAATAATT CAAATCTTTC TTTATCATT AATGAATTTA	5340
TATCATTATT GACATCCAAA ATATAATTTT TTATATCTTT TAGTTTATTT TTTAATAATT	5400
CAAATCTTTC TTTATCATT AATGAATTTA TATCATTATT GACATCCAAA ATATAATTTT	5460
TTATGATTTA AATTCTTAG ATCAATAGTT ATTTCAATTA TATTTTTTAT TCATAAAATC	5520
TCCTCGTTTA GTTTAATTTT ATTACTTTAT AAATGTCTG GCGCTGGACA GTTTATATTG	5580
GGGGTTTCCC ATTTTTTTGA ATAAGTTCTT ATATAAAATA TCAAATTATT TAATATATAA	5640
TATTATCCA ATATGGAATT TGATTTAAAA GCAAATACCA TATGTTTGCA ATTTTTTTTA	5700
TTTGGTTCCA TTTTCTGAT ACAATGCCTA AAAAGCATTC TTTCTTTGCA TTATTTTCAA	5760
TAATTTTTTG TGTGTATCGG GCTTTTAAGC CTAATGTGTG GCATTTAAAG AATATCTCAA	5820
TACTATATAG TCACAATTGA CTTTAAATTT TGTATTCTT ATTTTCAATT CTGAATCAAT	5880
AGCTTTGTGC TTATTTAGGT AATAGAAATA TCTATTTAAG CTGTATAATG TCAAATGGCT	5940

959

AGGATTAAAT CCAAATGATT TTCTATTTGT AAGTGTAGTT TTACCAACAT CACCTTTTAT	6000
GCTGGTAATT GTTATTATTT TTGTTCTTTT TCTATCCATT TTGTTATAAG CCCTCCATTT	6060
GATAATTTTT TGTCGTAAAA TTCATATATT TCTTTTTCCA AAGTTAAAAT AATTTTGATA	6120
AGAGATTTAT AATATTTTTT TTAATTTTAT CTTTTCTTAA TAAATAAGAA ATTCCTACAA	6180
TATAACAAAA TATGCTTCCT TTCTTAAATT TAAATTGTAT GTAGTGTATG CTTCTGTTTT	6240
TTCCCTATCA AACAATTTTC TAAATTGGAT AAAAAATCTG TGTTTTTGAT TCTTTTTTGT	6300
TTCAAATGCA TGAAAGTCTA AAAGTATTTT CGTATGATAT ATCTTTTTTT CGATTTTAAC	6360
AAAAATTTTG TTTTGTCTG TTTCGATTTT TTTGTATTTT TCTTTAAGTT TTTCTAAAAG	6420
TTTTTTCATA GTCTACCTTC TATCTAATAA AGTCTACCTT CTATCTAATA ACTTTTCGGT	6480
TGTCAAAAAA TTTATTTGTG TTTTTTATTA AATTTAGTAG ATCTAAATAG TATTTGTTGT	6540
TAAGTAGATA GGAATATTTT GGTTTTTCTA TTTGAATTAA ATACTAACAA CACAAAAAAA	6600
TATAAAAACC AATATACTTA ACATATTATT TGAACAATTA AAATCAAAAT TTGAAATTGA	6660
CAATGAAATT TACTAAGAA TGGTAAAAAA GTATATTAGG TTTATCTATG TTTTTTTATT	6720
ATTTGGTTTA AATCATCATA TTTGTTGTGA TCGATTATAA AATGAGGGCC TATGTTTGTA	6780
TTGGTAAATA TACCATTTTA AAAGnCCTTT	6810

(2) INFORMATION FOR SEQ ID NO: 21:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 5805 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

CTTGCA TGCC TGCAGGTCGA CTCTAGAGGA TCCCCGTGTA AAAATTGAAT CAGTGCTTGC	60
TATCCACTCA CCTAGCAAAA CTCTTGCTTT ATATGATGGT ATATCTTTAT ATAGCTTTTC	120
TTGTGTTTCG ACAAATCCTT TACTAAGTAG CACATTATCA TAAGTTGTAA AATTATATGT	180
CTTAAAGGTC GCTATATTAT CAATATAATC GGTTTTAAAA TAGTGTCTTG GATGATCtGG	240
ATTAGTATCA AAAATAATAG TTTCTTGCCC GCATCTTAGT CTTTTTAAGA CyTCCTCTAA	300
AGTTTGCTTG GTAAAGTTG TAGCCTCATT AACAAAAATA AGTGCCGAAT TACTTCCCCT	360
AAATCTTTCA AAATCACTTG CCTTATCTCC WCCATATAGA TTAATACGTA GTGAATCAAT	420
CAGAAATATAT GAATTATTTG TATGTCTTGG AATATAAGGA ATTTTAAGAA GTTTACATAG	480
CTTTTCAAAT TGyCCCAAAA CATTAACTTC AACTGArCGT TGTGAATTCC CAATAATAAA	540

ATTATTATTA	TCACyAGAGT	ATAACTTTTT	ATTTTCAATT	AAACTTTTGA	GAAAAAGATA	600
ACATGCAAGA	TACGTTTTGC	CGCTAGCTAT	GCCGCCGCTG	AGTATAATCT	TCTTTTCATT	660
ATTTTTTTGA	ATACTTTTTA	TAACATTTTT	TTGTTTTATG	GTTAACTGTT	CTTTTTCAAA	720
CTTATCAAAA	TTAATTGAAG	AATTTGTTAG	CTTTACAAAT	TGTGATATGT	CAACTCCATA	780
TTTATTTTTG	TATTCCTTTT	GTAGTGTTGT	AAAAAGTTTT	GTTTGATATA	AGTTCACCTG	840
TACCCTTTAT	AACTTTTGTA	ATTGCCTTTA	TTCTCAACTT	CATGAGCAGA	AGAAAGTTTT	900
TTCATACATT	CATAGTAAAG	CTCCATTTCT	CTTATTGAGC	ACTCCTTTAC	ATATTCATCA	960
AGCTCACTTT	TTAAAGAATT	AATTTCTCCA	TTAACAACCT	GCTTGTTTTT	TTTACTACTT	1020
GCTTTATTTA	AAGCATCAAT	TTCGGCTCTT	AAATTTTCTA	TTTTAGTATG	CATACTAAAA	1080
AGCTCAACAC	TAGAATATCG	CTTAAATGCA	TGTATAAACC	CTAATTCTAA	ATTGGCTCGC	1140
TCTAAATCCA	ATTGCGTTCT	AACTTTCTTA	GCGTTAACTT	CTGATCTAAA	GGTTTGGCAG	1200
AAAAGGTGTT	CAAAAGTATC	TTCACATAAT	GTTAGTCTAG	AGTCCTCGCT	AACAGAAGTT	1260
TCTCCACTTT	CCCACTTTTG	TCTCATTCTC	CACACATTTA	CTTTAGAAAC	CCTTAGTTTA	1320
GCTGCTATTT	CTTTATCACT	TAACGATCCT	TCTCTAAAGT	ATGCAACATA	ATCATTAATA	1380
GACCTTTTGG	CTCTTTTCAA	GAAAATTCTC	CTAAAATAAC	AAAATTAACA	ACTTATTACT	1440
CTAAATAGTA	ATTCAATTTA	TTAATTATTA	ACATTAACTA	TTATCTTATT	GATATCTATT	1500
GACAGATGTT	TGATATTTAT	TGACTTTTAT	TGATTTAGAA	ATAGCGATTA	ACTAATTTAT	1560
TAAATTTTGC	TACAACTTGA	CTATACCAAT	TTGGAAAAAT	CTTTTATTGT	TTTTATAAGA	1620
TACTTCCTTG	TGCAAATTCC	CTTATCATAG	TAGTGCATGA	TTATAAATAA	TATATCTACA	1680
AAGTTAAGAA	CCCCGTCTAT	TGATTCTCGT	TTTGGATCTT	TTCTACCAAT	CTCATCCATA	1740
ATATCAGAAA	CAATACTCAA	AAACCGGTCG	GAATATTTCT	CTCCCATTTT	TTTCAAACAT	1800
TTTTCTAGCA	TTCCTTTCTT	ATAGCTACAA	TCAAACCTCA	TATTTTGGAA	ATTTTATAC	1860
TTTTCTATTA	TATGCTTATC	TTTCAGAACA	TCTTTAATAA	AATTTTGTGC	AGGGTTTATA	1920
ATACCATTTA	TAATTTTCATC	AATACTTTTT	CCGGTTTTTC	TTTTGTATTC	TTGTATTGAT	1980
ACAAAACCTC	TATAAAAATC	CTTTTTTTGT	TCCAGAGTTA	ATTGCTTAAC	TCCATAAAGT	2040
TTGCTTATTT	CCTTTTTTGT	GCCTGGGCTC	AAACAATCAT	AAAAATCTGA	AATTTCAATT	2100
ATATACATCA	AAACTCTAGA	GAGTATATAA	ATAAACAATA	TTTTTAACAA	TAGTTTTTGG	2160
CATTTTCACT	TCATAAGTGA	TATAGCTTAA	ATAGAAAAAC	AAGACTATCA	ATTGGCCTTG	2220
TTTTTCTAAA	TTCGATTAAAC	AATAAAAACT	TTTTCTTTAT	TCTTTTTTAC	CTTCTACAGT	2280

961

TTCTCCAATA	TTTTTAAGTT	CTTCTTCAAT	CTTTTTTAAGC	GAATTAGTTA	TAACTTCATT	2340
GGTCATATCG	CTAGTATTAT	TACCACTAGT	CATATTTTTA	AACCCCAAAC	TATTAGCACA	2400
CTGCCAAGCT	TGTAATCCAA	CACCACCTTG	TCTTTGGACT	TGAGAACCAT	GCGTTACTCC	2460
AGTTGCAGAT	TCAGCTTGGT	TTTTATACTC	TTCAAATTTT	TTTTTAGCCT	CTTGTAAGC	2520
TTTTTTTCTC	TCCTCTTTTT	TCTTTTTTAA	GCTCTCTGAA	AGTTCATTTA	ATTTATCTTC	2580
AAGTCCTTTT	CCGTTTAATT	TTCTTTTTAT	TTTGTTTATT	TTTTCTTCAT	ACCCAGAATA	2640
TGTTTCAATA	GAAGTTTTTT	TAGAGTCTAA	TTTTTCTATC	TTATCTTTTA	ATTCTTGAAT	2700
TTGTTTTTCA	ATTTCTTTTG	TATCTAATGT	GTTTAAATCT	TTTGTCTCTA	AAATTTCTAA	2760
AAATCCTTCA	ACTGTTTTTT	TTATCTCTTG	TTCTGTTTTT	TTTACATTTT	GTTCTGAACT	2820
TTCTAAATCT	TTCAACGCCC	CTTCTAAATC	TTTACTAGTT	ACATCATTCT	TACAAGAACT	2880
TATCAGCATA	AAAATAGCAC	AAATAATAAA	CATTTTTTATT	TTTTTATTCA	TAAAGATTGT	2940
CTCCTATGTT	GTAAGCGTTT	ATTTCAAATT	CTTTTTTAAAT	TCATCTTAAA	TTCTCTAAT	3000
AAAATTGCAT	ATGTATTATC	TCTTCCTAAA	AATGTAATAA	ATTGAGAGTC	ATTAATAGTT	3060
TCTATTTTTG	TTTCTATGTT	TTTGATTTTA	TAATCTTCTC	CTTCTTGATA	ACCATAATAA	3120
TCCGCATTAA	ATGCTCCTCC	TCTAATCATT	GAATTTACAA	AGTTGTTAAT	TTCTGACTCT	3180
TTTACTGAAA	ATAATCTAGC	CGTGTGCCCC	CCAACATTTA	AATCTGTTAC	AATACTATAT	3240
TCTTCTTTTA	TTAGATCTAA	AGTTCCTAAA	TCTATCCAAT	TGCCGATATT	TGTTTTTTTTA	3300
TATTTAATAT	ATACATTAAA	ATCAAAAAAT	TCGTCAGTTT	TTATGCGAAG	ATATCCAAC	3360
AAAGCGCACC	TTCTGAAATA	AGTAATAGCT	GCTCCAACCA	TTTGGGGTAC	GGTCTTTCCA	3420
TTTTTAGAGC	TGTTTTTCAAT	GGTCCATTGT	AATTTTTCTG	TAAAAGTTGG	CGTATCAAAT	3480
GAGTATTTGT	ACACAGTGCT	TGTACTGTAG	AATGTCGTCC	TAATATAATC	AACTATGCCA	3540
TATTGCCCTT	CTACAGAAAT	TGGATCTTGC	GTAAAAAATA	GATCCAAATT	ATGCTTATCA	3600
ATAACGTTTT	TAATTTCTCT	AACATATGTCA	TCTAAACTTC	GATAATTATA	CTCGTACCCC	3660
TTAGAATTCT	TATTAATCCC	TGATAAATTC	ATTCTTAGGG	TTTTCATATC	TTTTCTGAAG	3720
CTTATTTTTG	CTTGAATATT	ATTTTGCATT	TCTTGATTTT	TTTCTGAAAC	ATTGTTTATG	3780
GGGTCCCCCT	TCTAATTATT	TTTCAAAATT	TTACCTAGCC	AATACTTTGC	TCATCATATA	3840
AAGATAAAGT	ATTATTTTTA	CAAGAAATTA	TCAAAACAAA	AACTGCACAA	ATAATTAAAT	3900
TTTTCATTTT	CTTATTCATA	AGTTACTCCA	TAAGTCCCAA	TATTACCACA	ACAGCTAATA	3960
ATTGCAATAT	TTCAAAGATT	TAAATATATA	ATTTTGTTAC	ATTTTGAATT	ACATTGTTAC	4020
AAAACATAAA	TGTAATTTTTA	ATCAAACCTCA	TAAAATCTCT	CCATTGCAAA	TGCACTACTC	4080

ATTATAAGAG ACTACAAAAC ACATACAAAT TAAATTTCAA AGTCTTTGCT ATATATTACA	4140
CAAAGTATTG TATCTTTCTT GTGTACCACC CTTAAAAATT GCCTCTTCTG TTTATCCCAC	4200
CTGCTCTACA GCCCAGATTT TGCATGCAAT GAGAACTCAC AAAATTTGAC TAAAAATTTT	4260
AGTTTTTGGT ACAATATAAA TTACATTTTT CATCTATTTT TATTACTTTT ACTTAATTTA	4320
AAAGTAACAC TTATAAGGAG CTTGTCTTAT GGATACTAAT AATTCTTTTA ATTTAAATAA	4380
TTTCAATATG GATTTTACGC TCAAACATT TCAAGAATAC CAAAATGCAT TAAATAAAAA	4440
CAAAATTCTA GAAAATGAAA ATAAATTTCT TAAATCTCTA GAAAATTCAC CTAAACGTAA	4500
GAAAAAAAAT TCAAAACCAA CTCCTAAGTT TTATTTGACC CCTAAAAGTA TTAAATTAAT	4560
TCTAAAATGT GCCAAAACCC TAAACAAAT TGACCCAATT TCTGGTTGGT TTGTGCATCT	4620
ACTCTTAATA AGTGGATGTA GAGGCACTGA AATGCAAAAA GTAAAAATGC AAGATATTTC	4680
AACTTTTTTA AGCAAAACCG GAAAACTTT ATATACTATT AAAGTAAATG TGGCAAAAAA	4740
AAGAAATACC TCTTGATTA GAGAAATTGT CATCAACTCA GAAGAGTTCG AGGCTATCCA	4800
AACAGCACAT AAAAATCATT TCCAAGAAAA AACTCTTGAC TCGCGACGTA CTTATCTTTT	4860
TCAAAAGAAC AAACATAAGT TTAAAGATAA CCAAATTGAT ATTGTCCATA TTTCTAAAAA	4920
ATTCAAAAAT CTTCTTAAAA AATCGGGATT TCGTGTAAT AAATCTCTCC ATCTATGTCG	4980
AAATTTATTT ATTTCAAAT TGAAATCTAA CGGCTACAAT TCTTTTCAA TTAAAGAACT	5040
TATGAAATAT TCTTCAACCA ATGAAATTGA TAATATCTAC GGmCTmTCTT CTGCTAATAA	5100
AATTCAAGCT TATGAATGTG CTAAAAAGTG CCTTAACTT TAGTAAACT ATTTCAAGTT	5160
AAATATACGC TTTGAAGTTA CTTTAAATAT TTTTCCACGw GGctTTcAAG TCAAGTGAAT	5220
CATATAATAT TTCTTTATTT TTTGTTGCTA TAAAGTGATA TCCATTAACC TTATCGATTT	5280
TAAC'TTCrCT TATTTCAAAT TCATTGGCTG CACCTAAATA ATTTAAAGay TCATATCTCA	5340
CrCTACTTCT AATTCCGTAr TAATTAAGTA TCATACATrG ATTTATAATA AAACAATTGC	5400
TCTTAATATA TCCAAGTCCT ATAAATCTAT AATACGCTGC ATTTATCTCA TAmrCAyTAA	5460
ATTCACGTTT CTTAAATAGA CTTGTATAAT AATGTAGACA CAAAAAGTAA CAACCCCATT	5520
TTTGTATCTC CAGTCTTAAA GTTCTATTGT CTtGTTTTAT TTTATTAATA AGCATTAATT	5580
AATCCTCCTA TATTAAATTA TTTTTTTAAT TTTTtagTGC ACCCATCACA TGGGGACACT	5640
AACACTATTT GCAAATGCTA TATTACTAGG GAAAAATACT GTACCACTTG TTGGTAGTAG	5700
TCCCTTTAAT CTATCTGATA TGCCCNtTTC TTAGGGnCAA GAGTAAACAC AAACCTCTCCA	5760
AATTTATAAT TAACnGCTCA ATAGTGGGTA nGTATCGGAA AATGn	5805

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

CTCAAGATTA AGTAAAGCAT TCGAACTGC ACTGTAAGTT GTGCTTTTGTG AAGAAATATG	60
TTCTTCAATA GCAGCCCAAT AAGTACCACC AGGTTTCATT TTAGAAAAAA AGAGATTGAG	120
CTCATTAATT ATTTCTTCTT CAATTAATGC CAAAGAAGAC GCAATAATGT TATAAATTGA	180
GCTTTGATTG TCGTCAATAT TAATmCCaTA ATTTACaCGC AAaTATTCTC TTTTmGmTCT	240
TACAAaTATCC yTAaTTGTAC GTTTTAAAAAT GCCAAAATCA GAATCAAAAA CTATrCTCAT	300
AAATTAAACT CCATATTyAA AACaTCGCCg aGAAAAAAA GGATATATGT GCTTTGTGTGT	360
CTTGATAGT AGTTGAAATA TTTATTAAAT CTAAGTTAAG CTCTTTAGAT ATTTTCATGAA	420
AATAATTTTT TACAGCGTGA AGATTGTTAA TTTTAAACAG CTTTAAAAGC AAGAAATAGT	480
CCAATCCCCA ATGAGGAGCA TAGCTTAAAC TACCCCTTAA GGTTTTTAAA AATATCAAAA	540
ATCTTTGTTT TTGTTCATCA ATTCCATCAA CAAGTGATAA ATCGTTATTA AATACCAATT	600
CAAAATTATT GCCTAATCTT AAATCCATAC TAGTAATTAT ACCATATTTA GCAAAAATTA	660
CTTAAACAAA CTATTAAATAT CAGAATTAAT TTGAGCGGTT GCTATTTTTA AGCTTGATTC	720
GTCAATTACT GAGTCCCCTA TAATTTTTAT ACCATTGATA GCACTAACAA TATTATCTAG	780
AATTTTTTTT AAGCTAGTTG TTTGGTTTGC TATTTCAATT TTATTATTCG CTCTAATTTT	840
AACAGTATCA GAGATTAGAT TTAAAGTCTT TGGGCTAATT GCACTAAGTA TATAAAAATG	900
ATGTTTGTC AAGTGAATAT CGTTATTTTT ATCAAAAATA TTAATGCTTG ATTGAAGTAG	960
TAAACGyWA TCACCTTTTG ATArTTCTAA ACTGATATTA GAGATATTTT TTGTGTGAAT	1020
TTCTAAATCT TCAAATTCGG GTATTGTAAC AATAGCyTCT TGAGTTTGWT GTTTAAACTC	1080
CTTTACAGTG CCAATTTTAA TTATAAAAAT GTTTGAATAA ATCCAATTTT TAACGTCCTC	1140
TTGTGCTAAA GCATGACCAT AAAGACGCTG GTTCATTCTG TAAATTTTAT AGTCTTTAGT	1200
CATTTTAATC CCCTTTACTT TATGCATTTA ATCAGAATCA TCAGAATCAT CCTTTAATTT	1260
AAGTATTAAT GAACACTCTC CTGCGTTGCT AAGTCTTGCA CTGTTTCTT TTATGGTGGT	1320
TTTTATCATT TTTCTAATC CATCAATAAA TGAAACTTTA TCGCCAATTT TTAATTTATG	1380
TGTGTAAAT GTTTGTGCGT TCCAATATAC ACGTTTTATC TTGTATTCAC CTCAATAGC	1440

AATTTCTTGT	TGTGGAATGA	ATTCAAGTCC	ATAATCTTCT	AAAGCTTTGT	AATTTTCATC	1500
TGCTTCAGTT	GTTATATCAT	TAGTAAATAT	AAAAATTACAT	TCAACATCAA	AGCTGTCACC	1560
ACCAACATCA	GCTATTACGT	CATGAATATA	TATTCCCTTTT	ATTTTGTCAA	CAAATTCTTT	1620
TGGTGTGTG	GCATAAATAT	CTTTTTC AAT	GATTTTAAGA	CGATCTTCCT	TGTCCATATT	1680
AATAATATTG	CGATTAGGAA	ACACAGATTC	TATTGCCTCT	TGCACCGTTT	TCCCCTTGAA	1740
GTTTTGTTC	TCTAATTTTC	GATCAAAGAA	GTTGCTACTA	ATTGCTAACC	GAACGTCAAG	1800
CTCAACACTA	AAATCACCAC	CAGGATAATC	AGTGCTCATA	GGAGTTCCTA	AATACCCCGA	1860
CATTATGAAA	TCAAAATTTT	TTTCATGAGC	AAATTTTTTA	TAGTGTATTT	TTACTATATC	1920
TCCTACTTCA	ATGTCGTTGG	TGAAGTCTAA	GGGCAAATTC	CAAAGTACAA	TTTTTGTTGG	1980
TTTAGATTTT	ACAAAATTAT	AATTTGAAAA	CTCATTAGAT	ATGGTAATAT	CAATATGAAT	2040
TCCATGTTGT	GTATTTATTA	TAATTTTGGG	AGTTTCCTCA	ATTAAAGAAT	CTCCAGAGCT	2100
TGTATCCTTT	TCTAAGGATT	GTTTTGCTTT	GTAAAATTCA	ATTTTAAAAT	CATATTGTAG	2160
TAGCAACATT	AATTATCCTT	TATATTTTTC	CAATTCAAAT	GTTTTTACAA	TTTCTATTGA	2220
TAGACTAACT	TCAACTTCAT	CAATGAAAGG	AACATCCTTA	AACGAAAGAC	TTGTAATTAC	2280
AGCTAATTCT	TTTAGGCCAA	AAGTTGGACT	GTAGATACTA	AAGGGAACCT	GAGCTTGTAT	2340
TCTATTTGCT	AGTTGTTCTT	TTGCAAGATG	CACGTCAAAA	CGTAGCATAG	TATTGCCAAA	2400
AACAGTCATT	TTGAGCAAAG	AAAGCATTTT	TTTATATAGT	GAGGTTAATA	CCCCACCATT	2460
TAATGAGATA	TTTTCACCAA	TCATTACTGG	ATTGTAGCTT	ACATATTCCG	CTTTTCTATC	2520
GTAATAGTTG	ATAACTGGTC	TTTTGGAACA	ACTGGTATTG	TAAGTGCGTG	CTATGAGTTC	2580
GGTTTTTGGT	TTTATAAAAA	ACAATTGAGG	AACATATCCA	AAACCTTTTA	AATCCATTCT	2640
TGGAAATAAC	ACTAAAAAAT	TATCTGCTCC	GAAAAGAGCA	AATATTTGGG	TTATTACATC	2700
TCTTATTATT	CGAGTAATCT	CCCAGAATTC	TTTCTTTTCA	ACATCTTTGA	TTTTTTCCTC	2760
GAATTTTTTC	TTTTCAAGAT	TATTATTGAT	AATATTTTTA	TTGTTAATAT	CCATAGAATT	2820
TCCTTTTTAT	TTGAAATTTT	CTAAATCATC	ACCCCCGGTG	TTATTGTTGT	TCTTTCCAAA	2880
AATCGTATTA	TTAATCCAAC	CAGTCGCGAA	GTTATAAGTA	TTACCAACAA	CATTACTAGC	2940
GGTATTATAT	AATGAGCTGC	CAATGTTTTT	TATTCCGTCA	AAAGCACCCCT	TTATACCGCC	3000
TGTTATGGCA	TCAACGATTT	GTTTTAAGAT	TTGTTCAAAA	TTAAGGTTCA	TAATCTTTTC	3060
AAGAATACCA	GAAATTTTGC	CAATTACTGG	CATCAAAACA	TTATTAGTTA	CGTCTTCAAG	3120
ATTTTGCTCT	ATTTTAGCTA	AATTACTTTT	AGCTAAAGCA	ACTTCATCAG	AATGACCCAT	3180

TATATTCAAA	GATGATATAT	CTTTTATTA	GTCTTTAAT	ATCTCTGGCC	TTAGCTTTTT	3240
TTTCCCTCCC	TCTTGAGTTA	GAAACTCTAA	CTTGTTTTTC	ATGGCTTCTA	GATATTTTTTC	3300
TCCAAATTTG	TCTATAGGTT	TCAATATATT	GAAAGCTTCT	GTAAGTTCCC	CTTTAAGTAT	3360
TTTTGAAACA	ACTTCAACAG	CACTTTCGTT	ATCACCAACA	AGCCCCGTAC	TTCTAAACAT	3420
AGCTGCTAGT	TTTGTTCGAT	TTAATACATT	CTCTCCCTCT	TCATCATTA	TTTTTAATTC	3480
CCTGATGTGG	CCTTTAAGCA	CACTCGATGT	TCGCAGAAAG	TCTTGTTGTT	CTAATTTCCG	3540
CTCAAATCCT	TTCAATCCCT	TAATAGCACC	CAAAATATTT	TCACGTTCTT	TTTCACTGTA	3600
AAACACTTTA	TTAAGTTGTT	TTAGTTGTTC	TTCTTTAGAT	TTATTTTCAA	CTGCTTTTTT	3660
AGCAAATCCA	TACATAAATC	CAATAAGCCC	GCCACCAACT	TTACTTACAG	CGTTGCCAAT	3720
GACATTTTCT	AAAGCACTAC	CTATTGCAAT	TTTGGCAACA	AGTCCTTTTC	CTTGAGAAGC	3780
TGCGAGCATT	TTACTTTTGT	CTTTTGATTC	TTTTGCAAGC	TCTTTATACT	CAAGGCGTCT	3840
TTTGTCTCTA	TCAGACATCA	AAGATCTTTT	GAAAGCTTCT	TTTCTTGCTT	TCTCAAACCC	3900
CATGCCCTGT	TTCATAAGCT	TTTTAGTCTG	TGTAAGTCTA	TATTTCTCAA	CACGCTCTCT	3960
TAAGCTTTCA	AATTTAGATT	GTTTGCTAAG	TTCTTTTTC	TTGTCCGACA	AATTATTTTT	4020
TACAATATCT	TTAGTGCTAC	CCAACTAGA	TTTTTTGGGT	TTAAGATATT	TTTCCATTTT	4080
GGAAATATCT	TGTTCAATAG	CCTTTTGT	TGCAGCATGA	TCAAGAATCC	CTTTAAATTT	4140
AATGGTGAAT	TTGTCGCTCA	TTAAGCCCTC	ACTTGCTTAA	AATTAATTCA	TACAATCTTT	4200
TTTCTAATTT	AATATCAGCA	AGTCTATTTA	CCTCTAAAAG	CTCGTCATAA	GGCAATTTCT	4260
TTACCGAGTC	GTATGAGCAA	ATATTCATAA	TTACTGGAAA	ATAGTATTTG	TCGTTCTTAA	4320
TTTCGTCAAG	CAAGTTAAAA	TACTTTTTC	TAGTCTCATT	AAGACTTGCA	ATGGCTTTAT	4380
CAATATCTCT	ATTTCTTTTG	ATCATTTAGC	AACCAGCTCA	TTGGAATTTG	ATGTACTTGA	4440
TGAAAGCGAA	GTGGCTACTT	TTTCATAATC	AAAGTTTTC	TTGATATAGT	CAAAAGTAAC	4500
AAAGTCCCCA	ACATTATTTT	CATACTCACT	CAAATATACC	AAAGCGGGTT	TTTTTAGATC	4560
ATTGTCTAAA	TGAAAAGTAT	TAAATTGTGC	GGTGTAATTT	ATTGCAACAA	GATAGTCTTT	4620
ATAATAAGAA	ATAAATCTCT	TATTTTGATC	CAAAATCACA	TAGAATTCGT	CTAAAAATTT	4680
TGGACTTATC	ATTAAACTTG	TGATTTCTCT	TAAGTATTGA	ACCTCATTA	GCTTTAAAC	4740
AGCGTCACTT	TGATTAAATC	CGAGTACTCT	ATCCCATTC	TAGACCGGCA	ATACTTTTAG	4800
TGGATATTCA	TAAGTTTAT	TTTTAGTTAA	AATTTTCATC	TTATATCTCA	TTATCATAAT	4860
AAGACTCTCC	TTTAAAGAGT	TGTTTGGTTT	AGATTTTGG	CAATTAATAG	CCCTAATTTT	4920
AAAAGATACT	TTTTCGGCCT	CAGCAGAATA	ACTTCTTGAA	GGCTCTTCAG	TAAAAATTC	4980

ATAGTTAGAA ATAATTTTGG TAGCAATTCT ATCATTGAAT GCTAAATCAA GCATTTTATC	5040
CTCTTTTCTC ACATCCATGT TGTAAACTG TTCATCAGAA AGTTCAGTTA ACAAATGTA	5100
GTCATGACTA CCCAAAGTAA CTTCAATGTT GAAAACATAA GTTATCGTTT TGGGATCTCT	5160
TAAGCTTAT ACAGGCATAC CTTTATCTTC ACTACTAATC ACTGCTCTTG TTGTGGGTTC	5220
GCTTGTAAGT TCTAGTTTGC CACTATGTAG CTGTGTACCA CCAATTGAAA AATAAACTTC	5280
TCTTAAATCA TAAAATTGCA TTTTATAGCCC TCCTTTTAAG CACTTAAGCT GTTTTGATAA	5340
TCAACTATAT CTTGAGTAGa ATTACTAAAG AAACAGC	5377

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5121 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

CnTTTGCTGT TATAGTATCT AGATTATCtT CTGCCGAATT TATTACAGCT GTTAATGAAT	60
TTAAGGATGC TACTGAAAAG TATGCTAATG GCAATAAAGG AGACCATGCT GTTGATGTTG	120
TTGTGGGTGC TATTGCAGGC ATAGCTTTTG ATAATGAGAA TAGATTGAA AGAGCCAAAA	180
TGTTTGCTAA TAAGGAAAAA GGTGCGGAGG TAGACAAAAT GATTGCTGCC ATTGAGAAGC	240
TAAGAGCTAC TTATACTGCA GTTAAGCCTA AAAATAAAGA TAAATAAATA ATAAATGTAA	300
TAAGTGGGAA AATACAGAGA ATATTCTTAA GCATTTTCTA TTGAGCTTTT TGTATACATA	360
ATTTATTTTG GTTATGTTTT ATTATGTTTT ATTTTTTATA GGATATAAAT AGACATATAA	420
GTCTATAAAA ATATTGTGCA CACAAGACAT TCATGTAATC ATTTATTTCT ATTATTATTT	480
GATAAATTTG CTCAATATGG CTTTTTTTAAA AAAATAGGGC ATATCTTTAA AACCCCTTATC	540
AATAAAGCAG CATTAATGAT AATTTTGGAA ACATTTGCTA CACGTACAAG ATATTAAACC	600
ATTTTTTTTC TTAGCATTA TATCATTATT ATATATTTAA AAATAAGCCA CGATTAAGGA	660
TCCAAATCCT CCTGGGACAA CATATGGGGT TGATCGTATA TATTTTAGCC CCTATTCCAT	720
TAAAAATAAC ATTTGATAAT TCATTTAATT TAAAAATGAA TTATCAATTA CAACAACTC	780
CATGTGATAA GATGGATAAT AACTATCGGA TTTTCTTAA TCCCATTATC TAGCATCCGG	840
AGCTTTCAGA GTAAACATTT ACATTTGATT TTTTATTAAA GAGCTGCTCT TTTAATATTA	900
CCAGACTAAA ATTATTTTAA ATAACATTTA CACATAATAA CACTATCTAT TGGACTTACT	960

967

GAATCATACT	AAGATAAAGA	AGTTGGCAAA	TATATTTTGG	TTGAACAAAT	AATTAAGAAG	1020
TGTTAAAACT	AATGAAAAAT	CCATTAATTT	TAAGGAAGGT	TTACAAAACA	TAAAAGATTT	1080
CTTCCTGCAA	AGTTATTTAC	CTAAATATGC	TTAATAGTAA	TAGCTTAAAA	GCGGATATAA	1140
ATATTATTGT	AAGAAGAGAG	TCGACAATTT	TGATACTACT	TAAAGGTTTG	GATTATTCTA	1200
TTTCTGCTTT	GTTTGTTTTA	AAGCGATTTA	TGGTTTGAGG	CTTAATGTTG	ATTTTTTTTAC	1260
CTTTTTTTTAT	TAAATTTTAT	TTACAATAAA	GCTTTTACTA	TAAATGAATT	ATGAATATTT	1320
TAATAAGAAC	AAGTCAKATC	TCATAATTAG	TGCAATCAAG	AAAAAAAaTT	AGCACATATC	1380
CATTTATGAT	TTAATTTCTA	CTATTTAGAT	CAGTGGTGAT	GCATTATTTT	AGCTTAAAGG	1440
AAArYATAA	CAATAGTTAA	AGTACAGTAG	ATGTCTTTTA	ACTTATCACC	TATATAAATA	1500
CAACACTAAT	TAATAYATAA	ATAGAAATGA	TTATTTTCAT	AATATAYCAT	AAGCAAGCCG	1560
TTTACAAGCT	TCCGCTATAG	mACTGGCAGC	TTCGCTTAGC	AATTTCAATG	ACTCGCCAAA	1620
CTGTCCCGAT	GCACTCTTAG	CACCCTGCAA	CAACTCACCA	CAAACACCAT	TGCCATTACC	1680
TTTAACGTCG	CCAAGGTATT	TCTCTACATC	TTTCATTAAC	TCATTTATAC	ATTTTTTTAAC	1740
CAAATCTTTT	CCTTTTGTCT	TAGGATAAGA	ATTCAAGCTC	ATTATAGAAC	AACTATACTC	1800
ATCCTTTTCA	TTTTTATTAA	ATTCATCTAC	CACCTTCTTT	ATTTTCTCGC	AGmTATTATC	1860
ATCAAAATTA	TCATTATCGC	TATCATTTAT	TTTTTGGCATC	ACAGCTTCTA	ATATCTTrTC	1920
TAACAAGCAT	ATTCTACCTA	TCCCGATCTT	CATATTGTCT	GAAAGAGGAT	ATGAGGCATC	1980
ATATCCTGAA	GCTATCAATA	GCTTTAAAGA	TTCAATCAATC	TTTTTGGCTG	ATTCTCTAAT	2040
ATCTCTTACA	AGTGAGGGAA	CCTCTCCCAA	TGCTATACTA	GCATTCCCCT	TTTTACTACT	2100
TAAAACCTTA	TCTTTAGATT	CCTTGGCAGA	AATACTAGCC	TTTTCAACCA	TATCTTTAGG	2160
ATTATCCTCC	TTACTTAAGG	CCTTAATTTT	CAATGCAGAT	TCAAACATAC	CTTTTACACC	2220
CACAACCTTA	GGATTGAGT	GGCCACCACC	TTTTTCCATA	GTGTCATTTA	AATTTGAATA	2280
TCATAATTTA	CAAGACATTG	CTAAAAAGCC	ACTAAACAAA	TATAAATATA	TTTTTCATCAT	2340
ATTTAAACCT	CTCTTTACAA	GAGTAATTTA	CATCAyTTTA	TTAGGATTAC	TACCTATCCG	2400
GCATTTAATC	TTTCTGAGAT	TATCTATTTT	ATCTATCAAT	GTAAAGTTAA	ATGAACTGCC	2460
AAATTATTTG	TTATATTTAT	ACTCTTTGTT	AGCTTTATGT	TTTTAAGTTT	TTAAACAATA	2520
TCTATCTTTT	TGCCyTATAA	TTTTATCTGC	GCCCAGCTTC	ATAATACACT	CATCTTGAAT	2580
ATAACATGAA	AAAATATAAT	ATrCCAACCTA	GAAATCTTAT	AATTCATTTT	TTAGTTCAAT	2640
ACTAAACATA	TTGTAAAAAG	GAGTATCCTT	AAGATTTATC	TTTTTATTAA	ATTCCAATAT	2700
ATTTGACACC	TTTAAAGAAC	ATTCTTTAAG	AATTAaaaaa	TTATTTTCAA	AATAGAATTG	2760

CAAGGAATGA	GTATTTAGAT	TGGTTCTTAA	AGAAACCGTC	GTTTGGAGTA	GCTCATAAAT	2820
CCATGCTAGT	TTGATCCCAG	CTCCCCAAAA	ATAATTATTA	TTCTTCGAAT	AACTCTCAAA	2880
TACTATTGAC	AAATCATTAA	AAACGTCATT	TTCAAAGCTA	ATATAATATC	TAAGACCAAG	2940
CAAAAACTA	TTGTCATCAT	CATCAAATTT	ATAATTTTTA	GACCAAAGTA	GGTCTTGTCT	3000
TAACGTAGAG	TAAAAAATA	TTCCACTATA	AAATTCAAAT	AAAAAATCAA	AAATAACAGY	3060
AATATCAAAA	GTTTTATTTT	CAATGCTAAA	TGGGAATTCA	ACCATTGCAA	GTAAATCAAC	3120
TTCATTAAAA	GATGCTTGAA	AATAAAGCCA	AGGGGATAAA	TATTTGGGAG	ATAAAAATTT	3180
ATCTAAGCTT	TCTTTGTCTA	ACATAGAACC	CAAAGAGACA	GAATAATTAG	AAATAAAATA	3240
ATAAAACTCA	AAAAACCATT	CTGGTTCTAT	TGTGGTCCCT	TTTAAAACAA	TATTTTCAAT	3300
TAATCCATTT	CCTAAATAAT	AATTTTGCCT	AACTAATTTA	AAAATAAAAT	CATTAAAGCT	3360
TAAATTGAAG	AATAATTTAT	TAAAACTAAA	ATATTGATCa	TTATTTTGCA	CAATAAAAGA	3420
AGGTGCAATG	CCAAATTCTA	ATATTTTATA	GTTTAATAAA	AATCCTAAAT	AAGCTTCATT	3480
GkCAAATTGT	AAAGCTCCTG	TACCAAAAAA	ATCTTTTTTA	TCTTCATCGG	GCAACAATAA	3540
AGAGGAATTA	CAATGCCAA	GTCAATAAGA	TTCCAATAA	TTACTACAAC	ACATAAAAAA	3600
GAATTTAAAG	AAAAACAAA	ACTTTGCGTT	GTGCGAAAAC	TTTAACTGCA	AATAATATTG	3660
AATCTTACAA	TCAAATTTT	GGAGATATTA	AAACAAATAT	AAAACATTTC	GAAGACCATT	3720
TTATGAAAGA	ATACTTTGAT	TTTATCTCTC	GGATTAAATC	TATTAAATCT	ATACAAATTG	3780
TTGTACTTGA	TTTTTTAAAA	AGAGAAGAAT	TATAACTTAT	ATTCTTAAAT	TTCATGCAAT	3840
CTAAATTTAC	GCTAAAAACA	TCAATGGAAA	TTAAATCTT	AATATTAAAT	AAGTTTAATA	3900
TCATTTGACA	ACAATATTAA	ATTGTAATAT	TATTATTTTT	AACTAAAATT	AATATTTATT	3960
AATTCAAATT	TATAAGGAGA	ACATTTTGAA	AAACCTTAAA	TTAAATATTA	TTAAACTTAA	4020
CGTTATTACA	GCAATATTAA	CTTCAATTTG	CATATCATGT	GCACCTTTTG	GCAATGTTAA	4080
TCCAAACGAA	CCAAAAAATC	CTACCACTTC	TAAAAGTCTA	AAAAAAACAA	AACGAAGCAA	4140
CAATTCTAGA	AATCTAAAAA	ACACAAGCAA	TCACACCAAT	TCAGAAAATT	TAACAGGAAA	4200
TTCAACAAAA	AATCCATCAG	AAAATAACCA	AAATCTTGAA	AATGAATCTC	AAAATTCAAA	4260
ATCTTCAAAT	CAAAATTCTC	AAGAAGAAAC	CACAATCTCA	AAATTAAAAA	ACATTGGTAA	4320
AGACCTGGAA	GCTCAAAAAA	AGAAAGAAGA	TACAGGAATA	ACTAAAATGT	CTAAAATTGA	4380
TAATGCTAAA	TATGATTTTC	TAGAGACTTT	TAAACTTAAA	CAAGATGATG	TTTTTATGTT	4440
TCATGCTAAA	ATGAAATTAA	AAAGAATAAT	TTACCCATCC	CTAAATTACG	ATACAAAAAA	4500

969

AATATTGGTA TTAAAAGAAA TTCTTGAAAA ACTTGATACA GAAGATAATA ACCGAAGAAT 4560
 AGCTGGTCAA TTTTGTAGAAA CATCAAGGGA TATTCAACTT CATCTAGAAG ACACGTATTT 4620
 AAAAAAATA CAAGATACAT TACAAACTCT AAGTGAAAA GAAGCCGAAA AGTTGCTACA 4680
 AGGTGTAAAA CTTGATTTAA AGAAAAACA AAACCTTGCT AAAAGTTTAA ACGCAACCAT 4740
 TGACGCTTAC AATAAAAATG TTGATAACAT TAAATAGAT AATAAAGCGC TAGCAAAACA 4800
 CATAAAGGAT AAATATTCCC ATCCTCTTTA TCTACTAAAC CAAGCTGATT AATCTAAATA 4860
 AAAAAATAAT ATGCTGCACT TTATATTTTA AAAAGAGAAG AATTAACTTC TCTTTTTTGT 4920
 GTTCATACAA TCTAGATTAT CACTAAAAAC ATGCAATAGA AATTAAATTT TCAATATCAA 4980
 ATAAAAATAA ATTTAATATT GTTATTTTGA ATTAAACTA ATGTTTAGTA ATTCAAATAT 5040
 ATAAGGAGAG CACATTTTGA AAAACCTAAA TTAAATATTA TTAAGCTTAA CTTTATTACA 5100
 GCAATACTGA ATTCAATTTT C 5121

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5107 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

GCTGTGAAGG GTAATAATGA GAAAGAGAAG GCTGAGGGGG CTATTAAAGA AGTTAGCGAG 60
 TTGTTGGATA AGCTGGTAAC ACTGTAAAGA CAGCTGAGGG GGCTTCAAGT GGTACTGATG 120
 CAATTGGAGA AGTTGTGGAT AATGATGCTA AGTTTGCTGA TAAGGCGAGT GTGACGGGGA 180
 TTGCTAAGGG GATAAAGGAG ATTGTTGAAG CTGCTAGGGG GAGTGAAAAG CTGAAAGTTG 240
 CTGCTGCTAA AGAGGGCAAT GAAAAGGCAG GGAAGTTGTT TGGAAGGCT GGTGCTAATG 300
 CTCATGGGGA CAGTGAGGCT GCTAGCAAGG CGGCTGGTGC TGTTAGTGCT GTTAGTGGG 360
 AGCAGATATT AAGTGCATG GTTAAGGCTG CGGATGCGGC TGAGCAGGAT GGAAAGAAGC 420
 CTGCAGATGC TACAAATCCG ATTGCTGCTG CTATTGGGAA TAAAGATGAG GATGCGGATT 480
 TTGGTGATGG GATGAAGAAG GATGATCAGA TTGCTGCTGC TATTGCTTTG AGGGGGATGG 540
 CTAAGGATGG AAAGTTTGCT GTGAAGAATG ATGAGAAAGG GAAGGCTGAG GGGGCTATTA 600
 AGGGAGCTGC TGCAATTGGA GAAGTTGTGG ATAATGCTGG TGCTGCGAAG gCTGCTGATA 660
 AGGATAGTGT GAAGGGGATT GCTAAGGGGA TAAAGGAGAT TGTTGAAGCT GCTGGGGGGA 720
 GTGAAAAGCT GAAAGCTGCT GCTGCTGAAG GGGAGAATAA TAAAAGGCA GGAAGTTGT 780

TTGGGAAAGT	TGATGGTGCT	GCTGGGGACA	GTGAGGCTGC	TAGCAAGGCG	GCTGGTGCTG	840
TTAGTGCTGT	TAGTGGGGAG	CAGATATTAA	GTGCGATTGT	TAAGGCTGCT	GGTGAGGCTG	900
AGCAGGATGG	AGAGAAGCCT	GAGGATGCTA	AAAATCCGAT	TGCTGCTGCT	ATTGGGAAGG	960
GTAATGGGGA	TGGTGCGGAG	TTTGATCAGG	ATGAGATGAA	GAAGGATGAT	CAGATTGCTG	1020
CTGCTATTGC	TTTGAGGGGG	ATGGCTAAGG	ATGGAAAGTT	TGCTGTGAAG	GGTAATAATG	1080
AGAAAGAGAA	GGCTGAGGGG	GCTATTAAAG	AAGTTAGCGA	GTTGTTGGAT	AAGCTGGTAA	1140
CAGCTGTAAA	GACAGCTGAG	GGGGCTTCAA	GTGGTACTGA	TGCAATTGGA	GAAGTTGTGG	1200
ATAATGmTGC	kaAGGyTGCT	GATAAGGCCA	GTGTGACGGG	GATTGCTAAG	GGGATAAAGG	1260
AGATTGTTGA	AGCTGCTrGG	GGGAGTGAAA	AGCTGAAAGT	TGCTGCTGCT	AmAGrGGrsA	1320
ATAATAAAGA	GGCAGGGAAG	TTGTTTGGGA	AGGCTGGTGC	TGATGCTAAT	GGGGACAGTG	1380
AGGCTGCTAG	CAAGGCGGCT	GGTGCTGTTA	GTGCTGTTAG	TGGGGAGCAG	ATATTAAGTG	1440
CGATTGTTAA	GGCTGCGGCT	GCTGGTGCGG	CTGATCAGGA	TGGAGAGAAG	CCTGGGGATG	1500
CTAAAAATCC	GATTGCTGCT	GCTATTGGGA	AGGGTAATGC	GGATGATGGT	GCGGATTTTG	1560
GTGATGGGAT	GAAGAAGGAT	GATCAGATTG	CTGCTGCTAT	TGCTTTGAGG	GGGATGGCTA	1620
AGGATGGAAG	GTTTGCTGTG	AAGAAGGATG	AGAAAGGGAA	GGCTGAGGGG	GCTATTAAGG	1680
GAGCTAGCGA	GTTGTTGGAT	AAGCTGGTAA	AAGCTGTAAA	GACAGCTGAG	GGGGCTTCAA	1740
GTGGTACTGC	TGCAATTGGA	GAAGTTGTGG	ATAATGCTGC	GAAGGCTGCT	GATAAGGATA	1800
GTGTGACGGG	GATTGCTAAG	GGGATAAAGG	AGATTGTTGA	AGCTGCAGGG	GGGAGTGAAA	1860
AGCTGAAAGT	TGCTGCTGCT	AAAGGGGAGA	ATAATAAAGG	GGCAGGGAAG	TTGTTTGGGA	1920
AGGCTGGTGC	TAATGCTCAT	GGGGACAGTG	AGGCTGCTAG	CAAGGCGGCT	GGTGCTGTTA	1980
GTGCTGTTAG	TGGGGAACAG	ATATTAAGTG	CGATTGTTAA	GGCTGCTGGT	GAGGCTGCTG	2040
GTGATCAGGA	GGGAAAGAAG	CCTGAGGAGG	CTAAAAATCC	GATTGCTGCT	GCTATTGGGG	2100
ATAAGATGG	GGATGCGGAG	TTTAATCAGG	ATGGGATGAA	GAAGGATGAT	CAGATTGCTG	2160
CTGCTATTGC	TTTGAGGGGG	ATGGCTAAGG	ATGGAAAGTT	TGCTGTGAAG	GATGGTGGTG	2220
AGAAAGAGAA	GGCTGAGGGG	GCTATTAAAG	GAGTTAGCGA	GTTGTTGGAT	AAGCTGGTAA	2280
AAGCTGTAAA	GACAGCTGAG	GGGGCTTCAA	GTGGTACTGC	TGCAATTGGA	GAAGTTGTGG	2340
CTGATGCTGC	TAAGGTTGCT	GATAAGGCCA	GTGTGACGGG	GATTGCTAAG	GGGATAAAGG	2400
AGATTGTTGA	AGCTGCTGGG	GACAGTGAGG	CTGCTAGCAA	GGCAGCTGGT	GCTGTTAGTG	2460
CTGTTAGTGG	GGAGCAGATA	TTAAGTGCGA	TTGTTAAGGC	TGCGGCTGCT	GGTGCGGCTG	2520

971

AGCAGGATGG	AGAGAAGCCT	GCAGAGGCTA	AAAATCCGAT	TGCTGCTGCT	ATTGGAAGG	2580
GTGATGGGGA	TGCGGATTTT	GGTGAGGATG	GGATGAAGAA	GGATGATCAG	ATTGCTGCTG	2640
CTATTGCTTT	GAGGGGGATG	GCTAAGGATG	GAAAGTTTGC	TGTGAAGAAT	GATGAGAAAG	2700
GGAAGGCTGA	GGGGGCTATT	AAGGGAGCTG	CTGCAATTGG	AGAAGTTGTG	GATAATGCTG	2760
GTGCTGCGAA	GGCTGCTGAT	AAGGATAGTG	TGAAGGGGAT	TGCTAAGGGG	ATAAAGGAGA	2820
TTGTTGAAGC	TGCTGGGGGG	AGTGAAAAGC	TGAAAGCTGC	TGCTGCTGAA	GGGGAGAATA	2880
ATAAAAAGGC	AGGGAAGTTG	TTTGGGAAAG	TTGATGGTGC	TGCTGGGGAC	AGTGAGGCTG	2940
CTAGCAAGGC	GGCTGGTGCT	GTTAGTGCTG	TTAGTGGGGA	GCAGATATTA	AGTGCGATTG	3000
TTAAGGCTGC	GGATGCGGCT	GAGCAGGATG	GAAAGAAGCC	TGCAGATGCT	ACAAATCCGA	3060
TTGCTGCTGC	TATTGGGAAT	AAAGATGAGG	ATGCGGATTT	TGGTGATGGG	ATGAAGAAGG	3120
ATGATCAGAT	TGCTGCTGCT	ATTGCTTTGA	GGGGGATGGC	TAAGGATGGA	AAGTTTGCTG	3180
TGAAGGGTAA	TAATGAGAAA	GGGAAGGCTG	AGGGGGCTTC	AAGTGGTACT	GATGCAATTG	3240
GAGAAGTTGT	GGATAATGAT	GCGAAGGCTG	CTGATAAGGC	GAGTGTGACG	GGGATTGCTA	3300
AGGGGATAAA	GGAGATTGTT	GAAGCTGCTG	GGGGGAGTGA	AAAGCTGAAA	GCTGTTGCTG	3360
CTGCTACAAG	GGAGAATAAT	AAAGAGGCAG	GGAAGTTGTT	TGGGAAAGTT	GATGATGCTC	3420
ATGCTGGGGA	CAGTGAGGCT	GCTAGCAAGG	CGGCTGGTGC	TGTTAGTGCT	GTTAGTGGGG	3480
AGCAGATATT	AAGTGCGATT	GTTACGGCTG	CGGCTGCTGG	TGAGCAGGAT	GGAGAGAAGC	3540
CTGCAGAGGC	TACAAATCCG	ATTGCTGCTG	CTATTGGGAA	GGTAATGAG	GATGGTGCGG	3600
ATTTTGGTAA	GGATGAGATG	AAGAAGGATG	ATCAGATTGC	TGCTGCTATT	GCTTTGAGGG	3660
GGATGGCTAA	GGATGGAAAG	TTTGCTGTGA	AGAGTAATGA	TGGTGAGAAA	GGGAAGGCTG	3720
AGGGGGCTAT	TAAGGAAGTT	AGCGAGTTGT	TGGATAAGCT	GGTAAAAGCT	GTAAAGACAG	3780
CTGAGGGGGC	TTCAAGCGGT	ACTGATGCAA	TTGGAGAAGT	TGTGGCTAAT	GCTGGTGCTG	3840
CGAAGGCTGC	TGATAAGGCG	AGTGTGACGG	GGATTGCTAA	GGGGATAAAG	GAGATTGTTG	3900
AAGCTGCTGG	GGGGAGTAAA	AAGCTGAAAG	CTGCTGCTGC	TGAAGGGGAG	AATAATAAAA	3960
AGGCAGGGAA	GTTGTTTGGG	AAGGCTGGTG	CTGGTGCTGG	TGCTAATGGG	GACAGTGAGG	4020
CTGCTAGCAA	GGCGGCTGGT	GCTGTTAGTG	CTGGTTAGTG	TGGGGAGCAG	ATATTAAGTG	4080
CGATTGTTAC	GGCTGCTGGT	GCGGCTGCTA	GTGAGGCTGA	TCAGGAGGGA	AAGAAGCCTG	4140
CAGATGCTAC	AAATCCGATT	GCTGCTGCTA	TTGGGAAGGG	TGATGCGGAG	AATGGTGCGG	4200
ATTTTGGTGA	TGGGATGAAG	AAGGATGATC	AGATTGCTGC	TGCTATTGCT	TTGAGGGGGA	4260
TGGCTAAGGA	TGGAAAGTTT	GCTGTGAAGA	ATGATGATGA	GAAAGGGAAG	GCTGAGGGGG	4320

CTATTAAGGG AGCTAGCGAG TTGTTGGATA AGCTGGTAAC AGCTGTAAAG ACAGCTGAGG	4380
GGGCTTCAAG TGGTACTGAT GCAATTGGAG AAGTTGTGGC TGATGCTGCG AAGGCTGCTG	4440
ATAAGGATAG TGTGAAGGGG ATTGCTAAGG GGATAAAGGA GATTGTTGAA GCTGCTGGGG	4500
GGAGTGAAAA GCTGAAAGTT GCTGCTGCTA AAGAGGGCAA TGAAAAGGCA GGGAAGTTGT	4560
TTGGGAAGGy TGGTGmTmT GCTCATGctg GGGACAGTGA GGCTGCTAGC AAGGCGGCTG	4620
TGCTGTTAG TGCTGTTAGT GGGGAGCAGA TATTAAGTGC GATTGTTAmG GCTGCKGrTG	4680
CGGCTGAGCA GGAKGGAAAG AAGCCTGCAG AkGCTAmAAA TCCGATTGCT GCTGCTATTG	4740
GGAAtAAAGA TGAGGATGCG GATTTTGGTG ATGGGATGAA GAAGGATGAT CAGATTGCTG	4800
CTGCTATTGC TTTGAGGGGG ATGGCTAAGG ATGGAAGTT TGCTGTGAAG GGTAATAATG	4860
AGAAAGGGAA GGCTGAGGGG GCTTCAAGTG GTACTGATGC AATTGGAGAA GTTGTGGATA	4920
ATGATGCGAA GGCTGCTGAT AAGGCGAGTG TGACGGGGAT TGCTAAGGGG ATAAAGGAGA	4980
TTGTTGAAGC TGCTGGGGGG AGTGAAAAGC TGAAAGCTGT TGCTGCTGCT ACAAGGGAGA	5040
ATAATAAAGA GGCAGGGAAG TTGTTTGGGA AAGTTGATGA TGCTCATGCT GGGGACAGTG	5100
AGCTGCT	5107

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5068 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

CACATTATTA AATCTAGAAT TGAATAATTA TTCTCAAAAA AAACATTATTA AATTTTACAA	60
CGAAATTCTT AAAAAAGATA ATAAAAATTC TTGCGATCTA CCAACAATGA ATAAATATCT	120
TGATATATTA GAAAAACAA AAACCATAGT AAAACTATCT TTTAAAAACC AGTCCAAATA	180
TATGATTTAT TATAAAATTA ATTACCCCT TAAAGTGTTC CGTTCAACAA TACAAGACTA	240
CTATCAAACA ATATCAGATA AACTAAACT ACGGTTAGAA CTAAACTATC CTACTACTAT	300
TTAATCGTAA AAAATATTTT TTTGCAAATT AAGCAATTTA GAAATATAAA TGTAAGACA	360
TATATTTTTA TTTGATAAAT AATAAAATT ACTGGGCAC TATTTGAAA AATTTTAAA	420
AGAAATATTA AGTATGAATA GCAAAAATAG GCTATCTTCA CACTTAATAA TTCTTATTTA	480
CACACTAAAC AACATTGACC TAAATTCAAA AAATATTGGA TACTATAGTA GGGGCTTTAT	540

973

ACGCCGTGCG TTTACTTTTA ACATAGATAG ATATTGCAAT ACTAGTAAAG ATATTGAAAT	600
AGACATAGAC TTATTAATAA AGTATCTCGA TTTTITAGAA AACAACTAA AAATTATAAC	660
TAATAAATAT AAAGTAGAAA AAAATATATT CAAACTTTAC TACATAATCA ATTATCCTTT	720
AAAAATATGT TACACAAAAA TTATGAACTA CTATAAATAG ACTATATAAT GATATTAAAA	780
AGAGAAACAT CTTTAGTATA TTACTAAAGG TGTTCCTCCC CTTAATCTAA AGTTGTTTTA	840
AGGTGTATAA TGGGGGTGAT ACCATATTTT AAATTATATA TCCCAAATTA ATtAAAAAAT	900
CAGGTATTGC AAATGTATTA TAGTGTCTCA TAGGCCTAAT AAAGAACAAT TAAAACTAAA	960
AAATATATAA ATAAAACGCA AATTAGAAAA AGAAATAACC GTCATAGTCA AACTTTATTT	1020
TAAGAAAAAT CCTAAATCTA TAATTTATTA TAAAGTTAAT TGCTCCTTAG AAAGAGTTTT	1080
ATTAAAAATA AAAGACTACT ACGTATTATT CTATGAAGAA TTAAAACAAT TTTTACAAAA	1140
AATCACTACT ACTTAATTAT AAATACATTA TAAATAAGC TTATGCAAAA CTTTAGAAAT	1200
ATATTGTTTT ACGCTAAAAA AATTTAAAAA AATACTGTGC TATATTTATA ATATAAATTT	1260
AATATAATAG GGGGCTAATT CATTATGGAT GGAGTAATTA ACAATACATT GGCAAGAATA	1320
ACAAAGCAAA TTTAATTTGC TAAGAATAAG TTAATCATTC TTGTCAAAAC ACTAGATCAT	1380
ATGAATAAAA AATTATTCCA TAGTGCAAT AAAAATTATG CTTATTCCTT AATAAGAAGC	1440
AAGTTTAATA AGGCTCTAGC TAAACTAAT CAACATGAAG TTGATTCTAA AACCCTGTTA	1500
GAATATCTTG AAATATTAGA AAAAATCCAA AAGTAATCTT CAAATGTTCC ACAAATAAAG	1560
AAAATGAAAG CTTTAGAGGC CTTTAGTAAG CTAATATAAT CCAGAAAATT TACTATAAAT	1620
CGATTATATA AATAGTAAAC CAATATCTAT CCTAGTGTAT TATGGCCTAT AATAGGCCCA	1680
ATAAGATAA TAATAAGCTT ACTATATTAC AAAACTAAAC CCTCGCTATA TTATGAAAAAT	1740
CAATACTAAA ATAATGGGCA CTAAAGCAA TTGGTTAAAA TAATTTCTAT AAATGCCTTT	1800
AAAAATTATT GAATATTAGA AAATATTATA TCAAAATCAT TTAATTGAAA TTAAATAAAC	1860
TAAATTAAAA GAAAAATTCA GATATATTTT AAATGTATTA TGGCATATAA TACTATAGCG	1920
CCCTAAACAA AATAAACAT AAATTATTAA AATAAATCAT TTATATAAAT CAATATATAT	1980
ATCTCAAACA AAAGAAAATT TATATAAATT TTAGGCCTAC TAGCGTATCG TAGACCTAAT	2040
AAATAATCAA CAAACACTG GTGTGTTTAT TACAATTAAA TTAATAATAT TATATATAAG	2100
ATTTAAAATT TTTTAAAAA AGAAATTTGT TATAAACATA TTGGTTAAAA TCAATATAAA	2160
TCAAAACAAA AAAATCTAAA TATTAATCTA ATAATATTCG AAATTAACAT CACTACAAAT	2220
ATAAATAACA ACAATAAACT ATTAAAAATAG TAAATACCT AAAATTTAGC TCTCAAAAAG	2280
ACATTCAATT GTCAAGCGAA ATTCAAGCAT TAAAAGATAC ACGAACCATT GCTAGTGCTA	2340

ATTCATCTAA	TCCGCCCTTT	AACTCCCCTA	ATTATATTAT	ATTCAAATTA	TCTTGAAAAT	2400
AGAAAAACAA	GTTGATAGAA	AAATTACTAT	TAATGAGATA	ATTAATGAAA	ATGGTAAAAA	2460
AACTAAAAAG	CTTTTGGAAG	TTCAAAAAGA	TAATATTTCC	CTACTTAAAA	ATGAATTCAA	2520
CATGGTGAAA	GTTTTAAGGC	TAAAGTTTAA	TGAAAACCTCT	ACAAACTCTA	CATTAAAAATC	2580
TACTTAGCAC	AGCAAAGTAA	TTCATACAAT	ATCTTAAGAA	AAGATTCAAC	TCTAAAAATA	2640
AAATTTAAAA	ATTGTGCTAA	TATTTTATTA	TCAAAAATTA	ATTATTAGGA	GGTTATATTA	2700
ATATAAAAAA	AACTTTCATA	TTAATATGAA	TTTTTAGTTT	AATAATGAAA	ATCTTTGCAC	2760
AAGATAAACT	TGAAAAAGAT	GTCGGACATA	TTACAAACAC	ATTGAAACAT	GAAAACTAAA	2820
AAGCAACCGT	AATTCTCTAC	CATTCATTTT	GAATGCAATT	GTAACTTTGG	AAATAGGATC	2880
TTTACAAAGT	TTTCATATAT	ACTCTTTGCC	AATATAAAGC	TAAAATAAAC	TATAAAAGTT	2940
TATCAAAGCA	CTATTCTTGC	TAAACTTAAA	AAGTTCATTT	AATAAGATAG	ATTACACTAG	3000
AATTAATAAG	CATAATGTAC	AAGTTTACAC	CAATTTTATC	TTTTCTCAAT	ATTTGTAAAT	3060
ATCAAAGCAT	TCTATTAAAT	CTATAGAAAT	TAAATATTTA	TGTAAAAGTA	TAATAATTAC	3120
GCTTAATAAA	AAAAATTATT	AACAGATATA	AAAATAATAT	AAACCTTCTC	ACAATAAAAA	3180
TATTGATATA	AATCTTCCAA	TATTTTACTA	TTCTACATTT	GATTAAATAT	ATATATTATA	3240
TTTAATATTG	GtTTATATTT	AATATTGGtT	TATAAATTTT	AGATTTTAAAT	TAAGGAGAAT	3300
ATTTATGAAA	TATAACATTA	TTGTAAGCTT	ATTTGTTTTT	TTATTTTTTAG	CTTGTAATCC	3360
AGATTTTAAAC	ACTAATCAAA	AAGATATGAA	GTACCAATCT	AGTAAAAAAG	GACTAAAATC	3420
TAATAAAAAA	AGACTAAAAT	CCAATAAAAA	GGGATTAACC	CctATAGCAG	AAGCAAGCTC	3480
AAATCAAAAA	GAAAGCTAAA	ATCAAGAAGC	AATCTCCAAA	AAAGAAAAAG	ACATTAATAA	3540
CCAAACAGAA	AACACACTGC	TTGATGATTT	AAAAAATTTA	ATAGAACAAG	CTAAATCGGA	3600
TAATGrTAAA	TATGTACAAA	AATTAAAAGA	AGAATCTTCA	AATCAATATG	GAATACTGGC	3660
TTTCAAAGAG	TTGTTCTAGC	CAGACGGAAC	TGAACAGTTA	TCTGCAAACA	CCGAAAGATC	3720
TAAAGCCTAT	AGAAAACGAA	CTTATAGTAT	CTTAAATGCT	ATCGATAATG	ATGCCTTAAA	3780
GAATTTTTTCA	GAAATTGTAA	TGGCATCAGG	CCAAACACAA	GGAATACTTA	ACAATCTCGA	3840
CTCACTTGGA	GGTGCCTTTG	AAGATATAGT	TGATTTTCTG	TATCCTAAAA	AAGATAATCT	3900
AGAAAAATTA	GAGATCCCGG	CCTTAAAAAA	GCTTAAAGAT	TCTTTTGAAA	ATTTTTTTAGA	3960
GATAAAAAAA	ATCACTTCGG	AAATGTTATA	CAAGTTCTTA	TTAGACTATA	AAAATAATGC	4020
AAATAGTATA	CAAACAGATG	CAAATGCACT	TAAATCTCAT	GCAAACACAC	TTTTTAATCA	4080

975

ACTGACAAAA	AAAATCGAAG	AATCAGAAAA	GCTAAAAAAT	GACATATATT	CAATAGAAAA	4140
CCTTTAATTT	ATATGCTATA	TATTGAAAT	GTCATAATGC	AAAGGCCAT	CTTTAATAAA	4200
AGATAGGCCT	AGCGTTATAA	AAACTGCTAT	TTCAACAATC	AATAATTATC	GAAATAGCTT	4260
ATTACCTCAA	TCACATGATA	GCTTTTTAAG	CTCTAACATA	AAAACAGCAA	TCTAACAGTG	4320
GACATAGTTC	CATAAAGCTT	TACTTCAGAC	AATTTTTACC	TTAGTTTTTA	TTTTTTTTAT	4380
AAGAAGAAAA	CTTAGAATTT	AGAGTTGCAT	TTTATATTTT	TATCATACAA	ATCGATTATA	4440
ATTACTCATA	GATCTACAAT	AGTATTGATC	GATTTTAGAA	TTATATTTTT	AATATTACAA	4500
TTGCTATATA	GTTTACTTTA	TGAAAAAAT	CTATCTATTT	TATGCAAAGA	AGATTAGTGC	4560
CACCCTGATT	TATATGATAA	TTGCCCTCCA	AATTAACAAC	ATATCGAATC	ATTAATACTT	4620
TTCCCCAAAC	ATTCATTTTT	AAATACCCCT	AATTGATAAG	CTCTCTATTG	TCAATGTCCA	4680
AGTGCTGCCC	TGCTACTAAA	ATGCAATATT	TATTATAAGC	AACTTTCTCT	ACTACTGTAT	4740
TTTTATTATA	TATTAAACAA	AAAATCAAAA	ACCTAATAAT	ATATTATTTT	AGGTCCCCC	4800
AAGCATCTCT	GATAACAAAG	TTATTTGATA	TTGGTTTAAA	TTCTTGTAAG	TTATTTGTAC	4860
ATACCATTTA	CTTTATTATA	AAAATAAAAT	TTCCCTTCAA	TATATTTCCC	CCACTTATCT	4920
AATTTAATTC	TCTGTGTTTT	TAAAAGCATT	TTTGTTTTTC	ATGTTTTTTT	GATTTTCAAT	4980
CATAAATAAC	AATAAACTTA	TTTATAATAT	TGAGAATATT	ATCTAATAAA	ATATTAAAGA	5040
TGTAATAAAT	AGTTACAAAA	AATTGCTG				5068

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4663 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

TTCTTTATTT	TGGCATTCAA	CTTTACATTT	ACCTTTTTTTT	ACAGTTTCAA	TAGGTTCTGG	60
TGCATTTTCC	ATGTTAAATC	CTTATACGGC	CTTTATGCTA	AATTCTTCTG	TGGTTAAAGA	120
ATTTTTTTCA	TTTTTTATTA	TTTCTAATAA	TTCAAGATGA	TATATACCAA	ATACTTTATT	180
GTATTCATTT	TTCTTTTGGT	TATTCAAATA	TTTTTTGATA	ATTGGCTTTA	GAATTTCAAT	240
ATTTGTTTCT	TTTTTTAGTT	GTTCAATAAG	GATATTGAAA	ATATTTTCCT	TTAAATTTTG	300
ATAATTTTGT	TGAGAATTTT	gCTTTTyyct	TTCAATCGmC	TTTCTAATT	TACGTTTTAT	360
GTTGTTTAAA	TCGyTATATT	TATGmyTTTC	AATAATAAAr	TGGGGCTTAA	ATTGTAAyT	420

TTCGTATACT	TTTTGTAAAT	TTTCTTTTAA	TGTTCGGGr	TTATATCCAT	TTTGTTyGAA	480
TTCTTTCTGA	GTGTTATTTA	rAATTyTyTT	TAGTTTCTCT	TGCTTTTCTT	TAAAGCAAGA	540
TTTATTTAAA	TTTGTTTTTT	TTAGCAATTT	ATTTTCAACT	CTTTTATGT	TTTGTATTAT	600
TTTAATCATA	GTATCTTTAT	CAACATTTAA	TGTTAATAAA	AAyGGAAGAA	TTTCTTTACA	660
TAAsAAGTTT	CTTTTtTTGA	ArTACTTTAT	TACTTGATAT	TTTTCTATTT	CTTTAATCTT	720
TCTTTCTTCT	TTTATATTAT	TTTTATTACT	TAAACACTCC	ACTGAATTTA	CACTACyATT	780
TTTAGAAyA	TyGTCTTTAA	AATGGTTATT	AACTCTAGAT	TTAAATCTAG	AGTTTTTTTCG	840
yTCTTyAAAG	TACTTGTTGA	TTTTCTGGTA	ACATTCTTTT	TTAGGATACT	TTAGTTTATA	900
rTAAATTTCA	GTyCCACAAT	TTACACCCAT	rTGTTGGTAG	TAATTAGTTG	TrACTTTTTAr	960
TACTTTTTCT	AATTTtTAAA	GATAATTTTG	CATTGTTCTT	AGwGTAGTGG	GAGCTAGmCC	1020
ATTTCTTTTT	AGATTTTCrT	TAAAGCAGTA	GAGTATGTTT	TGTTGTGTGT	ATTTTTTATC	1080
TTTTTTGTTT	AGAAAATCTA	GCGTTGAAGT	AAGAGATATT	AATTTGTGTT	GGTGTTTGTT	1140
GTGGCAAGTT	GGAATTTTTG	TTTTATTGG	GAAATTTTGC	ATTTTTTTTC	TCCGTTTACA	1200
TGTATTAGTA	ATTACTAATA	TAGTGCAAAA	TTTTGATTTA	AAAGTAAATA	CTTTTCTAAA	1260
AAAATATTAA	ATTTTAATTA	TTAATTTTGT	TAAATTAATA	TAAAAATTTG	TAATTTAGTA	1320
AAAATATAAA	TTGATTTTAA	TTCTAAGTTG	ACTTATACTA	CAAATAGCGT	AGTAAATGT	1380
TCGCATTTTT	TCTACCGTTT	ATATGAATTT	ACAAGAAATA	AAGATATGGG	CTTAACTAAG	1440
TTCTTTAACA	AGAGAATTTA	GCTAAGCCCG	CACTTTTTGT	AAAAATTTTT	TGTAAAGAAG	1500
TTGGCAAAAA	TAGTTTTTGC	TATATACTTA	TATTTATTAA	TACATATAAA	CGGAGGAAAA	1560
AGATGGAAAA	TCTTTAAAAC	AATAATAATC	CACAAGAAAA	TATTCAAGCA	GAAATTAAAT	1620
TCTTAAATGA	TATGAAAACC	CTAATGAAGA	ACTTGCCACG	TATTGACAAA	AGTCTTAAAG	1680
GGTACGGATA	TAAGTATCAG	GATTTCAATG	ACATATTAGA	AGAAATTGAA	AACGTTATTG	1740
AAAAGCATAA	TTtGGATCTt	AtGTTTAGGC	AATTTCCAAC	TTTTACACAT	GATCCATATG	1800
GTATAGTTCA	TGTTATTAGG	ACCACATTCT	ACAGCACAAG	CAGTGGGTAT	AGAGAGTCAT	1860
TTGATACCCC	AATTTCTACA	GAAAATTTGC	AATGGAACAG	TGAAAATGGT	TCTAAAAATG	1920
TAAATACATT	GCCACAATTT	GTTGGTTCAG	CTATTACTTA	TTTCAAAAGA	TACGCTTTAG	1980
TTGCATGTCT	TAATATAAAA	AGCGAAATGG	ATACTGATGC	AGCACCTATT	TACAATAATT	2040
ATGAAAACAG	AAATCTATG	CCTAACAAAC	AAGTTAGTGT	TAATCAAAAG	TAAGAACAAA	2100
AAAGAGAACA	AAAACAAGAG	ATTAATCAAA	TTCAGAAAAA	TAAyAyTATT	CAAAACCAGA	2160

977

AAAGAGATAT	TAAGCAAGAA	TAAAAAAAAG	ATAGGTTTTA	TTATTACAGT	GTTTTTAAAG	2220
AAGCGTTGTC	TAATATAAAA	GATTGGGTAA	ATAGCCCTAC	AACAAAAGAT	AATATAAACT	2280
CAATTATTCA	AAAAATAAGC	TTTATTCAGA	ATATAGACCC	CAATAATGTT	GATGATATCA	2340
AGAAAATTGA	ATCTGATTTA	ATCTCGTATT	TTGAGAAAAA	TAGTGATTTT	AAAAGTATAA	2400
ACTATTGGGC	GGAGATTATA	AAAAACTATT	TCAAGAAAAA	TAATArATTA	AAGGATTTAC	2460
AAGATTTTGA	AAAGTTTGTG	gTgTTTAAGA	GGACTGCTTA	TGGTCCTAGC	CCATTAATAT	2520
TCTTTAGTGT	CTTAAAAGAA	TATGAACGGT	TTGATGAGAT	ATTTGCAGCA	TAGCAAGATT	2580
CTTACATGGT	AAAGCCCCCC	TATTTGGGGG	CTGCTATATA	TTATGAATTT	TTGCACGTAC	2640
TACTTGCAGT	ATTTTCAAAG	CCGTCTATGC	CCCCTTTAAG	GGCCTCCTGA	ACGACCTGCT	2700
TGAAGGTATT	TTTATTTTCA	ACCTTATCTC	CAGTACAAC	GTCAAGTTCA	CTCTTTATAT	2760
GATCAAGTGC	AGATTTTATT	TTGCTTTCAT	CATATCCTAA	AAATTTATTA	AATTCTCCAT	2820
CATTGCCCAG	agCTtCTTTT	AACCAGTCAA	GrTGtGTtTT	TTGrTywTCA	kwTAGCTTTT	2880
CTCTAAGmAG	kTCTTCTTTA	GATTTwGGTT	TTTCTTGtGT	TGCTTCTTTT	TGGGTAAAT	2940
CACGTTTTTG	TCTACTTTTT	GTTTGGCTAK	TATTAGTATC	ATTAGAATTA	CAGCyGTTTA	3000
GCATTAGTAA	AAATAAACAA	AATAATATGT	TGATAATTTT	CATTfTTATT	CCTTTTTTTA	3060
TTATTAATAT	TCACTTAATC	AATTATTAAT	ACTAAATATT	GGATAAACAA	TTATTATTTG	3120
AATTGATATG	TTTTAAGTGA	GGTAGTAGCT	ATTTAGAAAT	GAAAGCAAAT	ATTAGCCCTG	3180
CTATCATTGT	GATAGACATT	GCTCCCATAA	TTCCCAATAC	CCATTTAAGC	ATTTCTGAAA	3240
GAGACATTAA	ATTCTTTTCT	ACATTGTCTA	TTTTAGCAGT	AAGTTCATTT	TTAACACTAT	3300
CGATCTTAGC	ATTAAGTTCG	CTTTTAACAC	TATCTATTTT	GACATTTAAA	TTCTTTTCTA	3360
CAGTATCTAT	CTTAGTATCT	AAACCATCTA	TTTTTAGATT	TAAATTCTTT	TCTACAGTAT	3420
CTATCTTAGT	ATCTAAACCA	TCTATTTTFA	GATTTAAATT	CTTTTCTACA	TTGTCTATTT	3480
TAGTATTAAG	TTCGCTTTTG	ACACTATCTA	TTTTAGAAAT	AAGATTATCA	AATTTTATAT	3540
CAAATTGTTT	TTCTAAATTT	TCTAAATCTC	TATATGTTAG	CTCATTGTGA	TAATATCTTT	3600
TAGATAAATC	TTGTGCTATT	AATTGTTCCA	TGCCCAGTCT	AATAAATCTT	TTATATATTT	3660
GTTCTTGAGT	TACACTTGCA	ATATTTGTTG	ACACTGTTTC	CATAAAATTT	TCCCTTATGG	3720
TCATATTATA	TACTATTTTA	GATTAATTGG	CTTTAGAGAT	TTTTATATGT	AAAGTAGAAT	3780
TTCTTGCAAG	AAAAACCTTT	TTGTAATTTA	CATTTTTAAC	TTCAGATATC	AGTTTTAAAT	3840
TTTTTACTGT	AGATTTTTTA	CAAAAACAGT	ATTGCAAAAA	CTCTTAGATT	ACTTTTTCTT	3900
TTCTTTGTAT	ACTACAATAA	CTCCAAAACC	CACTAAATGG	TTTAGTGATT	TAACCTCAAG	3960

AATATTTTCG GCACCTATTT GGTAAATAAA ATTTTCTAAC CCTATCCCTA TAATTTTCGAA	4020
TAGAGTTTTCG TTTTATCTT CTTTTTTTAT AGGAAAGTTA ATGTTATGCT TATGATCATC	4080
ACCGCCTTGA TCTAAAGCTA TTAAAGTTTT AACTTTTATA ATTTTCATCTT TTTTAATTTTC	4140
ATATGAAATT AAATTACCAA TACTGATAAT AAACATAAAT AACATTAATA AATTAATTTT	4200
TTGCACATTG TGTTCTTAA TAAATAGAAT ATTAACAATA TTATATCTTT ATTAAGATTT	4260
GCCCTAAAAT ATAAAATTTT ATTAAAATAT AGCAGTAATA AACGACTTTA AGAATATAAA	4320
TGGGAATTTT TTGCAAGAAA AAcCTTTTTCG TAATTTACAT TTTTAATTGA GAATATTTAT	4380
TATAGACTTT TTCCGCTATT GGTTTTGTTC TTTTAATGTA CTCTAAATAT ATGTTGATAT	4440
TATGTTTTAC AGCAGTTATG GaGTGTTTCGT CTTTTATGTT TGATAAATCT GGaTAAGGAT	4500
ATTCTGGaTA ATTTGGaTCA TTAACTTTAA CTTTTGTTCG aGCTAAAAAT GTTACTAGGT	4560
ACATAACATA CTCTGAAAGT TGTGTTTCAT ATTTAGCTAA AGATTTTAGT GTTGAATAA	4620
TTGGAGGTTT TGGCTCTTCT GGTAGGTTAG CAATAGTGGT GCA	4663

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4312 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

CAACTTCAGT TTATATTATC AAACGACAAA TAAAACATTA AGTACAATAA CCCAATATTT	60
CAAAAAGGAT GCACATTTTA ATAAAAAACT AAAGCTGTTT AACTACAATT GTTGCACTTG	120
AAATTTTTTA TACTAAAATA TAATACAAAT AATTATATTA ACAAATATCG ATTTTTATAA	180
AAAATAAGTA AAAGTAGTTT AGTTTACCTG AGTATTTAAA TACTTTTAAT TGAGGATGTT	240
TTATTTTAAA AAGGAGTGTA AAACATATGTC AAAAATGTTT GACGAAGTAT ATTGCTATTC	300
TTGTGGCAAG ATTTAAAAAA GATGCTGAGA TTTGTATTTT TTGCGGGGTC AGAAATAAAC	360
AAACCGAAAA CTACAATAAA CTTATAGTAT TTTTACTATG CTTACTTTTT GTTATTTAG	420
GAGTTCACAG ATTTTATGTA GGTAAAATAG AAACGGGCTT ATTATAATCA TACCTCTTCA	480
CTTTTAAATA TTGTTTATAA GCAGTGGGTC TAGGCATATT ACGATTATAC TCATGGCTCC	540
CCTCGCCAGA ATACTTAATA TCTAGAGAAT ATAACTCCTC TATACATGAA TACAGCCAAC	600
GAACATACG CATAAATTTA TTATTGTTCT GCTCATTTTT TACCATAATA AACAACTTAA	660

979

TCAGGTCTTT	AGATTGCTCA	GACCCTAAAT	CTAGAAAGAA	TTTATTAAAA	TACTCCTCAT	720
TATAGTCACT	CACTGGGmGT	ACTACAYCAC	GATAATTAGG	ATCTTTTAAA	CTAATTAAAG	780
TCTTTTTFAT	CTCAACCAAT	AAACGATGTT	CAGACGCATA	TAATTTTAAA	CTAGAAAATA	840
TGCCPTCAGT	AACAATCTCA	TCGGAACCCA	TATCACTACT	TTCCGAATTC	TCAAAAAAAG	900
TTTGAACAGC	TTGTTCTCTGA	TTATCAGGCA	AATAACAACC	CAATAAAGCC	AATGyTATTA	960
TACAAACGCC	AACCAAAATC	CTCATATATG	CTCCTTACCT	ACCTTACTAC	AAAAATAATC	1020
TGTTGTAAAT	ATACAAGTTT	ATCTAAGCAC	TATTTTATTA	AACATTTAAA	GTCCTACCAA	1080
GATAGATTTT	TCTATAACAA	GTAAACATAT	ACCAATTTTA	CCTTTTCTCA	AGAATTATTA	1140
AATACTAAAA	TATTAATTTT	AGCTTTATTA	TTATCTAGTG	AACTGCTATT	TCTAAATCAA	1200
AGATTATAGA	AATAGCAGTT	CACACAAAAT	GTGCTTAAAA	AATTAAAAAA	TAATTTTAAC	1260
AAGACTAATA	AAAAATTTAC	TAAAGAATCC	TTTTAATTAC	ATTTAAACTT	GTTTGTGTGT	1320
ATTCTAACAA	GATCGATTAA	AACTCCAACA	TATAAAAATC	CAAATGTAAA	TAGAGAAATA	1380
GAAAGAAATA	CAATTAATGG	AAAAATTTTA	TGAAAAAGAA	CATATATATT	TTGAATATAT	1440
TTTTATATAT	ACCATTATTT	TATTCGTGTT	TTTTGACTCC	ACCAAAATCT	TCAAAAATCA	1500
ACAGTATCAA	AACCGAGGTT	TTGGATTTTA	AGATAATTGA	AGAGGGAAAT	ATTATAAAAT	1560
ATGATAAAAA	GCCCATTGAA	GAGCGTAATG	AAAATACTTG	TCTTTCTTTT	AAAGAACCCG	1620
AATTAAATGA	AATAAAAGAG	GGGGACGTGC	TTGAATTACT	TGCAGGTGGT	TATGTTACAT	1680
GGGCAAAATC	TGGTGACTTA	AGGGTTTTTAA	AAGATAAAAA	TAACAATTTA	ATTGAAGATC	1740
TTAGAGAACT	TAGGTACTCT	TATATTTTTT	CACCCATTCG	ATTCAAAAC	TTTTTTAGTT	1800
ATAATTATAG	CATTAATGAC	AATAACTATA	AAATACTCGG	CAAAAAAGCA	CCTATAGTTA	1860
AGATAATAGC	ATTTGAATCA	ACTAAAGAGT	TTGAAAAAAA	ATACGAAATA	AATAGTTTAA	1920
AACTAAATTC	TGAAGAATCT	AATATTGATT	TTGAACAAAA	TAGAACTGGT	TTAGCCAAAA	1980
TTAATTTAAA	AGAAACTTCA	AAAGAACCTA	ATTACATTTA	TTCATATAAT	TTTGGAGTTT	2040
TTGACAATTC	TTTAGCAGAT	TATTTTAAGT	TATTTTATAA	AAAAAATAAC	TGTAACATA	2100
TGCCTGCATA	TCTTACTATA	AAAGATAAAG	AAACCGATAA	ATATAAAACC	TACGAAATTA	2160
TATTAAATCT	AAAGCTATTT	AACGATACCA	TTAAATTATT	AATTAATAAG	TATTCAAATT	2220
TATCAAAAGA	AAAATTAAAA	CTTTTTACTG	ATGAATGATA	AAAATTGAAT	AAGAAAAGCA	2280
AAGACAAAAA	TTTATCAATT	AATGTAAATA	AATACAATTC	AAAATTGATA	AAGTTGTGTG	2340
ACATATTCGG	TATCTCAACT	TGTCGATTTA	AAAGTATTGA	TAGTGAAC	CTATTTCTAA	2400
ACAAAGATTA	TAGAAATGGC	TTCTTGATATC	TTCCCATGAT	AGCTTTTTTAG	GCCTTTTGTG	2460

CAAGAACCTT TAGTTAAAGA AACTATTACT AAAC TAGTAA TAGCAGTTAA ACTATAAAGA	2520
ACCTATTTTT CAAGAATAAA TATTTTTGAT ATAGATTCAG CAATACATAA CTCTAAAATA	2580
CTATTTAAAA TCAAAATAAA TTTATTTATC CTCAAATTCA TCTCATTCTA ATTTTTATTT	2640
AAATCTTAT TCTATGTTAT TTAGTTTTAT GATATCTATC TTAACATCTA GCTCATAATC	2700
TTGATTGCTA CTATATATGT GATATAATGA TAAAATATTC TAATAATATT CTATTTTAGA	2760
TAGAGGTAAT ATAATGAATT TAATAATTAA AGTGATGTTG ATATCCAGTT TATTTTCTAG	2820
CTTTATCTCT TGTAATTAT ATGAAAAGCT TACAAATAAA TCGCAACAAG CTTTAGCTAA	2880
AGCTTTTGTC TATGATAAAG ATATAGCTGA TAATAAAAGT ACAAATTCTA CTTCTAAACT	2940
AGATAATAGT TCTCTAGATT CTATAAAGA CAACAACAGA AGTGGTCGCA CATCTAGAGC	3000
TTTAGATGAT GCTGAAGAAA TTGGGGTAAA AGAAAGTAAT CAAAACAGAA ATGATCAACA	3060
ACAAAATAAT GAAAGTAAAG TAAAAGAAAG TGAAAAAAC AATAGTTCAG GTATACAAGC	3120
AGATGATAGT GTTTTAGACA CAGCTCATTC CGATGCTAGT GAAGTAGAAA ACAAGAAACA	3180
TGATACTAGC AGACAACCTC AACTACTTAA TAAGGACTCT AGTGAAGCTA GAGAAGCTAG	3240
TAAAATTATA CAAAAGCTT CTACCTCTTT AGAAGAAGCT GAGAAAGTAA ATGCAGCTTT	3300
AAAGGAAACA AGATCAAAAC TTGATAAGAT AAAAGATTA GCTGATAGCG CTAAATCTTA	3360
TTTAAATAAT GCTAGAAAA ATTCTAGAAC TAATGGTCT ATACTAGAAA TATTGCCTAA	3420
CCTTGATAAA GCAATTGAAA AGGCTATTAG TAGTTATGCC TCTCTTAATG TTGCTATAC	3480
TGATGCAATT GCTGCTTTAG CAAAAGCTAA GAATGATTTT GAGCATGCAA AAAGAAAAGC	3540
AAATGATGCT TTAGAAGAAG CTTTAAAAGA TATACCTCAT TTTAGGGGGT ACAATTATCT	3600
TTACCATTAC CGGATAAATA ATGCTAATGA TGCAATGGAG AGTGCTAAAA GTTTGCTAGA	3660
GGTTGCTAAG AATAAACAAA AAGAACTTAA TGAAAATATG ACTAAGACAA ATAAGGACTT	3720
TCAAGAGTTA AATGATATAT ATAAAAAATT GCAAGATATG GACTCTAGAT AAGTAAAAGT	3780
AAAATATTAA AGATAAGAAG CCAGACAATA CTTTATGAGG TTTAGCTTCT TTATTTATAA	3840
TATTCTTTTT CTAAACAACA CTTTATTTTC TCTTAACTTT ATAGTTTGAC TTAAAAATC	3900
ATTATTTTTT AAAATATTAC ATGAATTAAC TTTAATATCT TTATTTTTAT ATTATAATTA	3960
TTATTAATAT AGATATTATT TGCCATATAA GTACATAACA AAGTTTATT AAAAAGGAAA	4020
TATAAATATT ATGCGATTAT GTTAAATAAA AATTTTTATT ATACCTAATT TAGTATTTAG	4080
TTCTCTTTTT TTATTTGAAA GTTGTTCTGG TTTCTATCT AAAAAATCTA TAGAACAGTT	4140
TGCATTAGCA TTAAAAGATC ATCAAGAAAA TAAAAATACT ACTAATACTT CgTAGaTAAA	4200

981

AATAGTAAGG AAATTGAATC GCCTAAAGAC GTTACATCAT CAAATAAAAA AACTTATGAT 4260
 CCAATCTTAC AAGTAGGTTT TAAATCCCCC AAAAAAAnC CCCnAAAATT TT 4312

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4305 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

nAATTCGAGC TCGGTCCCCA AAAGTAAAAG CAAGCCTTGA TAAGATAAAA AGCTTACTTA 60
 GTACAGCTAA ATCTTATTTA GAGCAGACTA GAAGAGGTGT GGGATCTAGT AAgCTAACTT 120
 AGCCTTATTG CCTAGCCTAG AAGAAgCTAT TGCTAAGGTT AAGAGTAATC ATGCTTCTGC 180
 TGATACTCAT TGCAATGATG CTATTGCTGC TTTAAAAaGA GCTAAGAACG ATTTTGAGTA 240
 TGCACAAAGA AAAGCAGATC GGGCTTTAGA AGAGGCATTA AGTAATAGCA ATGCTTCAAG 300
 GCATGAGAGC TACTACTATG CTGGCTACCA CCAATTTATG GCTGATGCTA AAGCTTCAAT 360
 GAGTAGTACT AAAAGTTTGC TAGAGGTTGC TAAGAATAAG CAAAAAGAAC TTAATGAAAA 420
 TATGACTAAG ACAAATAAAG ACTTTCAAGA GTTAAATGAT ATATATAAAA AATTGCAAGA 480
 TATGGACTCT AGATAAGTAA AAGTAAAATA TTAAAGACAA GgCCAGACAA TACTTTATGA 540
 GGTTCGGCTT CTTTGTTTAT AATACTCTTT TTCTAAACAA CACTTTATTT TCTCTTAACT 600
 TTATAGTTTG ACTTAAAAAG TCATTATTTT TTAAtAATT ACATGAATTA CCTTTAATAT 660
 CTTTATTTTT ATATTATAAT TATTATTAAT ATAGATATTA TTTGcyATAT AAGTACATAA 720
 CAAAGTTTTA TTAAAAAGGA AATATAAATA TTATGCGATT ATGTTTAATA AAAATTTTTA 780
 TTATACCTAA TTAGTATTTT AGTTCTCTTT TTTTATTTGA AAGTTGTTCT GGTTTTCTAT 840
 CTAAAAATC TATAGAACAG TTTGCATTAG CATTAAGA TCATCAAGAA AATAAAAAATA 900
 CTACTAATAC TTCAGTAGAT AAAAATAGTA AGGAAATTGA ATCTCCTAAA GACGTTACAT 960
 CATCAATAA AAAAACTTAT GATCCAATCT TACAAGTAGG TTCTAATCAA CATATGTCAG 1020
 ATGATCCTGG TGCTAATAAT AAAGAATCCC TACCAAAATTC AAGTCCAGCA ATAATACAAA 1080
 ATGACTCGCA TGCTCAAAAT AATGTAAAGA TGGAAGAAAA TAAATCAGCT ACTCCACAAC 1140
 ATGATCCAAT TGAACAAAGT AATTTTAAAA ATAGCCTTAC TACAACAAGT AAAACTCCTG 1200
 CTATTCCTTC AGAAGAAGAA ATTAAAGCTA ACTTAGATGA ATTTGCACAA GAAGAGTATG 1260
 AGCAAACATC TCTTTCAGAA ATTAAAAATG CCACGCAAAT TGTTAATCAT GCTAATCCTG 1320

AAAACAAATT AAACAATACA CTCCTTGAGT TTGAAAAAGA TTATGAAACT TTATCAAAC	1380
TGTTATTTCTC TAATTTAGAC GCATCTCCTT TGAATAGAAA AATAAAGACT ATTATGCCTA	1440
AATTACAAGA AATGCGTTCT TTTATGGAGC AAGCAACTAA TTCTTGGGTA TCTGCTAAAG	1500
GCATGCTAGA TGAGGCTAAG GATAAACTAG CAGAATCTAT TTATAAAAGA CTATACAATG	1560
GCAATTCATA CCGGTTCCGT GGCAGTTTTA ACGGACGTGA TATGCAACAT GCAAAAAATT	1620
TAGCATACAG AGCTATAGAC TTTGCTTCTG CATGCATTGA ATATACACAA AAAGCTATTG	1680
ATTATCTTCA ACAGGGAAAT TCTTGCAAAA AAGAAATAGA AAATATATTC AAGCTTTAAA	1740
ACTTCCAGTG TAGGCTTTAG TTTCTTTAAT ATCTCTACTC ATATATAATC CCATCTTTAC	1800
TAGAAAAGCT TATATATCGG CTTACCTAAA TTAACATATT CACTTCCCTC TTGCCTTTAC	1860
AAGCACTACT CTACTTCTTT CAAATTTATA GTTTGGTTTG CATTTAGCAT TCACTATTTT	1920
TCTATTTTTA TAAATGTGAT ATATTTATTT TTTAAGAATA AAGCATAAAT ATCATCAGAT	1980
TCTAAGAAGA GGTACTAAGA TAGATGAATT TAATTGCTAA ATTATTTATT TTATCCACTT	2040
TAGTTTCAAT TCCAAATATC CTCTCTTGTA ACCTATATGA TAATCTTGCA GACAACGCTG	2100
AGCAGGTAC AGACATACTA GACAACAACA AGTCTTTTAA TACTTTAGGA AGCAGCAATG	2160
AGAGTAGAAG TCGCAGGCCT AGAAGTACAA ATAATGCTTA TATGAAACAA AACATAGACA	2220
AAAATCATTT AGTTGTTGCA GATATGCAAA ATGATAATAG TAGCAGCAGT CTTCCCCAAC	2280
AAGTTAATAG TGAATCCAGT AAAGCTAATG AAGATAGTAA TATTATGAAG GAAATTGAAT	2340
CTTCTACAGA AGAGTGCCT AGACTAAGAA AAGATTTAGA AACTATAAAA CAAATACTTG	2400
ATAATATAGA AAGCTTGCTT AATACAGCTA ATTCTTATTT AGAGAACGCT AGAAAAGCAC	2460
CTAAATCTAA TCAAGATAAT CAAACCTTAT TGCTTAGCCT GCACCAAGCT ATTGCTAAGG	2520
TTAAGAGTAG TCATACTTCT TTTATCATTT GTTATAATGA TGCATTTAAT TCCCTGGGAA	2580
TAGCTGATAC TGCCTTTAAA GATGCAAAGA GAAAGGCAGT TGAGGCATAA AATGCTTCAA	2640
AGGAAAATTA TGAATGGTAT AACGGTCATT ATCATTCTTT TATAAATGAC GCTAAAGATG	2700
CAATGGAGAG GGCTAAAAGG ATGCTAGATA ACGCTAAGCA TAAACAAGAA TATCTTAATT	2760
CTAATATGTA TCAGGCAAAT GCAGACTTTG AAGAGCTAAA TAAAGCATAT GAAGCTGCTT	2820
ATTAAATAAT ACTAATCTTA GATAGCTCAG CTTTAAAGAA AAAAGCTCTA TGCTATAAGC	2880
TTAACATATA ACTCATATTC TTGATTACTA ATAATAAATG TAATATAATG ATATTGTATT	2940
ACAATAATAC TCTATTTTGG CATAAAGTTA GCACAATGAA TTTAATGATT AAAGTATTAA	3000
TATTCAGTTT ATTTTAAAGC TTTATCTCTT GCAAGCTATA TGAAGCTGTA GATAAATCTC	3060

983

TTATAAAAGA CAACAAAAGA AGTGGTCGTA AAGCTAGAAG TATTAGTTAT AAGGAAGTAA	3120
ATAATCAAGA ACAAATAAT GAAAAGAACC TAAAAGAAGC AAAAGAAAGT AAAAAAACA	3180
ATAATTTAGG TATACAAAAA GATGGTATTG TAAACACAAA CCCTTCCGTT GCTAGCGATG	3240
CTAGTGAAAA ACATACTAAT AGACAACCTC AACAAAGTTAA TAATAACTCT AGGGAAACTA	3300
GTGAAGCTAG AAACATTATA CAAGAAATTT ATACCTCTTT AGAAGAAGTT AATAAAATAA	3360
CTACAGATTT AGAAACAATA AAGTCAAGAC TTAATAATAT AAAAAGTAA GTTGACAATG	3420
CTAGTTCTTT TTTAAATAAT GCTAGAAAAT CTAATAAAGC TAACCCAACC TTATTGCCTA	3480
AACTTGATCA AGCTATTCGC AAAGTTAGTA GCAGCCATGC TTATGCTAAC TCTAATTATT	3540
CAGATGCAGT AAGTGCCTTA AAAAGTTCTA AGCACGATTT TGAGTATGCA AATAGAAAAG	3600
CAGAAGATGC TTTACAAGAA GCGTTAAATA ATAGCAATAC TCAAGGTTAC CAATATGCTC	3660
GATACCACTA TTATATGAAT GATGCTAAAG AAGCAATGGG CAGGGCTAAA GTTAGCCTTA	3720
AGACTGCTAA GCAGAAACAA GAAAACTTA AAGACAAGAT GGATCAAGCA AATAAAGAGT	3780
TTGAAGAGTT AAATAAAGCA CATGAAGCTG CTTAAGTAG TAGAGAATCT TAGCTGGTGT	3840
AGCTTCAAAG AAGACATGAC ACTTACTTAT AAATAAGGAA GCTTTTGGAT TTTAACAAAA	3900
ATAGTCTGGC TTTTTTGCAC ATATAAAACA ACTCCATTAT TTCTAAGATA AATATTTTAA	3960
GCTCCCTGGT AAAGTAATTC ATTTATCCTA GATTTACTCT TCCACTTCTA TACGTCCCGT	4020
CCTGCTTAAT CATTAATTTT TAAAATTAAA TGTTTCTTTC TAGTTACGCA CTATATTGTT	4080
ACTATAACAA AAATTGAATC TTAAAAATTA ACATATTACT TTAAAAAAGT ATACTTATAG	4140
GAGATGCTTA TAAAGCTTAA CAACTTATT TTTACCAATA TATATATCTA ATATCTCTTA	4200
TACTTAGTTG CTCAATATCT AAAGATTTAA GTGATAAGCT CTCTTCACTA AAATCTAATG	4260
ATTTTTTTTAA TTCAGACACT TTAGTTTATG ATTCTAGCAA TTATG	4305

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4293 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

CGATAGCTTT AATAAGcAAG CTCAATTACA ACAwTTAAaC CCAGGTGTTT CACAAAAACA	60
AGAwATAGAT AAAAAACAT AGAAAAAGA AGCCTAGACA ATTCTTCACA AGAAAAAGAA	120
CTCACAAACC CTGCTTATTC AACACAAGAA CATAAAAAA GTGCTACAAA CTTAGACTCA	180

AAAAAAGATG CTCTTATTAA AGAAACTCTT GAAGCTATAA AGGAAAAAAT TAAAGAAGAA	240
AAGAAAAGCT ATTCTAGAAG AGCAGCAAAG ACAGAAACAA CAAGAGCTTG ATAAGATTAA	300
AGCACAAATAT GAGGAAGAGA AGAGAAAGAG AGAAGAAGAG AGGAGAAGAG AGGAGAAAGA	360
GAAAAGAAAG CAAGACTTCA AAAATTTCATG CAACTACTT CTGACTTAAC TAATCTTGTT	420
AAGATGGCTG GGCTTGAGGC TTATAGCATT TCCCATAAAT TAAAAGATCT TGA AAAAGGT	480
ATTGAAAATT ATGAAGACAA CAATAATTCT ACTAAAGACA CACTAAACCA ATCTCTTAAA	540
GATGTTATTT aTGAGATTAC AAAGCTTAGT AGTCTTATAG AAGCAAAAGA TAAGATTGAT	600
CAGCGTAAGA AATTGGGTTA TCAGACAGAA CAAGAGTTTG ATGCTAAATT TATAAACTTA	660
AAGAACATCA AAGATAAGCT AAAGACTTTA TGTGGTAAGG CTAAAGGCCA TCTTGGTAGC	720
AATCTTTCTA GCGTTACTAT TGATGGGATT ACTAAAGAGA AGGTAGCTCm AGCTTATCTT	780
ATCATTAAAC TAATACACAA AACATTAATT TATATGAATG ATGATAGTAA AGGTAGCCTT	840
GCTACTATAC TTAATGACTT AGAAAAGGAT GCCAAATCAA TATAACTAGC ACAACAATAT	900
CTTCTTATTT TAAAAAAGCC TAAGTACTTA TATCTTAGGC TTTTPTAAAA ATTATCTTGC	960
CTCTTAGACC ATTCTTGATA ATAATAATAC TGTTAAGAAT AAATTAATGC TAAAATGGAT	1020
AAGTACACTT AACTAATTA CTATTTTTGC AGTAAATATA AAAACATAGA ATAAAAATTC	1080
TTATACTAA AAGAGTATAA TCTTCTTCAA GAGAAATATA TTATCAAGAA ATTAAATAGA	1140
CCTTAAATTT ATTTTTTCTA TATATTCAA ATTACTTTAA CTATAATATT ACCTATAGAG	1200
AAAATCGTAT GGTAGTGGAC GAATGGTTTT TCCTAAAAAT AAAGAAAAAT AGTAAAAATG	1260
GAAGAAAAGA AAACAAAAAA AAGATATAAT TCTGTATAAA AAAATCTTTT AAGAATTTTT	1320
CCATTTTTTA GAAAATGGTT TTCTATAATA GAAATATTAT ATTTTTTTCT CTATGTCTTG	1380
TAATACCATT AATAATATTG ATCAAAATAT TAAAACCTTC TATTGACCAT ATTTCTGATT	1440
GAACTGGAAT TATAATATAG TTTGCAGTAT TTAAAGCGCT CTTTAAAAGA AAATTTTGAA	1500
TCGGAGAAAA TGTTTACCAA AATATAATCA AAATAGCAAT TGATTTTGGA AAGAGATATA	1560
AATATTCTAC ATATTTATTT TTCATAAAAA CTTTTTTTAA AGATAAGATT AATACCAATG	1620
CTATGAGATT TATTTTTATC ATTTTAATTT TCTTTTAATA AAAAACTTA ATAAGTTATC	1680
AACTTAGGTC AACCACAGTA AAACAATTAA AATGACATTT AAAAAGATTG AAATTTAGTA	1740
AACAAAAAAA AGCCCTTATG GGCATCCTTT TCCGGTTTAG GATAAAGAGA AATCTTTATC	1800
TTATACATTA AGAATAATAT ATTATAAAAA AATAATCAAT GGATTATTTT TTTTATTCTT	1860
CTTTATTTTC ATACTCCATC ACAAGACTAA ACAAGATATC CCTTCTATCC TTAATAATTT	1920

985

TTTCCAAAAT AAAAAGCTGCT CTTTGGTAT CTCTTATGCA AAAAGAATAA ACTTCCTTAT	1980
CTTTTATTAA AAATTTAACA GGGGGCATAC ATGAATTATC ACAATCTTTT TTTCTATCTT	2040
TTTATGTTT AGATGATTCT AATGATTTT TCAATATTTT TCTGTATACA GATGAAAAAC	2100
CCkGTTTTTT AATCTCCTCA ACAGAAATAT TTCCCTCTAA GACTTCCTGA TAAATTTTTA	2160
TATATATATA CGCTTGGCTT TTATTAATTA CATAAGACTT AATAAACTGT TCGAAACTGT	2220
CGAACCCGTC ATATTTATAA AGATTTTTTT GTTTGATTTT GTATAAAATT TTCATTCTTT	2280
GAAATTTACT ATCAATATCT AATTTTAAAT TGTATGCTAG CTATTCCTTT AATTCATTGT	2340
AATTTTTTAA TTCCCTGTTT TGATGATAT CCATTTCTTC TATTTGAGTT TCTACCTTTT	2400
TATACAAAAT TATGCTTTTT TTGTTTTCTT TTTTTCCAT TTTTACTCCC TTTCTTTATT	2460
TTTAGAAAAA GACCATTCGT ACACTAACAC GATTTTCTCT ATAAGATAGA TTACGGTTAA	2520
AACAATTTTC ATTATAAAGA AAAAATATTT TTCAAAGTTT CTTTAATTTT TTGATAATAT	2580
ATTTCTCTTG AAGAAGGTTT GAGTCTTTTA GTTATAAGAA CTTTTATACT ATTATAAAAA	2640
TGTATCTTGC CCTTGATATA TTCTTTGTAT TCTTTATGAA TCAGATTTTC TACTTCTTTA	2700
AGAATATTTT TATTTTTTAT AAATGGGTTT TCTACAATAG AAATATTATA TTTTTTTTCT	2760
CTATGTTTTG TAATGCCATT AATAATATTG ATCAAAATAT TAAACTTTT TATTGACCAT	2820
ATTTCTGATT GAACGGAAT TATAATATAA TTTGAAGTAT TTAAAGCACT CTTTAAAAGC	2880
AAATTTGAAC CTGGAGAAGT GTCTAACAAA ATATAATCAA AATCGCAATT TATTATATTT	2940
CTATTTAAAT AATATTCCAA GAAAGTTTCT TGATCGGTTT CTGTATTAAA TTTTCTAAC	3000
ATAGGATGAG AAGGAATTAT ATACATATAA TCATTAATTT TATTTAAGTA TTTTTTAAAA	3060
TAGAAATCTC CTTTTAACAT ACTATACACA TTATATGTTT CGGCGTCAGG AATATACTTG	3120
GTAAAATATG ATGTTAAAGA ATTCTGTGGA TCCAAATCAA TTAGTAATAT TTTTTTACCC	3180
AATTCCTTCA ACAAATAAGA AAAAAGTATA GAAAGTGTGC TTTTCCAAC TCCTCCTTTA	3240
ACTGATGTGA GTGCTATAAT ATCTGGTTTT TTAATATCCA TTTATCTAAA ATTCCTCCAT	3300
TTGTTAGTTT TTTGTTGTAA AATTTATATA CTTTCTTTT CATTTTTTTT AAATGTTTTA	3360
AACTATACTT GTAGTATTTG GTGTCTTCTT TTTGTCTTTT TCTTAGCAAG GTTCTTAGAG	3420
ATAATAAGTA ACACTTAATA GATCCGGTTT TAAATATAAA TTCTATATAA TATAGTTTTT	3480
TTATTGCGTA ATTTCTATTT TTTCCTATTT TATGAAGAAA TGGTTTTTCA AGTCGATCGT	3540
ATCCATACCT TATTCCTAAA AATTTATTTT TTCCTTCTAT TGGGAAAAGA TTGAAAGAAT	3600
ACTTATCTTT ACTATTAAAT TTTTAAATTT CTAGTTTCAG TCTTTGTTTT TTGCAGTTAT	3660
TTCTAAAATT AACTAGATGG TAGAATATTT TTGTGTAATA TATTTTCTTT CCATTCTTTT	3720

CTTCTATTTT GTTAAAAATA TTTTATTATG GATTTCATC AATATTCATT AACGCTTCT	3780
TTGTTTTAG TTTTCTAAAA ATTGAATTCA AATCTTTTTC CTTATTACAT TAATCAAATA	3840
ATTGTTTAAT GTTTTATTAC TTGTAATGTA AATATGTAGC TTGTTTAAAG TAAAATAATT	3900
AAAGTTCTAG TTGTAAAAAA GTATTGTGGA TAAGAAAAATG GATTTCGTCA ATTTACAAAA	3960
GGTATATTAA CTGATTTAGA TAAAAGTCAA AAATATTGTT TTGATTTATA TCAGAAATTGG	4020
TAGATTGCKa TGTTTTAAAG TAAGTATTTA GAATAGCTTT TACTATTAAAG CTTGCrkACA	4080
AAATGGTGTT GTCAGCTTTA TTCCAATCTT AATTCATTT TATCAAATCA AATTAAGATT	4140
GGAATCAAAT GAAACAAAAA AAGTGAATAA GAATTCATCA AAAGAAATTC GCAAATATGT	4200
TAAAGGATTA CTTAATATTG TTAAAAATAT TGTGCCTGTT ACAACTAAAA GGTTGAAGAA	4260
CTATATTTAA AATGTGTCAG GGTATCTAAT GAA	4293

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4228 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

TTGGAAAGGG AAAnGCAAAT TCTCAACAAn ATTATCAAAA TTTAAnGGAA AATATTTTCA	60
ATATCCTTAT TGAACAACTA AAAAAAGAnA CAAATATTGA AATTCTAAAG CCATTATCAA	120
AAAATATTTG AATAACCAAA AGAAAATAGA ATACAATAAA GTATTTGGTA TATATCATCT	180
TGAATTATCA GAAATAATAA AAAATGAAAA AAATTCCTTTA ACCACAGAAG AATTTAGCAT	240
AAAGGnCCGT ATGAGGATTT AACATGGAAA ATGCMCCmGA mCCTATTGAA aCTGTAAAAA	300
aGGGTAAATG TAAGGTTGAA TGCCAAAATA AAGAACGyTT TATTTTGATT GAAAAAGAAA	360
ATGGTAAAGC AATGTACCAT ACAAAAATAA TGATGGAYAT TTATAAATTT GGAGTTTATG	420
AGAAAAACA CGAATTTAGA TTATCATTGA GGCCTTATT TAAyGGGGAA AGAATTGTTG	480
AAGAACTCA TTTTrTACCCA ATTAAAGAAG GAGATAAGTT yATTGGTATT TTTTATGGCT	540
ACAGAAAACC AATTAAAAAG CCGTTAATAA AGTATCAAAT AAAYGGGACT ArAAAAAGCAT	600
ATGCATTAGC AAGGGCATAT TATATGGAAT TTAGATTTAA AGCAGGAAGT GTTTTTTGCT	660
ATTTyAAgGG mTaTATCGAT TATTAGATAA AAAAAGAACA AATAATCACT ACAACAAAGT	720
TTTATTTAGT ATGTTTACAG ATTTAGAACA ACAAGTATAT AAATTTTATG GGAAaAAATA	780

CCCGGAGCAA GGACCGTTAA TAAAATGGAT ACTAAAAAAC CTAAAATAAT AACAAATAGCG	840
TCAATTAAGG GCGGTGTTGG CAAAAGCACA AGTGCAATAA TTTTAGCAAC GCTATTATCA	900
AAAGACAACA AAGTACTTTT AATTGATATG GATACACAGG CTTCAGTTAC TAGTTATTTT	960
TATAAACAT TAGTAGAAAG TGAATTTGAT TTTACTTGAAA AAAATATATA TGAAGTTTTA	1020
AAAGGAAATC AATTAATAAA TGATGCAATT ATCAATGTTG ATCATAATTT TGATTGTTG	1080
CCAAGTTACT TAAGCTTGCA CACTTTTAGT GAAGAGCCCT TGCCTTATAA GGAACATAGG	1140
TTAAAGGATA GCTTTAAATA TTTAAAATTT AAATATAATT TTATTATACT TGATACTAAT	1200
CCCCATTTAG ATTCTACGTT ATCCAATGCT TTAGTTGTTA GTAAACATGT TATAGTTCCA	1260
ATGACTGCAG AAAAGTGGAC TATTGAGAGT TTGCAACTAT TAGAGTTTTT TACGGATAAA	1320
TTAAAGTTAA AACCCAAAGT ATTTTATTTT GTAACAAAAT TTAACAAAAA TAAAACTCAT	1380
AAAGATTTAT TAGAAATGTT GCAACAAAAA GAAAAGTTTT TGGGGATAAT ATCAGAACGT	1440
GAGGATTTAA ATAGGAGAAT AGCAAAAAAT GATAGATTTG ATTTAGATAA AGATTATATA	1500
AAGGAGTATG TAAACGTTTT AAATAATTTT ATTTTGAAAA TATGAAATTT GTCCGATAGT	1560
TGGATGAATT TTTTAAACAA AAAGGATAGG AGATTAATTA TGGACGTGGG AATAAAAAA	1620
AACGATAGGG TAATATCAAA AAAGGAAATA AAAAAAGAAT TAAGCAATAA AGATGAAATA	1680
TTAAAGCATT ATAATTTGTT GAAGGAGCGC TTGAAATCTA ATTTTCAAAA AGAAATCTAT	1740
AATAAGATAG AGAGTATGAA AATTTTAAAA GAAATAAAG ATAATGAATA CTATAAACTT	1800
GATGGTTATA AAAGTTTGA TGCTTTTATA AAAGATTATA AGTTAGCCAA AAGTCAAAC	1860
TATGAATATT TGAAGATAGC ATCAGCTATA GAAAATGGCG TAATAGAAGA ACTTTTTTTA	1920
TTAGAAAATG GAATTAAAGA AACTATAATC TTTTAAAGAA ATAGTAATTC AGATACGGTT	1980
AAAAATCAA AACAAAATCC AATAAAACCA TTAAGATTTT AACTTAAAAG CAAAGAAAGT	2040
TATGATTTTT ACAAAAGTAA TGCTAAATTC ACGGGATTTT TATTAGATGA ACTTTTTGAA	2100
AGTCAAAAAG ATTTGATTAA TAAATCTTTA AGAAGATATA AGCAATTAAA AGGATAGTAA	2160
AGGTATTTTA TGACTAATTT AGCGTACAAA ACGTATAACA TAGAAAGCAT AAAAAATGAG	2220
TTTTTAAACA TAGGATTTAG TGAAGAGGCA ATAGATTTTG TTTTGCTTCA TAATGAAAAT	2280
TACAGCTTTG AGGTTTTTAA AGAAAAATTG ATTAATGTAG AGAAGAATTT GCAAAAAGAT	2340
ATATCTAGTT TGGACATTAA GATAGATACT GTAGAAAAGA ATTTACAAAA GGATATATCT	2400
AATTTAGACA TTAAGATTGA TGCCGTGGAA AAGAATTTAC AAAAGGATAT ATCTAATTTA	2460
GACATCAAGA TTGATAATGT AGAAAAAGAT TTGAAAAAG ATATATCTAG TTTAGATACT	2520
AAGATTGATG TTGTAGAGAA GAATTTAAAT CTAAAAATAG ATTTTGTAGA AAAGAGTTTA	2580

AATGCCAAAA TAGATAGTTT AGACGTAAAA ATAGATAATG TAAATAATAA AGTAGATTAT	2640
ATTAAAAGTG AACTTATTGc CAAGATAGAT AGTGTAGAAA AAGGGTTAAA CGAAAAACTT	2700
AATACaGGAA ATAGGCTAAT ACATTTTATG ATATTAACAG CAGCGATTCT AGGCCCAGTT	2760
TTAAATGCCC TATTTATGAG ATATTTACAA TATATCAAAT AATGATGTAA TGCATAATTT	2820
GCTTTTTTCA AATAGTTTAT TATCAATTAA AGCTTATTTA AGCTTTTTAAA TAAAGTAACT	2880
TAAATAAGTT CTTTTATTTT AATAAATACA AATTGATTTT AATTCTAAAT TGAAGTGAAT	2940
TTAATTGTTT AGTGAGTTCA CCTAAAATAA ATTAAGCTAA GCCCGCGGCT TTATTAAGCT	3000
CTTTAACATG AGAATTTAAT AAAGCTTTTA TTTATTATAA TAATTTCTGT AAAAAGCCTG	3060
ACAAAAATAG TTTTGTATAT ACATATGTAT ATGTATAGCT AAAAAATAT ATTGCTATCA	3120
AAAAAATCCA ATTAAGTTGG GTTTAGCTAA GTTCTTTAAC AAGAGAATTT ArMTAAGCCC	3180
tATTTTTTTG TAAAAATTTT TGTAaaaaAG TTGGCAAAAA TAGTTTTTGC TATATACTTA	3240
TTTtTataAA TAACaaGGAG kAAAAAGATG GAaAATCTTT CAAACAATAA TAATCCACAA	3300
GAAATATTC AAGGAGAGCT CAAAATGATA AGTGTTAATC AACAAAGTTT TACTGGTTGT	3360
GAAATAATTG AGGAAAAATC TTCTCCCATTT AAAGAAAAAA GTAAATTAAG TAAGATAGGT	3420
AAGAAATTGC CAGGAATAAG CAGTCAAGAA TGTTTTAGAT TTAATCGAAA TATTGATTTT	3480
AGTGTGCAAA GAAACAAStT aGATAAATAC GGTGCTAGTG AAGTAGGCAA TATTCTTGTT	3540
GGAGGTGCTG GrCTkAAAGA TTTAATGATA AACAGAGTGC TTAAATATTT TrrwATGAGy	3600
CTACCTTTTG AAGAGAATTT rTATATGCTC AAGGGCAAAG ArTTAGAGAA TTTAGGATTT	3660
AGAGArTTTG TTAAAGCACA YrGTGATAAT ATTrATrTTT TGTATAAAAA CAAATATGCC	3720
AAyGGwGTTG ATAAGTATAA yTATTTCAAA AAAATGGGyA GTTCAsAAAC TTTAGTGGGC	3780
TCAACAATTG ATGGCTGGTT TATTAATAAT AATGGCGATT TAGAACTATT AGAGATTAAA	3840
AGTAGCGACT CTCATTATAT GAGTAGTGCT ATTGCTGAGT ACAATAAAAA TGGCAATTTT	3900
TTAAGCAGTA AATATTTTTT CAAATATTAT GTACAAGCAC AAATGCAGCT AGCATGCACT	3960
GGGCTTGAGT ATTGTAATTT GTTCTTTTTA ATAGATGCTG CACCAATTAA CTGTAAGATT	4020
AAAAGAGATG AGGCCTTAAT ATCAAAAGTG TTTGAATTTG TTAATAAATG TGAATTAGAA	4080
ATTATAAATT TAAAAAAGA TATTTATAGT AACTATAGAG ACGATTACTT AATGGCACAT	4140
AATTTTAATG AGGATACGTT TATAAACTT GTTGAAGATT TAGTAGAAAG GAGTGATTTT	4200
TATAGTTCTG GAGTTGAGTT TGATTGGG	4228

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4137 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

TTATTTTGAA TTAAACTAA TGTTTAGTAA TTCAAATATA TAAGGAGAGC ACATTTTGAA	60
AAACCTAAAT TAAATATTAT TAAGCTTAAC TTTATTACAG CAATACTGAA TTCAATTTTC	120
ATATCATTTT TACCTATTGG AAAGGTCGAT CCAAAACCCG ATATCAATAC TAATCCAGAA	180
AATATCCAAA ATTAAAGTTT AGAGAAGCTT TTCGCATAAA TATTTTATAA TTTTATAGGAT	240
TATATCGGCA ACTATGTTAA ATATTACTCG AATGGCTGTA CTTTGATATT AAAATCTGTT	300
ATTTGTGGAG TTGGTATTTT TGATTTTTAA ATAATTTTCAG GAGTAACTAT TTCTTTGAAA	360
ATTTTCAGGAA TTGTTGTTTT AGGAATGATC ACTTTTTCAG TAATTTTCAGA AATAATTTCA	420
CCAAGGCAAT TTTATTCTTT GCAAGAATTT TGTTCACAAT TGTACAACAT AATCAAAAAA	480
TTAAAAAAGT AAAATGCAGT ATGAAAACTG ATAGTGAGAT TTCTTATTCA AATAGGAACA	540
TCTACAATTC TATCCCAAAA GTAAAATAGG AAAGAGTTTG TTAGAAAGAA AACCGTATTA	600
ATTTCTTGGT TAAGTTATGT AATAGTAATG TATTGTTATT AATTTATTAT ATAAAATTTA	660
GGCATAAAAA ATAGGAGGTA TCATCCAAGC AACTTTTAGG TGCTAATGAG AAAATAAAAA	720
TTTTTTAAGT GGAGAATAAA GAGTAATCTT TGGGCAAATC GAACAAAGAT TGCTTTACTG	780
TCTTATTTAA CTATAGTAAG TTTATCTCTA AAATAAGATT ATCCAAGCTT ATTTTAAGCT	840
TTTATTCATA TTTCTCAGCA AAATCAATTT AGAAATCTTT TAATTTTAA TTCTTGATA	900
ATGCTTACAA AAAATCATAA GTATAGAATC CGCACAAATA CCAAATGTTT TTTTATTCAT	960
CATAACTTGA TCCGTAAATT TACGAACACC AATAATACGG TATCGTAAAA TAAATAACTT	1020
TATCAGCCTC AATAATAACT AAGAATACAA ACTTGGCATT GCTAGTAAAT TTTAGCAAGA	1080
TGCTAAAGGA TGATGTGCCT GGTATAAGG ACAACCAACA ATACTTTAGA GAATGCAATT	1140
GTAAAGTATA AGGAAGCCAT AAGTAAGACT ATTTGGGGCT AAGAGTCAAA TTAAAATAAA	1200
GACAGAAAAC AATAAGTAAG AGAAAAAGAA TGAAAGCTTA ACTCATTTAA GAATAGTTAG	1260
AGGTGTTCTT TCTGTTGTTA AAAAACCCT GAAACAGCTT TGCCTAGCTT GCGCTGATTT	1320
TATTGCTACT GCTGCCAGTC TATCTTGTA TGAATTTAGG CAACTGCTG AAGATTTTAG	1380
TGTTTGCTGC TAAGGAGTAT GCTAATGGAA AAGGAAAAAT AATGATTTTG ATGTTATTAG	1440
GTGCTATTTT TAGTATGGCC TATAATGAAT TTGAATAGGA GGTTCAAAG AGTAAAGACT	1500

TTTGCTAATA ATGAAGGGGG CAAATTAAAC AAGATGACTG CTACTATTGA TAAGTTATGT	1560
GCTGTTTATA AAAAAGTTAT ATCTTAAATA CCTTAAGTTT TTGGCCAACT CTTTTCTCTC	1620
TTTAAACAC TTTGCCTCTA TGCTTGCTTT ATAATAAAAT AATACTTGGA TAATGAATAA	1680
CTAAAAAAT AAGGAGGTAT TAATGAAAAG GAAAAGCAAT ATATGTATTT CACTTCTAGT	1740
CACAATATTA TTTGTGCTT GCAAGTTTTT TGGAAATAAA AGCGCAAGTA AAGAAAAAGA	1800
AGAAACTTCT TTTTCTGATA CTGCTAGCAA GATTAGTAAG TCGGGAACAG CTGCTTCTTC	1860
AGACAAACAA GAAAAAATA CAAGTGATGT TACAGGTGAC GCCAAAAAGC ATACTAGTAG	1920
CCCTTACATG CTTGCTGATG CCCTTATTGT TAGTGATACT ACTAATAGAG ATAGAGATAA	1980
GCAAGAAAAT AAAGATAAAT TAAATGAAGA AGATAAAAAA AAGCTTAATG CTTTTTTTAG	2040
CACAAC TAA ACATATCAAT CTAGCCTAGA TTCCATTTAT AACAAATATA CAGGCTATTA	2100
TAATACCATT GATACCTATG GCAGCTGTGA TACGTATCGC ATTGAGTGTT TTAGTGTAGG	2160
ACCTTCTGAA AAACGTAAAC AAGCTCTTGC TGATCTAGAG AAGTTAAAC TAGACGAAAA	2220
GTACACTCAG CTTAGCACAA TGTTAAAGAG TGCTGTGCCT AGTTATTACA AAAAAATTT	2280
AGATGATTCT ATTGCACAGT ATAAGGAAGC CATAAAGCAG GCTATTGAAG CTGAAAGTAA	2340
AATAGAGACA GTAAAAGACT ATGCAACAGC TCAAAGTGCT GCCGATGACG AAAAGAAAAAG	2400
AAATATAGAT AATTTAAAA TAGTTAGAGA TGTTCTTCTT ATTATTAAAA AACTATTGA	2460
GAAAGCCAGC CGATCTTATG CTGATGCTTT TGCTATTGCA ACATCTAGCT TATCTGTAG	2520
CGAATTTAAG CAAGCTGTTA AAGAGTTTAA TGATGCTGCT AAACAATATG CTAATGGAAA	2580
TAAAGGAGAC AATGCTGTCA ATGTTATTGT AGGCACTATT TCTAGTATGC CTTATGTCAA	2640
ATTTAAAGAT GAGTTTGCAA GAGCAAAAT GTTTGCTCGT AATTATAGAG GAGACGAGGT	2700
AGACAAGATG ATAAGAGCTA TCGACAAGCT GTGTGATGTT TATAAAAAAG TTGCGCTTTA	2760
GAATAAATA AATTAGGGT TTACACCAA AACTATGTT CTGTAATATT CAATATAATT	2820
TTCTTTATCT ATGATAGAAG AGTCTTTAAA CAAAACATTA ATCTTATAAA ATTCTTCTCT	2880
CCTCTCACAT ACTTTCACAT CCTATTTAAA ATTAATACTA ATGCCTCCCA AGAAGCCCAT	2940
TATTGCCATA TGAATTTAAC TAAAATACTA TCGAAAAAGA AGATATGAGC TACAAAAC TC	3000
TTTAAAAAGC CCCATATCCA AACTAATCAA TTTAATCACT TTATGTCTGT CTTACTTAAT	3060
AAATCACTAG AATCAACTTA TCAAAAGTAC TTTCTTACCC CCCCCAATCA TCGTAGTTAT	3120
CTTTTAAAT CATATATGAT ATATGTATTA TTATCAGCTT ATCTTCCCTA TATATTAGGT	3180
AAAAATAGA AACAAACAAC CGTGCAATTG CGACTCAATA AAACACCTAT CAAAAACCAA	3240

991

TATTCTACTT TCATTATACA GAATAAAGCA ATATAATATA TTTAATATAT ATTATCGCTT	3300
AAATTTATTT AAACCTTAATA AATAAATTAA GGGGAGAATA AAAAAAGAAT GATAAAAGGC	3360
AATACGTTTA TTTTAATATT AGTAACAACA ATGTTTGTAT CATGCAAATT CTATGGAAGT	3420
GATGATACAA ATAAAAAAA TACATCTCTA AATGGTGATA CTAGAGAGAT TGACAATATA	3480
GGTTCAGTCA TTTTAGAACA AGACGGAAAC AAAAAAGGTG ATACTACTGC TAGTAAAGTT	3540
GCTTTGGATC AAGTTACAGA ACATGCTAAT AGTGAACCTA TGCTTAATGA TGACCCTGAT	3600
TCTAGTATTA GTAAATACAA CCAAGAAAAT ACTACTGGCA AATTAACCGA AGAAGATATG	3660
GATAAGCTTA AGGCTTTTTT TGTA AAAACT ATAACATATC AAGGGATACT CAATTCTATT	3720
TATAACAAAT ATACACGCTC TTATAATACC ATTGCAACTT ATTCTGGTTG TGCCAATTAT	3780
AATAGTATTG GATGTTTTAG CGAGGGCCCT TCTGCAAGGC GTAGTCAAGC CCTTAACGAC	3840
CTAGAAAAAA ATAAACTAGA TGAAGAGTAT ACTAACTTA ACCAAATGCT AAAGGAGACT	3900
ACACAAGATT ATTGCCCAA AGCTCTAGAC AATGCAATTG AGGAATACAA GAGGGCTATA	3960
ACAATAGCTA AAGAAGCTGA AGATAAAATA AAAAAATAA CAAGCTTTAC AATAGATGAA	4020
GGCAATAATA ATGAGGAAAG AAAAGAAAAT GTAGATAACT TAAAAAAGT TAACAATATT	4080
CTTTCTATTT CCGAAAAGAC CATAGAAACA GCTAGTGTGG CTTATGCCAA TGCTTTT	4137

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3760 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

ACTTTTTCAT TTTTGAAGCT TTATATATTt TTATaCAGTG ATTAATTCTA AATTTTTCtT	60
TATTTyaTAA AATTTTGTGAT AAATCAATAA TCTACAGCCA ATATTAAAAT CAAAATATAA	120
TAACAAATCT ACAAGTAGAT AAGATGCCTT CCAAATCTTT TTTACTCGTA GACTTGATTA	180
AAAAAAAGA ATAAATTAAA TGCAATTAAT AATTAAAAT ATAATAAAAA AAATTATAAA	240
ATAATATCAA AGTACAAAT TTATATTTTA GTCGTATAAT TTTGATTCTA AACTATCCTT	300
TATATGATAA AATTTTGTGAT AAATCAATAT AGATTCTGCA TAAACAATAT TTATATTTAA	360
ATTATCAACA TTATTGCTAC ACGACAAATA TAAAAGCTTA AAAAAATTTA TATCACTAAT	420
ACTCAAATAG AATATGAAAA CCTCATTTTC AAAAACATTA TTTCCATAAT TTGTCTTAAT	480
TTACAAAAAT AATTTAATTA ATTCTTTAGC TCTTTTAGAT CCTAAACTAA ACAAGAACTC	540

ATTCAAAATG TCATGACTTT TAATTGGAAA CAATAAAGAT AAAGGGTTTA TATCGGTTTC	600
CATATCTGAT AGTAACTTAT AAAACTCATA AAGACTTTTT TTTATGTCCT TTAAAGTAAT	660
AATTTCAATG GCATTTAGTT CTAAATAAGT GTATATGTTT TCCACCATAT ATTTTTCATA	720
AAAAAACATT TCCATTTTAA ATGGAATACA TTATATTCTT TTTTAAAGAT ATTTTAAACG	780
TATGCTTTTA ATTTTACATT TATTATTAAT GAATTTATTT GAGCTAGCTT TTATATTTGC	840
TAGTAATAAA AAAGGAAGCG AAGTAGATAC TATGATTACA GCTATTGATA AGTTAATTAC	900
TATTTATAAG AAAGTCAAGT CCTAAGGTTT AAAATAAGAG AAATATATAT ATAAAGAATT	960
TTTTGTGCTA TATTTATTTA CAACAAAAAT GAAGATTAAA TTTTAACTA TAAGTTTAGC	1020
TATCTTGCTA GCTAACTTGA TTATTATTTT ATTAAACTTG GTTTATTTA TTGTAAATAC	1080
ATCTACTAGT AGCCCTTATA TTGTTCCCTC AGAAAAGATT GATATTTTAC ATCAAAGTAA	1140
TACAGGTGCG GTTAAATTTA AGATTTCCTT AATAAATCAT TTGGGCTCTG TTGCTATTGT	1200
TTATGATTAC AATCTGCTA GTGAAAGATT TTATTTAGAT TTTGAGATTG TAACAAACAA	1260
GAAACCTTTT AATCTTTTAG ATGTTTCTCT TAATGATGTT GTTATTAAAC CTGAGGTTTT	1320
ACTTGCATCC AATAGCAAAT TAAGATTCGA AGAGGGTCAG TATGTTTTGA ATTTTGACGA	1380
CTCTATAGAA AAAACAGGAT TTTTGTGTTA CTTAGACCTT AGAAATGAAT ATTTAAATCT	1440
AGCAGAAATT GCAAGAATCT CTGGCATTAA TTTTCGTGTT AAATGCATAG AAAGAGAAAC	1500
AGGTGTTTTA CGAAATGTTT TGTTCAAATT AAGTGTCGAA AAGGGTAAAA AATTCTTTGA	1560
CCTTATTGAA AGATATAACA ATAATATTGG CAAGGTTTCT TGATTATTTG ATTTGTGGG	1620
GAAAAAAGT TTGATTTAAG GAAATATGAG GAATATTAGC AATtGTATCA AATATATTAT	1680
ATTAACAATG CTTATTGGAT TATTAATTTT TTGTTGTGCA ACCTTTGTTT GGTTGATTGG	1740
AATTTTTTAT TCAAATAACT TTAAAGAAGA GCGGAATTAT TCAATAAGCC CAATAGATAG	1800
TGTTATTATG CGTAAATGTT ATTTTAAAGA ATTTAAGTCT GGACTTATTA AAAGCGTATT	1860
CTTTAAGAAA TTAGATGTAA ATGTTAACTC TAAAAATTTT AAGGAGCTAA ATAAGGTAGA	1920
TAAACAAAT CTGCTAAATT CTTATCCATC TTATCATATG GAGTTTGTCG TAGTTGATAA	1980
TGGATTTTTA ATGAATTTTA AAAATGTTAT TTTTAATGGT ATAGATGATG CTAAATTATA	2040
CGATCAACGT GATATGGTTT ACGGAGGATT TAGATACTCA AAAGAGGCTT ATTTCCAAAT	2100
TATTGGCAAT TATGATGTTA AATTAAATAA AATGAAACAA TATACTCCAG CAATTGTAGT	2160
AAATGTTTTT AAAATTAACA TTAATGATGC TTTATTTAAC TCGTTATTAA AGCAAAAAAC	2220
TTTAAAAGTT ACTTTGATTT CCCATAATAA TAAAGAGTAT ATTTTACAAA CTAATAATTT	2280

993

CTTATCAAAG TATAATTTTC AAACACCAGA AAAGGAGAAT AGTTCTTACT AAGAAATTAA	2340
AGAATTTTAT TTTAAGTTTA ATAATGGGTT GATCATGTCT TATGGTCAGC AAACCAAATA	2400
TGCCTCCCCCT TTATCAGAGC AATTATTCTC TATACCCCCT CTTTTATATA CTTTCTATAT	2460
AATAAATATA GTTTCATAAA ACAATTTTTTA TGTAACAAAA GCTAACTGCC TTATTATTGC	2520
TATATATTTA TAATATTATA TTATATAAAA AGATAGGTCT GAAACAATAT GGATAAATTT	2580
TTAACATCTA ATCATCCTCC AATAATAATC TTTACTATTG GGGCTTTGTG TGCAACCGTG	2640
CTAATATGCT TAATTATAAT ATTTATTATA CATGGCATAA TAAATCCCAT TCTTATAAAG	2700
AAATTCAAAT CCATAAACAA CAGTCTACAA AAAATAACAA AAGAATTTGA AGAGATGAAA	2760
AAAAGAGTAG GACAATTAGA ATCCATATCA AAAAAATTAG AGCTAAATAA TAAACCTGCA	2820
AAAAAACCTA TAAGCTTATA TGGACTAAAA AAATCCCAA TCTAATGTAG ATTTACAACC	2880
GATTATTTTC ATTTTTTTGA TTTAATAACA AATAATCAAT AAAAATAATT TACAAATAAT	2940
TACATACAAA AAGCTACACG CAACAAGGCA AGGCAAAATA AATTATTAAA AAGCGAGCAA	3000
CAATATCAAG CACCCCTTCC CCTATAACTA TTTTAAAAAA AATTAAAAAG GTTTAACGGT	3060
ATACTTATAA ACCTTTTTTA TAAAAAACAA AATTTATTAT AAACCTCAAT AACAGTAAAT	3120
GTTTAAATA CATATAACTC ATTTTAGCCC ATCAAAGAC ATTTTCAACT TTATTTTACA	3180
ATTTTTTAAT AAACCTCTACA TTGGGTGGA CAATGGAATC TAAAAATTCT TTATCTTTA	3240
ATATTTTATA CTTTTCATAG TATGAAAAGT ATGAAAAAAA TGATTAATAC TACAATACAT	3300
TCCTAAATTT TATTGTGTTT TTTTATGATA TAACAAAAAA ATGTTTATA AATTTCCAAT	3360
TCGGATATAA AAATTACCAA AGAGAAATTT TTATGAAAAA AGACATATTA TATACTTTGA	3420
ACGTATTTTT ATATATATCA TTACTTTATT CGTGTCTTG GATGCCATTA AAATCTTCAA	3480
AAATCATTAA AATTAAGAAG TGTAAAACT AATGAAAAAT CCATTAATTT TAAGGAAGGT	3540
TTACAAAACA TAAAAGATTT CTTCTGCAA AGTTATTTAC CTACATATAC TTAATAGTAA	3600
TAGCTTAAAA GCGGATATAA ATATTATTGT AAGAAGAAAG TCGACAATTT TGATACTACT	3660
TAAAGGTTTG GaTTATTCTA TTTCTGCTTT GTTTGTTTAA AAGCGATTTA TGGTTTGAGG	3720
CTAATGTTGA TTTTTTTACC TTTTTTTATT TAAATTTATT	3760

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3653 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

CTTGnGTGCC TGCAGGTCGA CTCTAGAGGA TCCCCGTGTT CATAAAATCC TCTCCTTGAA	60
GGTGTACTTT TTAATTAAG TAAAAGTAAT AAAAATAGAT AAAAATAGTA ATTTATATTG	120
TACCAAAAAC GAAAAATTTT AGTCAAATTT TGTGAGTTCT CATTGCATGA GAAATTTGGG	180
TTGTAGGGAG GCTGTTATAA ATAGAATGGG CATTTTCTGA GGGTGTCCGC TAAGAAAGAC	240
TACATACTTT AGCTAATATA TAGCAAAGAC TTTGAAATTT AATTTGTATG TGTTTTATAG	300
TCTTTTGTA TGAAGTAGTC ATTTGCAATG GAGAGATTTT GGGGAGTTGT TTAATTTAC	360
ATTTGCGTTT TGTAAAAATG TAACAGCTGA ATGTAACAAA ATTATATATT TAAATCCTTG	420
AAATATTGCA TTTATTATGT ATTGTGGTAT GATTAGGACT TATGGAGAAA TTTATGAATA	480
AGAAAAATGAA AATGTTTATT ATTTGTGCTG TTTTATACT TATAGGTGCT TGCAGATTTC	540
ATACTTCATA TGATGAGCAA AGCAATGGAG AGGTAAAGGT CAAAAAATA GAATTCCTCTG	600
AATTTACTGT AAAAATTAATA AATAAGAATA ATAGTAATAA CTGGGCAGAC TTAGGAGATT	660
TAGTTGTAAG AAAAGAAAAA GATGGTATTG AAACGGGTTT AAACGCTGGG GGACATTCGG	720
CTACATTCTT TTCATTAGAA GAGGAAGAAA TTAATAACTT TATAAAAGCA ATGACTGAAG	780
GTGGATCATT TAAACTAGT TTGTATTATG GATATAATGA CGAAGAAAGT GATAAAAATG	840
TCATTAAGAA TAAAGAGATA AAAACAAAGA TAGAAAAAAT TAATGATACT GAATATATTA	900
CATTTTATAGG AGATAAAATT AATAACAGTG CGGGGGGAGA CAAAATAGCT GAATATGCAA	960
TATCACTAGA AGAGCTTAAA AGAAATTTAA AATAGAAGTT AGAAATATAG GAGAGAGCGT	1020
ATATGAATAA AAAACAATT ATTATTTGTG CAGTTTTTGC GCTGATACTT TCTTGTAAGA	1080
ATTATGCAAT TAAAGATTGA GAACAAAATG CAAAAGGGAA AATTAAAGGA TTTATAGATA	1140
AGGCTTTGGA TCCAGCAAAA GATAAAATTA CTTCAAGTAG TTCAAAAGTA GATGAATTAG	1200
CAAGAAAATT ACAAGAAGAA GATAAAATTA AGGGTGTAGA AGAAAACAAT AAAGATGAAT	1260
TAATGCAGGG TGATGATCCT AATAGTGGTG TAATAAATTC GTCACCAGTA TTGCCAGAAA	1320
ATAGTCAAGA TAATACACCA ATATTAAAAG CAGCGGAACA AAGTGATGGT CAACAAGAAG	1380
AGAAAGTGAA AAAAGTAGAA GAATCCGAAG CTAAAGTTGA GGGAAAAGAA GAAAAACAAG	1440
AGAATACAGA AGAACGAAAC AAACAAGAAT TAGCTAAACA AGAAGAAGAA CAACAAAAAC	1500
GAAAAGCAGA ACAAGAAAAA CAAAAAGAG AAGAAGAGCA AGAAAGACAA AAAAGAGAAG	1560
AAGAGCAAGA AAGAAAAGCT AAGGCAGAAA AAGAAGCTAA AGAAAAGCA GAAAGACAAA	1620
AACAAGAAGA ACAACAAAAA CGAAAAGCAG AAAAAGAAAG AGAAGAACAA CGAAAAGAGG	1680

CAGAAAAAAG	GCAaGTTGAT	AACGAAATTA	GAACACTTAC	AGGCAAAATA	GATGAAATCA	1740
ATAGAAATAT	TGATGTTATA	AAAGAGCAAA	CTAGTGTGGG	GGCACAAGGT	GTTATAGATA	1800
GAATTACAGG	GCCTGTATAT	GATGATTTTA	CTGATGGGAA	TAAAGCTATA	TACAAAAC TT	1860
GGGGGGATTT	GGAAGATGAT	AACGACGAAG	GATTAGGAAA	GCTATTAAAA	GAATTGAGTG	1920
ATACTAGACA	TAATTTAAGA	ACCAAATTAA	ATGAGGGTAA	TAAAGCATAT	ATTATTGATA	1980
CTAGAAGCAC	TGAACCCCAA	TTAAAAGAAA	ATGTAAGTGT	TAGCGAAATT	AAATCAGACT	2040
TAGATGAACT	AAAATCAAAA	TTAGAAGAAG	TTAAAGAATA	TCTTGAAGAT	AAAGATAATT	2100
TTGAAGAAAT	TAAAGAATAC	GTTGCTGGTA	GTGAGGATAA	TTATGATGAA	GAAGATTAAT	2160
TTTAGATATA	ACTAAATTTT	GTATACACAA	AATAACAACT	AGTAAAAAAA	TGACTAGTTG	2220
TTATTTTTTT	GTAGATTTCA	TTGTTATAAA	TATAGAAATG	TTTTCTATCA	AAACTTTTCAT	2280
TCAAAAAATG	CCAAAACTA	TTGCTCAAAA	TATTGTTTAT	TTATATACTC	TCTAGAGTTA	2340
TGATGAATAT	AAATGAGATT	TCAGATTTTT	ATGATAATTT	ATATAAGAAA	ACAAAAAAG	2400
AAATAGATAA	ACTTATAAAC	AAGCTCTATT	TAAGTAGCCA	AATAACTCTA	AAGCAAAAAA	2460
GACAAATATA	CAGTGCTGTT	GAAAAAATGC	AAAAGTACGT	AATAAAAACC	GGAAAAAGTG	2520
TTTTTTTAGA	ATCGGAAAAA	GAATTTGTTA	AAGACACTTT	GAAAAGAAAA	AATCTAACAA	2580
AAAAATTTCA	AAGTTTCAAA	GTTGATTTTA	GCTACAAGGA	AGGAATGCTA	GAAAAATGTT	2640
TAGAAAGATT	AGGAGAAGAT	AAATCTATCG	AATTTTTGAT	TTTTGTTTGC	CAAATTCTTA	2700
ATGGGATAAG	AGAAAAAGTA	TCAGAATTAG	ACTTTCAAAT	AGATGCGATT	AAAGAATTTA	2760
GAGATATTTT	ATTTTTGAGT	ATACACTATT	ATGATAAAAG	ACTTTTCACC	AGTAAGAATC	2820
TTATGAATGA	AATGAAATAC	TTTTTCGAAA	AAGTAGAGTT	AATTTATAGT	TATATGCAAT	2880
AAATTAGTGA	ACTGCTATTT	CTAAATCAAA	AATTATAGAA	ATAGCAGCGA	ACTAAATCAA	2940
TAAAAGCTAA	CAGATATTCC	CTGTTAAATA	TCAAGAAGTT	ATCAGTTTAT	GTTAACAATT	3000
AACAAATTGC	TTTACTATTT	AGAGTAACAA	ATTGTTACTT	TTGTTATTTT	AGAGGATTTT	3060
TTTGAAAAAA	GTTAAAAGAT	CTTTTGATGA	TTATGTTGCA	TATTTTAGAG	AAGGATCGTT	3120
AAGTGATGTA	GAAATAGCGA	AGAAATTAGG	AGTTTCTAAA	GTAATGTGT	GGAGAATGAG	3180
ACAAAAGTGG	GAAAGTGGAG	AAAGTGTTGT	TAACGGGGAC	TCTAGAGTAA	CAATTAGTGA	3240
AGATACTTTT	GAACACCTTT	TGTCGCAAAC	CTTTAGATCA	GAAGTTAACG	CTAGGAAAGT	3300
TAGAAGCGAA	TTGGATGTAG	AGCGGTCTAA	TTTAGAATTA	GGATTTATAA	ATGCATTTAA	3360
GCAATATTCT	AGTGTGAGC	TTTTTAGTAT	GCATACTAAA	ATAGAAAATT	TAAGAGCCGA	3420
AATTGACGCT	TTAAATAAAG	CAAGTAGTAA	AAAAACAAG	CAAGTTGTTA	ATGGAGAAAT	3480

TAATTCCTTTA AAAAGCGAGC TTGATGAATA TATAAAAGAG TGTTCAATAA GAGAAATGGA	3540
GCTTTACTAT GAATGTATGA AAAAAGTTGC TACGGTTAAT GGAGCTGAAA GCAAAAGTAA	3600
CTACAAAAAT AGTAAAGGC ACAAGTGAAC TTATATCAAA CAAAAGTTT TAC	3653

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

CAnTTTTATG GAGGTTCTTA GATTTTTnG TATTGCTTCT CATAATTAAA AAAATAGAGA	60
ATAAAAAGGT CTTCCCGACT TTTCTTAATA TGAACAATT GnCAATAAGG AATTCATAAG	120
GAAAAGTTAA AGCTAATATA TCATCTATAA ATAATAAAAA ATATTAAAAA ATAGAGGTTG	180
AAATTTTTAC ATATTTTATA CATAATAATA ATTATTACAC GAACAAATAG GAGAAAAGAT	240
GGCATTAAT TTGCTTAACC ATAACCACAA CAAAACCAAT ACCAACAAAC TACTTTCAAA	300
AGATTCAAGG CTCAAAAAA TTATTTTCAGT AATTAATTAC TTAAATAAAA GTTTTGAAAA	360
AAAATATGAT ATTTCAATAT ATAGAATTCA TTTTAATTCT GAAAACTAA AAGAGCTTTA	420
TCCTCATCAT CAAATAGATA TCCTTAGAGT TTAAACTCT AATATAAGCA AAGAAGGCTA	480
TAAACCAACT GTAATAAGAA CCTTAAGAGA AGACCTAAGA TTTTTAATTC ACATAAAGC	540
AATTGAAAAA AAAATATTAA CATCTCAAA TAACTTAGGA AAATTTAAGG GAAAATTATG	600
TATATATAAG GTGTCGCCTA TTGCATATAA ATTAATATCT GCTTATTTTG AAGCTTATAA	660
AGCAGACCTC TATAGAAAAA TAAAAAGAG TAAAGACGGG CTTGATACAC AAAATGTAAC	720
TAAAAATGTT ACTGTATATA TAAATATCA TAAAAATATA TATAATAAGA ATTCTATTGA	780
AACCGTCTTT AAAAAATCCT AACTAAGAA AAAACAAAA AAGAAAAACA AAAAAGAATT	840
CACAAAAAAT AATTGAAAA AAAGGTTGAA ATTACCTGAA GAAATAACTA AAGAAATTAT	900
AAGTATAGCA AAAAAACTA AAAATCCAGA TAAACTTAC AAAAAACGC TTTTAATTA	960
CAAAGATTTC TTAACTATT TATCATATGA CTATAAAAA GAAGATATTT CATATTTCTT	1020
TTTGAGCAAA CTTAAGAAT ATAAAAATAA AATTCACTTT ATGAGAAAAT ACGCTCCTTA	1080
TAAACAGAC TTTTACCTAC TTGCAGGAGA ATTCAAAGAT TCGTACCATT CTAAATGGAA	1140
AACAAATAAA AAAACCAATT TTAGCGGACA TGTAAAGAA ATAGCCAACA ACATTCTAAG	1200

TAAATTTTA	GAAAAGGAGC	TAAAGTTTGA	ATGATTTACT	AGAAAACTA	AAAGCGAGAA	1260
AAAAAGAAAT	AATAAGCAAG	AAAGAAGCGG	AATATAACAA	TAATATAAAT	AAAGGAACAA	1320
AAGAAAGAAC	TGCCTTTT	AGAATTGAAG	AAATAGATAA	TAAAAAATA	TATTATACAA	1380
AAATCTTTAA	ATATTTAGTA	AAATTTAGAA	TTGCCAATAA	AGACAATAAG	CTAAGTTTAA	1440
CTTTCCAAAA	ACTTAATAAT	AAAAAAAATT	ATTATTTATT	TAATCTTTT	CCTCTAAAAG	1500
AAGACAACAA	GTTTCTAGGA	ATAAAATATG	GATGGGACAA	ATTAGAAAAG	CCTTTTTTTT	1560
TAAGGCAAAA	TAATAAATCT	TATGTAATAA	AAAAACTTTA	TTATTTAGAA	TTTAAATTTA	1620
GCAAAGGGTC	TATTAAGTGT	TACGTTCACT	CTCTTAGAAC	ACTATTAAGA	AAAAAAGACA	1680
AAGAAAGTAC	CAAATATTAT	AAGTTTAATT	TAGAACACAT	AAAAAGAATG	GAAAATACCG	1740
TATATAAATT	TTACAGTAAA	AAGCTAAAAA	ATAAAGGAGT	AATATATAAA	TGGATAGAAA	1800
AAAATCAAAT	ATTATAACAA	TAGCAAATCT	TAAGGGAGGT	GTAGGCAAGA	GCACACTATC	1860
AATACTGTTT	TCTTATGTAT	TAAAGGATTT	GGGTAAAAAA	GTATTGCTTA	TTGATATGGA	1920
TTACAAAAAT	GCTTTAACTT	CATATTTTAG	AAAATATGTT	TTTAATTTTG	ATAAAAAATA	1980
CATTTATAAT	TTATTAATAG	GCAATGTTTA	TTTTGATCAA	TGTATAAGTA	AAATCAACGA	2040
TAATATTTTT	ATAATCCAT	CACATCCTTT	TCTTGATGAA	TTAATGATA	AAAATTTGGA	2100
TAATAAGGAA	AATTTATTGA	GTTTTTGTTT	AGACAAAAAT	GTTTTAGGCC	ATGATTTTGA	2160
TTATATTTTT	CTTGATACTC	CCCCTAGTTT	TAGTTTTATT	TTAAAAAATG	CATTAAATAC	2220
TACAAATCAC	ATTATTATTC	CAGTTCAACC	TGAAACATGG	TCAATAGAAA	GTTTGGAGAT	2280
ATTAATGAAA	AAAATTACAG	ATAAAAGCTA	CAATATTTCT	ATTGTTGTAA	ATCAATTTAT	2340
TAAAAACAGG	AATATACTTA	AAGAGGTTGA	AGATGCTCTA	TATAAACGAT	ATAGTAACATA	2400
TATAAAAGGT	AAAATTCATT	ATTATAATAG	TATAAAGGTT	TTTATAATTA	ACCGTTTGGA	2460
ACCAGATATA	AAGAGCAAAT	ATTATAAAGA	AGCAAAAGAT	GTATTAAAAA	ATATTTTAGA	2520
TTTGTAACAT	TTTTTTATAT	TCCCCCGGGG	GAATATAAAA	AAGGGAGTTT	AAAATGAAAA	2580
TAAAAGCCGA	AAAAGATAAA	GAAGCATTTAT	TTAGTAATCG	TTTTGGGGAT	TGCAATGAAG	2640
AAACAAATTT	AAATGACGAT	CAAGATAAAG	AATTGGCAAA	TTATAATAAT	CTAAAAGAAC	2700
AGCTTAAGTA	TAATTTAAAA	GATGATATTA	ATAATAAAAT	TCAAAGAATG	AAAATATTAT	2760
ATGAAATTAA	ACAAAAAGAA	TTATATAAGT	ACGATGGTTT	TGCTCGTTTT	AATGATTTTA	2820
TAAATCTTT	TGAAGTTGCA	AAAAGTCAGG	CTTATAGGTA	TTAAAAAATT	TATCAAAAAG	2880
TTCTAGAGGG	TAAAGTGTC	ATTGATAAAA	TAAAAGAAGT	GGGCTTTAAG	GCTATATTAA	2940
GAGATATAAA	GGCCAAAGAT	TCTTTAAACG	AAGATAACCA	TAGTGAATCT	GAAGGCGCTA	3000

ATGAAAGCAT TCCTATTAGA ATTTTAGTAA AGGATAAAGA ATTATATAAT TTCTGTAAAC	3060
AAGATACTAA AAGATTGTAT TTTATTATTG AAAAAATTTA TAAAGAAAAG AGAGATGTTT	3120
TATCTGAGCT TATAATTGAG TATGAAAAAA ATAAAAAATA AAAAAATAAA AATAAGCCTA	3180
TTGATTAATA ATGTATATTA TGATAGCATT TAATCAGGTT GGGATTTAAT TTCCTATACT	3240
ATTTGTTTCGT TGTAACGGA ACTGCCATA TCGGGCTTTT TTGCTATATA TAATCTTAAT	3300
CAAAAGTAAC TATTAACTAT TAACTATTAA CTATTAACTA TTAAGTATTA ACTATTAACT	3360
ATTAAGTATT AACTATTAACT TATTAAGTAT TAACTATTAG TAGATTTAAG TTTTTCCTCCG	3420
ACTTAATTTG AA	3432

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3398 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

ATAATAATAA TGATTATGAA ATGCTCAAAA ATCTTGGTAA AGGGGTTTTA ATGAAAAATG	60
CCAATGAATT TCTTAAATTT AATTTAGCAA AGAATGAAAT AACAAGATTT AGTAATAATG	120
AGGATGGCGT TGCTAGGTTT TTAATTGATT TTTTAAAGCT TAATATTAAA TATTAATAAT	180
TTGTATTTAA ATGTTTAATC CATTTGATTT ATTTTATGCA GGATTTTCTA TTTAAATAT	240
AAATTTTTTA CTTATAATGT ATTTTGTAAA ATTTATTTAT TAAATATTG GAATAAGTAT	300
TGACATGGAT TAAACAAAGA TATATATTAT TTTATGTTGy ATAAACAAAT TGGCAAAATA	360
GAGATGGAAG ATAAAAATAT GGTCAAAGTA ATAAGAGTCT ATGGTGAATG CCTAGGAGCT	420
TTAAGGCGAA GAAGGTCGTG GTAAGCTGCG AAAAGCTTGG GGGAGAAGCA AACATTTATT	480
GATCCCAAGA TTACCGAATG GAGTAATCCA GCTAGCAAGA TGCTAGCTAT CTATTATTTA	540
AATAATAGAG GCGATACCAG GGGAAAGTAA CCATCTAAGT ACCCTGAGGA AAAGAAATCA	600
AAGAGATTCC CTTAGTAGTG GCGAGCGAAA AGGGAGTAGC CCAAACTTTA AATGTGTCAA	660
GCTGCAGAGC GTTGCATTTA TGGGGTTGTA GGACGTTTAG GCTTAGTCTG TAATAAGCAA	720
AAAAGTTACA AAATATTTAT ATAGAAGAAT AATCTGGAAA GTTTAACCAA AGAAGGTGAT	780
AGTCCTGTAA TTTAAATGTA AATATCTTTT TAAATGTTC CTGAGTAGGA CGAGGCACGA	840
GAAACCTTGT TTGAAGCTGG GGAGACCACT CTCCAAGGCT AAATACTAGA AAGCTACCGA	900

TAGAGAAGAG	TACCGTGAGG	GAAAGGTGAA	AAGAACCCCG	GGA _g GGGAGT	GAAATAGAAC	960
TGAAACCGTA	GACTTACAAG	CAGTCAAAGC	CGTAATTTAT	TGCGGTGATG	GCGTGCCTTT	1020
TGCATAATGA	ACCTGCGAGT	TATCATGTCT	AGCAAGATTA	AAGCATAGAA	GTGCTGGAGT	1080
CGAAGCGAAA	GCGAGTCTTA	AAAGGGCGAT	TTAGTTAGAT	GTGGTAGACC	CGAAGCCGAG	1140
TGATCTATTT	ATGGCCAGGC	TGAAGCTTGG	GTAAAACCAA	GTGGAGGGCC	GAACCTAGT	1200
CTGTTTAAAA	AGGCAGGGAT	GAGCTGTGAA	TAGGAGTGAA	AGGCTAAACA	AACTCGGAGA	1260
TAGCTGGTTC	TCCCCGAAAT	GGATTTAAGT	TCAGCCTTAT	TTTAGTTTAA	TAGAGGTAGA	1320
GCACTAATTG	AGCTAGGGCC	TGTCAAAGGG	TACCAAACCTC	AGTTAAACCTC	CGAATGCTAT	1380
TAAATGATGA	ATAGGAGTGA	GACTATGGGC	GATAAGGTTC	ATAGTCGAGA	GGGAAACAAC	1440
CCAGACCAAC	AGCTAAGGTC	TCAAAAATGT	GTTAAGTGGA	AAAGGAGGTT	TAGGTACGTA	1500
AACAGCCAGG	AGGTTGGCTT	AGAAGCAGCC	ATACCTTTAA	AGAGTGCCTA	ATAGCTCACT	1560
GGTCGAGTAC	TTAAGCGCCG	ATAATGTAAC	GGGGCTAAAC	ACATTACCGA	AGCTTTGGAT	1620
CTTAACGAAA	GTTAAGATGG	TAGGGGAGCG	TTCTGTAAGC	CAGAGAAGTT	AAGCTGGAAA	1680
GT'TTGATGGA	GGTATCAGAA	GTGAGAATGC	AGGTATGAGT	AACGAAAAAA	TGGGTGAGAT	1740
TCCCATTTCG	CGAAAACCTA	AGGTTTCCTG	GGTAAAGGTC	GTCTTCCCAG	GGTTAGTCGG	1800
CCCCTAAGGC	AAAGCTGAAA	AGTGTAGTCG	ATGGGAAACG	GGTTAATATT	CCCGTACCTC	1860
TTATAGTTTC	GATGGAGTGA	CGCATGAGGT	TAACACTGTC	TAGGCGATGG	TTGTCCTAGT	1920
TTAAGCATT	AGGCGATGAT	CTTAATAGGA	AAATCCGTTA	AGAGAGCTAA	GATGTGATGA	1980
TGAGTGCTAT	TTAGGTAGCA	TGAAATGTAG	GTAGTCAAGG	TGCCAAGAAA	TAGCTTCTAA	2040
GGTTAGGCTA	TAAGGGACCG	TACCGCAAAC	CGACACAGGT	AGGTGGGATG	AAAATTCTAA	2100
GGCGCGCGAG	AGAATCCACG	TTAAGGAACT	CTGCAAAATA	CGTACGTAAC	TTCGGGATAA	2160
GTACGACCTA	AGCAATTAGG	TAGCATAAAA	ATGGTCCAAA	CGACTGTTTA	CCAAAAACAC	2220
AGGTCTCTGC	AAATCTGTAA	AGAGAAGTAT	AGGGACTGAC	ACCTGCCCCG	TGCTGGAAGG	2280
TTAAGAGGAG	ATGTTAGTTT	ATGCGAAGCA	TTGAATTTAA	GCCCCAGTAA	ACGGCGGCCG	2340
TAACATAAAC	GGTCCTAAGG	TAGCGAAATT	CCTTGTCGGG	TAAGTTCCGA	CCCGCACGAA	2400
TGGTGTAACG	ATTTGGACGC	TGTCTCAACG	TGGAGCTCGG	TGAAATTGAA	GTATCGGTGA	2460
AGATGCCGAT	TACTTGTGGT	TAGACGGAAA	GACCCCGTGA	ACCTTTACTA	TAGCTTG GTA	2520
TTGAGATTTG	ATTAAATATG	TGTAGGATAG	GTGGGAGACT	TTGAAGCTAT	CTCGTCAGGG	2580
GTAGTGGAGT	CAATCTTGAA	ATACCACCCT	TGTTTAATTA	GGTTTCTAAC	TTATAGAAAT	2640
ATGAGGAGAG	TGCCAGGTGG	GTAGTTTGAC	TGGGGCGGTC	GCCTCCTAAA	GAGTAACGGA	2700

1000

GGTGCGCAAA GGTACCTTA GAGTGGTTGG AAATCACTCT GTAAGTGTA AGGCATAAGG	2760
TAGCTTAACT GTAAGACTGA CAAGTCGAAC AGATACGAAA GTAGGTCTTA GTGATCTGGC	2820
GGTGGCAAGT GGAAGCGCCG TCACTTAACG AATAAAAGGT ACTCCGGGGA TAACAGGCTT	2880
ATCCTTCCCA AGAGTTCACA TCGACGGAAG GGTTTGGCAC CTCGATGTCG GCTCATCGCA	2940
TCCTAGGGCT GGAGCAGGTC CTAAGGGTAT GGCTGTTTCG CATTAAAGC GGTACGCGAG	3000
CTGGGTTTCAG AACGTCGTGA GACAGTTTGG TCCCTATCTG CCACAAGCGT TGGATATTTG	3060
AGAGGAGCTA TCTTTAGTAC GAGAGGACCG AGATGGACGA ACCTCTAGTG TrCCAGTTAT	3120
CCTGCCAAGG GTAAGTGCTG GGTAGCTACG TTCGGAAGG ATAACCGCTG AAAGCATCTA	3180
AGTGGGAAGC CTTCTCAAG ATGAGATATC CTTTAAGGGT CCTGGAAGAA TACCAGGTTG	3240
ATAGGTTAGA AGTGTAAGTA TAGCAATATA TTAAGCTGAC TAATACTAAT TACCCGTATC	3300
TTTGGCCATA TTTTGTCTT CCTTGTAATA ACCCTGGTGG TTAAAGAAAA GAGGAAACAC	3360
CTGTTATCAT TCCGAACACA GAAGTTAAGC TCTTATTC	3398

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3203 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

GAGAAACCAA GAATTAAATG TAAAAATAAA GATCGTTTCA TAAAGATTGA AAAAGAAAAT	60
GACAAAACAA TGTATCATAC AAAAATAATG ATGGATATTT ATAAATTAGG AATTGACAAT	120
AAAAGAAATG AATGTCGTAT ATCATTAAGA AACTATTTA ATCAAATGAA AGTAGAAGAA	180
GTTCGTTTAT ATTCTATAAA AGAAGGGGAC AAATTTTGTAG GTATTTACTA TGGATATAGA	240
AAACCTATAA AAAACATTTT CGTAAAATAT GAAATAAACG GAACCATAAA GTCATATGGA	300
TTATCAAAAG CACATTACAT AGAATTTAGA TTTAAAAAAG GAAGCGTTTT TTGTTACTTT	360
AAAGGATTAT TTCGCTTATT AAAAAAGAA AAAGAAAATA CACCATATAA TATGGCTTGT	420
ATTGATATGT TTACAAAAC AGAGAAACAC GTATATGAAT TTTACGGTAA AAAATATCCA	480
GAAAAAGGAA TAATTATAAG ATGGATAGAA AAAAATCAAA AATAATAACA ATTGCAAGCC	540
TTAAAGGGGG CGTTGGTAAA AGCACAACCT CAATAATACT TGCAAATCTA TTATCGAAAA	600
AGCATAAAGT ACTTTTGATC GATACAGATG ATCAAGCTGC TACTACAAGC TATTATTATA	660

1001

ATGAATTAGA	AACAAAAAAT	TTCGATATAT	CTAAAAATGAA	CATAGGAAAT	GTTATAAAAG	720
ACGGTACAGA	TATTAAATAAA	AGCATTATTA	ATGTTGAAAA	TAACATAGCT	TTGATACCCA	780
GTTATATAAC	AGTCGATGAA	TTAAATGGAG	AGTATTATTA	TGATAACCGG	CATCTTCCAA	840
TTGAATTTTC	ATTAAAGACG	AAATTAAATT	CCATAGCAGA	CAACTATGAT	TATATTATAA	900
TTGATACTAA	TCCCAAAAGG	AATTTACAT	TAAAGCTTTC	CCTAATTAGC	AGTAATTATG	960
TAATATCTCC	AATGACGGCA	GAAAAATGGG	CAGTTGAAGG	ATTTGAAACA	TTAAGAAGGT	1020
ATATAAAAGA	AGTTGCTGGA	ATACCAATAT	TTATTGTTAT	TACAAGGTTT	AAAAAAAATG	1080
TTACCCACAA	GCAATTAATG	GAAATAGTAA	GCATGAAAAA	CGGGTTTTTG	GGATACATAA	1140
GCGAAAGAGA	AGATTTAAAT	AAAAGAATAG	GGTGTAATGA	AAAATTTGAT	TTTTCAAAAG	1200
ATTACATTAT	TGAATATAAA	AAAATATTGG	ATGTTTTTTT	GGGAAAATTG	TAAGAATTGA	1260
CAAACCTAAT	AAGTCCGGCA	TGCCGGACTT	ATTGGAAATA	AGGGCAAAAA	TATGAATAAA	1320
AAAAACATTA	ATTTAAAAAT	TAATAAAAGA	ATTTTCAGAAA	ATAATTTAAA	TTATATTCTT	1380
GATCAAAGCA	ATGAGAATCA	AAGAAAAGAA	GAATTTGAGC	GATTAATTAC	ACAATTAAAA	1440
AATAATATTA	AATCAGAAAT	ATACAATATT	ATTGATACCA	TGAAGATCCT	TAAGAAAATA	1500
AATGACAAGA	GGCTCTATTT	AGAAGGAGGA	TATAAATCTT	TTAAAGATTT	TTTATCAGAT	1560
TTTAAATTAG	CAAAGACACA	GTCTTATGAA	TATATAAAAT	TAGCCGCTGC	AATTGAGGCG	1620
GGAAATATTAG	AAAGAAAATT	TTATTACCAA	TAATGGAATA	AGGGCCTCTA	TAAGATATAT	1680
TAAAAATCAA	GCAAATGGTA	CAATAAAAAA	ATCAAAACAA	AATCCAATAA	AACCATTAAAG	1740
ATTTCAACTC	AAGAACCAGG	AAAGTTATGA	CTTTTATAAA	AGCAATTCTA	GGTTTGTAAG	1800
TTTTATGATG	GATGAGATTT	TTAAAAATCA	AAAAGATTTT	CTTAATAAAC	TTTTAAAAAG	1860
ATATAAGGAA	TCAAAGGGAC	AATAAGAAAA	TTTTATAAGC	AATTTAATCT	TTAATATTAT	1920
TGAAATATAA	AATATAAAGT	TAGAAATTGT	AAATAAATTGA	TTTAACAAAT	AAGGAAATAT	1980
ATACAAAAAA	GCAACTGAAA	ATTTAAAAAGA	TCATTTGCTA	AGCAGAGGAA	TTTTATTG	2040
TTAAAGTATT	TGAAAAAAA	TTAAATATTA	TCAAAGAAAA	AGGTAAATTG	ATCTCAATTG	2100
ACAATAAATT	GTCAGTAATA	AGCAACGAAG	AATGTTTTTA	ATTTTGATTA	TAATAAATTT	2160
TGCAAGAAG	CACGCTTAAT	AAGCACGGTG	TAATAAGTTG	GGCAATATCT	TGATTAGCAA	2220
CAATGTGTTT	TGATAATCAA	TGGTAAGACG	AACACTTAAA	AATATTTTAG	AAGGAACAGG	2280
GCATTTAAAG	TAAATTTATA	TATATTTAAG	AGTAAGGATT	TGAATAATTT	ATGATTTAGA	2340
GCTGTAGAAT	TTATTAAAAAT	ACAAGAGCAA	CTATTAAAAA	AATGGGCAAA	TTAGAACTT	2400
TAGCAGGGGT	AGTGATTTAT	AAGGACGGGG	TGTTAATGAC	GATATTATAT	AGGCTCAAGG	2460

1002

GCCAGCAAGG ACTACTATTG ATTATATAAA CACTGTTGTT TAAGATTTTA AAAAAAAGAG	2520
GCTATTTTAA AATAACAAAT ATTTTATAGA ATTTATATTC AAGCATAAAT TTAGGAATTA	2580
AAATCAATGA GTTTACTATG AATCTTGAAT TTGTTTTGTT AAATTCAAAA CCACCACACC	2640
CCTATTTTTT AGCTATCTAA TTAAGGGATC CATATGTGTC CCCTTTATTT TTAAATAAAA	2700
GATATATATT TAAAGACAGT TAGGCCTCTT TTAGGCATAT TTTTGTTTAA TAAAAAATAT	2760
TAAATTAGGG TTTATAATTT TTATAGATGA AAATAAAATA GAAGAATCTA ATTTAACTAA	2820
ACAATTTTTG TTTAGTTAAA ATGATATAGG GCTTTGCAAA GTAGATATAA TTAAAGAAAA	2880
TCTAAAATCG CTAAATAAAA CTATTTAAAC TAAGCCCCAT AATGAAAAAG TTTTAGTAAA	2940
AATATTAAAG AATATTTTTA CTAAATAAAA AATTAAACCA GCATTAATAA TACTTACATT	3000
AGATGATTAG CTACTTTTTT TAATTAATAA ATTTTGCATT TAAAGTTCTA TTCCACTTAT	3060
AAATATTGAC TATATCAATA ATTTTCAAG CATTTGGTACA TTTTATATTC TAAATATTTT	3120
GTTTTGTCGC TAATTTGTTG ACATAGGAAT TATAAAAAGG CCATCATCTT TTAAATTAAA	3180
AAGTAAAATA ATACTAATAA ATA	3203

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3189 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

TTGCTAAAAA TATATTTTTT TATATCTtGG CTCTACTACA ACTCCTTTAT TTTTAGAGTA	60
ATAAATAAAT CTGCTGCCAA ATAACCTATA AGATATTTTT TAAACATAAC TTGGATCGAT	120
ATTTATAGAT TTAAAAATTT TTAAATCTAT AATAACTTCC AAAATACAGA ATCTTCACCT	180
AGATTATAAT TGTTTATAGC ATATTCTTCT TTTGAATATG TAAATTCTTA AGCTTATTTA	240
AAAGCTTTTT TCTTGATAG TCAATTAGCT ATTTTAGCTT TTCTGGTTG AACGCCAATA	300
CTAAAATTAT TGAAAATATC TTTTAAAGAA ATCCCATGT CATAAATATC TTTATTTGAA	360
AAATCTTTTT AGTAAAAAAA TAATGGGGAT ATTTGTATTC AAGTTTTTCA AAATTAATAG	420
TAAAGATATT GTTTTTTCCT AAAAACCCAT ATTTTTTTTC TCTTTTGCCT TTAATACTTT	480
TGTAAAATAC TTTAATCAGC TTAATTTTTT TAGTCCATCT TATATTTAGT AAAAATAGCA	540
ATAGTAACTC CGGTTTGGAT ACAAATACA TTCTCACCTA TACTGCCATC ATCAGTTTTT	600

1003

TTCTTTCTTG AACTATCGTG TAAATTTAAT ATATAAATTT CATCAAATGT TTTTAAGAGG	660
TAATCTCATA CCTCTGAATG CCACCTTGTC AAGGTATCCA TTTGTTTGTT ATGATACCTA	720
GCAATCCTtC GTTAGAACTT TTAATTCCTAT GTTCTGCAAA TCTAATAAAC TTAGTGCGGT	780
CATCATTAAAG TGGCCTTAAA TTTTTCAT TTATAAACTT ATTTCTATTT TTTTATAAAT	840
CATTAATAA ATTTAATATA TATTCATTAT TATTTTGA ATCTGAATTA TAAGGAGGAT	900
TTCCCAGTAT GACAAGTATT TGCTTTCTT TAGCTTTATT TGTAAGTTTA TTTTCTCTC	960
CAATTGCAGG GAAAATACCT TAAAAGATTT TTGATCTGAA GGGTCTGCTT TATCAATAAA	1020
ATTAGTCAAA AATATTTATA ACTTTATGTT TTCATTATTT AAGCTGTTCG TACAAATTTT	1080
TCTTTCAAAT ATTGACTTGG CTTTAAATGA TCAACTACAT AAGGAACCAT TAAACATTCA	1140
AAACCATAGA CATTTTAAAG TATGTGAAAA TTAATGTAAT CTTCTTGTTT TTCAGAGTCT	1200
ATTGGAATTT CGTTAATAT AATTTAATT ACTTCAGGTA AAAATGTGCC AATACTTATT	1260
ACAAAATCAA AACTGCAAC TTTATCCCTA TTTTAAAGC CATAATTTAA TTTAATTTTT	1320
TTAAGTGCCT TATGTAAACT GTTAACAATA AACTTACAC CCGAATAGGA AGTGTACTAC	1380
ACTCCTTTGG CCTTCTTAA TTTAACATCG TACTTAGCTA GAAAATCCTC ATAAAAATAA	1440
AGATAGGGGA TCTTTTGAGC TTGTTTGGC TCTTGTAATA GAAAATCTT TAAAAATAA	1500
GCTCTGTATC AATTTATTTA TTACATTAAT AATTTCTTCT AAAATCTATC TTGGACTATT	1560
ATATTCATTA TTTGTATCAA TATCACTAAT TAATTTAAT ATATCTCTTA TAAGCGAAAA	1620
GTTAGAAAGT ATAACTTTT TAATATTATA AAAAGCTATT TTTCATTAAA TTTAAGCAAA	1680
GACATAATTA CCTTATCTTA AACTTTTGA TAATTATAAT TGATTTTAA GGAAATCAAA	1740
ATGATGCCCC AAAAGCTTTT AATAATAAAA AATTGTTATT CTTGCCAAAA GCTACTTAAG	1800
AAAAATAGTA AAATTTGTTG TGTTGTTTAT AGAACTAGAA ATAAATACCC CAAAACCCTT	1860
ATAACGAGCT AATAATTGTT TTTATTGGGA GGTATTTAG GGATTGTAAA TTTTATATA	1920
CAAAGCCTAA AACAAATTTT ACATTTTAT ACTCATATCC TTTCTATTT CTGCTTGCT	1980
GTTTCTTTAT AATAACGAGT TTTAATCAA TTAAATAAA ATTTTCTTT CTAACATCTT	2040
TCTTCTTCT TTCAAACCAT CTTmAGACA CTTAATTTA TCTTTATAAC TCTTCTTAT	2100
CTTTTGGTTA TTCTCTTTT TTAAATTTCT CTTACTTTTT GTATTCTTT TCAATCTTTT	2160
CTAATCTTG TATtCCTTTT TTATTAACCT CTAATCTTAG ATTTCAACA ATATTTAAG	2220
CTACCAGATT TTTAGATTC TCTGTATCT CTGCTTGGCA TCTTAAATTA ATTTCTCTTT	2280
TATCTCTTCT TTTGTATCTA TAAAATCTAA AAATCTTTA GCTTGTTTTT TTAAATCTTA	2340
TTCTAAATTT TGTATATCTA CAACTTATAT AATGTTTATA AGAACTTATT AATATAAAAA	2400

1004

TAGCAGACAT AGTAAACTTT TCCTCATAAT TATCCCACCA AGCTTTAGGA ATATATTAAA	2460
TACCTATAATT TACATATATA AAGCTTAAAA GCAATTTAAT TACATTGCAC ACTATAAAGC	2520
AAAAAATAA AGCCCCAAAA AACTACTCCC CCCAGAGCAC AAATTCCAAA ATCACCAAAG	2580
CAGATCACAA TAAAGACAAT TAAATGCAAA CAATAAAAAAT ACAAGATATT CCAACTTTAT	2640
TTAATAAAGT TGAATAAATT TTTTGCAACA TAAATTTTGA AAGCATTATC AAAATAAACA	2700
TTTATTATAA AAATTGTAAA AAAGAAAAAC CGATATTAAA TACAAAGCTC AAATATCTAT	2760
AAGTTAATTT AGTTTTACAA CAACTAGCAA TAAACTACA TTAATAAAAT TAATAGATAC	2820
ATTAAATTTT AAATCTTCAT TACAGACACT ATAAACAAA ATTTTGTATT TTAATTTTTC	2880
TTATTATTAT ATTAGTTACA ATATCAAGCA AAACATCTTT TCTATTCTAA AAAGCTCCTT	2940
AAAAATATAA TTTACTATTA TTATCTCTTT TTTACAAACT CACATAATTC TTTATCTCTC	3000
ATGAAAATTC TAATAGAAAT ATTCTTATTA TTTAATTTAC TTATATGATT ATTAAAATTT	3060
AATGATTTTT TTTCTAAACA TGTGTTTTTT TATATTTTAA AATCCTAATT CCTTAATCTT	3120
ATCAATAGAT AAAACTATCC TCCAAAACCT TTGACTAAAG TTTTAAATAA AAATAAGTTT	3180
GCnTTTAGC	3189

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

TTGTAAAAAG TTTTGTGTTGA TATAAGTTCA CTTGTGCCCT TTAATTTTTT TGTTAGTTGCT	60
TTTACTTTCA GCTTCATTAG CAGTTGCAAG TTTTTTCATA CATTATAGT AAAGCTCCAT	120
TTCTCTTATT GAACACTCCT TTATATATTC ATCAAGCTCG CTTTTTAAAG AATTAATTTT	180
TCCATTAACA ACTTGCTTAT TTTTTTTACT ACTTGCTTTA TTTAAAGCGT CAATTTTCAGC	240
TCTTAAATTT TCTATTTTAG TATGCATACT AAAAAGCTCA AACTAGAAAT ATTGCTTAAA	300
TGCATTTATA AATCCTAATT CTAAATTAGC CCGCTCTAAA TCCAATTCGC TTCTAACTTT	360
CCTAGCGTTA ACTTCTGATT TAAAAGTTTG CGACAAAAGG TGTTCAAAAG TGTCTTCACT	420
AATTGATAAT CTAGAGTCAT CGCTAACAGA ATTTTCCCA CTTTCCCAT TTTTCTCAT	480
CCTCCACACA TTTACCCTAG AAACCCCAA TTTATCCGCT ATTTCCCTAT CATCTAACAA	540

1005

TCCTTCTCTA AAATATGCAA CATAATCATC AAAAGACCTT TTAAC TTTTT TCAAAAAATC	600
CTCTAAAATA ACAAATTAA CAAATTGTTG CTCTAAATAG TAAAGCAATT TATCAATTGT	660
TAACATTAAC TATTGTCTTG TTGATATCTA TTGACCACAG ATCTATCTTT ACAATTCTTA	720
TTAAACATGA ACCAGTATCA TTATTGTCGC CATTAAGAAG ACCCCTCATA AATTCGTTAG	780
CATTTAAAGA AAATAAGCA AATATAAAAT AATATAAATT CTTTTATTT ATCATGATTC	840
TCCAATATTA ATAAAATAAC AAGACTAGTA GCTAATCTTG TTATTCATAA TTTATGCTTA	900
TAAAAACCAT TTATTTTATT TCGAAATCTT TTTTAGCTTT TCTTAATAAA TATCTTATAA	960
GATTCTTTTT TCAAATTAAA ATCTAATCTT TGGGCAAATC AGCCAAAATT TGT TTTAAAA	1020
TTTGT TTAAC TGTATTTGCT TTATCTTCAG AATAATCTTT TTTAAAATTA TTTCTGGCGT	1080
TATCTCCATA TTTCTCAGCA TAATCAATTT TATCCGAATT TAATTGTATC AAATAATTAA	1140
AAATCGAATC TGGATAACTC CCTATAAGTC TAATCATATC CTCAGACAGG AAAATACTAT	1200
CAGTACTTAT CTTAATTTTT ATAAGATATT CAATAGCCTC AAGAGCGTCC AAAAAACAC	1260
TTTTTTCTTT AATTCCAATT TTTCTTAAAT CTCCTCTAAT TCTAGGAGCA TCGGAAAAAA	1320
CATGACTTTT TTCATACTCA TTTTAAAAAT CATAATTATC TAGTCTTTTA TTTATTAGGT	1380
TAAAATCTTC TTTAGAAAAA GCTCTTTTAG TTTCTGTATA ATTTCTTCT ATATTGCAC	1440
TTAAACTTAC TACAAATAAA AACAAAAATA TTAACAGACT AATTTTTTTC ATATCCCCTC	1500
CTAGCTTTAT TGCCTAAATT TCAGCAATGT AAATGCTAAT AAACAATAAG ACTGATTGTT	1560
AGTCTGTGTT TTTATAATTT TTAATATCAA AACCCATTTT TTATTATTT TTATCTTCTA	1620
TATTTTGAGG CTCTGCTAGC TTTTCAAGTT CTTCTCAAT ATTTTAAAGA GCATCATCTA	1680
TAACCTTTTT TACAAAATCA TTAGTATTAG TACCATCAT AACAGAATAA CTTCCATTTA	1740
CACCCAATTC TTTAGCATAC TTTAAAGCTT TTTGTCCAAT ATTTCTTGT TTTTAACTT	1800
TCTCAGTACT TTCTCCAGTT GCAGATTCAA CTTGTCTTT AAATTCCTGA AATTTCTTTC	1860
TAGCCTCTTC TAATCTTTT TTTCTTTTAT CTATTTTATC CTTTAAATCT TGAATTTCTT	1920
TTTCTTCTC TTCTTTTCCT TCTTGTGAC CACCATCTTT TGCTTGCACC GCTTTTAATA	1980
CGGGTGTGTT ATCGTGGGAA CTTGCCGGCA ATACTGGTGG TGGATTAAAC AGACTGTTAT	2040
TAGGATCGTC ACCTTGCAAT AACTCTTTAT CTAAAAATCC TTCAACTTTT TCTTTTACAT	2100
TTTGT TTTAA ATCTTCACTA CTCGCATCAA TCTTGCAAGA AATTATCAA ACAAAACTG	2160
CACAAATAAT TAAATTTTTC ATTTCTTTAT TCATAAGTTA CTCCATAAAG TACTAATATT	2220
ACCACAACAC CAAATAATTG CAATATTTCA AAGATTTAAA TATATAATTT GTTACATTC	2280
AGCTGTTACA TTTTAACAAA ACACAAATGT AATTTTAACC AACTCGCCAA AATCTCTCCA	2340

1006

TTGCAAATGC TCTACTCATT ACAAAGATT ATAAAATACA TACAAATTAA ATTTTCAAGT	2400
CTTTGCTATA TATTACACAA AGTATACTAT CTTTCTTGTG TACCACCCTC AAAAATCACT	2460
ACTTCTGTTT ATTACACCCA CTCTACAGCC CAGATTTTGC ATGCAATGAG AACACTCCAA	2520
ATTTGACTAA AATTTTTCGT TTTTAGTAAA ATATAATTTA CATTTTTTAT CTATTTTTAT	2580
TACTTTTACT TAATTTAAAA GTAACAACCT CAAGGAGAGG ATTTTATGGA CAATAATAAT	2640
TCTTTTAATT TAAATAATTT CAATATGGAT TTTACGCTCA AACTATTTCA AGAATACCAA	2700
AAACTAATAA ATGAAAACAA AATCTTAAA AATTCATAA AAAATTCATC TAAAAGTAAA	2760
AAAGAAAATT CAAAACCAAC TCCTAAGTTT TATTTAACCC CTAAAAGTAT TAAATTAATT	2820
CTAAAATGTG CAAAACCTT AAAACAAATT GACCCAATTT CTGGTTGGTT TGTGCATCTA	2880
CTCTTAATAA GTGGATGTAG AGGCACTGAA ATGCAAAAAG TAAAAATGCA AGATATTTCA	2940
ACTTTTTTAA GCAAAACCGG AAAAAGTTTA TATACTATTA AAGTAAATGT GGCAAAAAAA	3000
AGAAATACCT CTTGTATTAG AGAAATTGTC ATCAACTCAG AAGAGTTCGA GGCTATCCAA	3060
ACAGCACATA AAAATCATTT CCAAGAAAAA ACTCTTGACT CAAGGCGTAC TTATCTTTTC	3120
CAAAAGAGCA	3130

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3029 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

AGTTTCCCA TTTGCTCCG TAACCTGTGA TTACACTATC ATTTGmGwcy CCTGATATkT	60
cTGTGGAKaT TATTGTgAA GmTTTTCctC TTTTcCTCCT TATTTGTAA TAAaTatTAT	120
ATgCAAAAC TATTTTGGCC AACTTTTTTA CAAAAAATT TACAAAAAT TAGTTGGGCT	180
TATTTAAATT CTCTGTFAA AGAAGTTAGC TAAACCCAAC TTAATTGGAT TTTTTTGATA	240
GCAATATATT TTTTGTGTA TACATATACA TATGTATAAC TAAAGTATT TTTGTCAGGC	300
TTTTTACAGA AATTATTATA ATAAATAAAA GCTTTATTA ATTCTCATGT TAAAGAGCTT	360
AATAAGCCG CGGGCTTAGC TTAATTTATT TTAGATAAAC TCACTAAACA ATTAAATTCA	420
GTTCAATTTA GAATTAAGAT TATTTGTAT TTATTAAAT AAAAGAACCT ATTTAAATTA	480
TCTTGTTAAA AAATTCAAAT AAGTTCTACT TTAGAGCTAT ATACTAAGCT ATTACTTTAT	540

1007

AAAATTTTAA TCATTTTCAA TTGAAAAAAC ACTTATTAAA TATAGAATAG ATAATTGGGG	600
CAAACGTTAT TCCCATTATT AGAATTACTT GTATTGTTCT ATTGCTTGCA TTAAGTTCAT	660
TTTTTTAAAT ATCTATTTTA TTGTCTAGAC TAGATATATC TTTTTCGAAA GTTTTTTCTA	720
CACTATCTAT TTTAGTATTT ACACTATCTA TATCTTTTTG AAAATTCTTT TCTACATTAA	780
TTATTTGTTG TTCTAAAGAA TTCATTTTCT CCTTTAAAAC TTCAAAGTTG TAATTGTCGT	840
TCTGAAGTAA AACAAAATCT ATTGCCCTCT CACTAAACCC CTTATTTAAA AATTCTAACC	900
TTATATTTTC TATTTTAAGA GCATTGTAGG CTAAATTACT CATAAAATCC CCTTTATTAT	960
CCTTTTAATT CTTTATATTT TTTTAAAAGT TTATTAATCA AATCTTTTTG ATTTTCAAAA	1020
ATCTCGTCCA TCATAAACT AGTAAATTTG GCATTTTTTT TATAAAAATT ATAACTTTCC	1080
TGTTTTTTAA GTTGAAATCT TAGGGGTTTT ATTGGATTTT GCTTTGACTT ATCCTCTTTA	1140
ATTTCTACGT TTAATATATT TCTATATACA CCCTTTAAGC CTTTTTCTTT AATATCATTT	1200
ATTGATATGC TCCCCTCTAA TACTTTTCTA TAAATTTTAA GGTATAAAAA AGCCTGACTT	1260
CTAGATATTA TAAATTCTGA CAAAAAGTCT TCAAATTTTT TATAACCATC AATCAAATAA	1320
AGTTTTTTTT CTCTTATTTT ATATAGGATT TTCATTGTTT TAATTTTATT CTCAACATCA	1380
TCAACAGTAA TTCTACGAAG TTGATCCTTA TAGCTTTTAT ATTCAAGTTC CTCATTTTCA	1440
AATTCTTGAA CATCCTCAAT TCTATTATTT AATAATATTT TTTTACTTT TAACTTTGAC	1500
ACTTAATCCT CCTAAGTTTC TGATTTATTT TAAAAGTCT TCCGGAAGAC TTTTAAAACA	1560
TATTGTTTAA TATTTTTTTT ATTTCTTGAT AATAAATTC TTTATTATTA GGCTCTTTCA	1620
ATTCATTTAT AAAAACCTTA ATTGAATTAT AAAAATGAAC TCTTCCTTTA ATAAGATCTT	1680
TGTATTCTGA CTGCAAAATA CTTTCAATAT CTTTATACGT ATTTCTATTT TTTATAAATT	1740
GATTTTCTAT TATTAACACA TCAATATTTT TCTTTCTTAT TATTTCAACT TCCTTTATTT	1800
CATTCATTAA TATTGGCAAA GACTCTACAG ACCACCTTTC TGCTTGAATA GGTATTATAA	1860
CTTTATGTGT AATGTTTAA GCATTAAACA ATAAAGAACT TAAACTAGGG GGAGTATCAA	1920
TTACTACATA ATCAAAATTA TAATAATGTA AATTTTTATC AAATATATGT TCTAACATAA	1980
GCTCTTTATA AGGAATATCT CCTTTTTCAA ATTTACATAA AATTGGATGG GCCGGAATAA	2040
TATACATATT ATTATTTATT GAATTTATAT ATTCATTAAA AGCAATGTTT TGATCTCTTT	2100
TTAAAAGATA ATAAACATTA TTCAATTCAA TATTTCTGAT ATATTGTAAA AAATAACTGG	2160
TTAAACTATT TTGAGGATCT AAATCTACAA TCAACACTTT ATTGTTCAAT TCGCTTAAAA	2220
TATATGAAAA TATAATTGAC AACATGCTTT TGCCAACACC GCCCTTAATT GACGCTATTG	2280
TTATTATTTT AGGTTTTTTA TTATCCATTT TATTAACGGT CCTTGTTCTG GGTATTTTTT	2340

1008

CCCATAAAAT TTATATACTT GTTGTCTCTAA ATCTGTAAAC ATACTAAATA AAACTTTGTT	2400
GTAATGATTA TTGTCTCTTT TTTTATCTAA TAATCGATAT AATCCCTTGA AATAGCAAAA	2460
TACACTTCCG GCTTTAAATC TAAATTCCAT ATAATATGCC CTTGCTAATG CATATGCTTT	2520
TCTAGTTCCr TTTATTTkAT ACTTTATTAA wGGyTTTTTh ATTGGTTTTTC TrTAGCCATA	2580
AAAAATACCA ATAAACTTAT CTCCTTCTTT AATTGGGTay AArTGAGTTT CTTCAACAAT	2640
yCTTTCCCCA TTAAATAGGG CCCTAATGA TAGTCTAAAT TCATGTTTTT TTTTCATATAC	2700
TCCAAATTTG TAAATGTCCA TCATTATTTT TGTATGGTAC ATTGCTTTAC CATTTCCTTT	2760
TTCAATTAAA ATAAAGCGTT CTTTATTTTG ACATTCAACT TTACATTGTC CCTTTTTTAT	2820
AGTTTCAATA GGCTCCATTG CACTTTCCAT ATTTAAATCC TCATATAGCC TTTATGTAA	2880
ATTCTTCTGT GGTAAAGAA TTTTTTTGTT TTCTTATTAT TTCCAATAAT TCAAGATAAT	2940
ATGTACAAA TACTTTATTG TATTCTATTT TCTTTTGGTT ATTCAAATAT TTTTTGGTAA	3000
TTGGCTTTAG AATTTCATA TTTgTTTCC	3029

(2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3000 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

CnCACAGnAC CTTTTAAAAG AGTATTCTAT TTTCTTAATT TATAAAAAAA TAAATCAAG	60
GTAAGAACTA TTTAAATAA ATCTTGTAAG TCTTTAGTAG TGAATGATTG TCTGTCCTAG	120
TAACCTTAGAA CTTAGAAAGT TAGCAAAGCA AACTTTCCAT CCTTCTTCAT CTCATTACCA	180
AAATCCGCAT CCTCATCACC CTTTCCAATA GCAGCAGCAA TCGGATTTGT AGCCTCCCCA	240
GGCTTCTCTC CATCCTGCTC AGCCTCACCA GCAGCCTTAA CAATCGCACT TAATATCTGC	300
TCCCCACTAA CAGCACCAGC CGCCTTGCTA GCAGCCTCAC TGTCCCCAGC ATTAGCATTA	360
TCAACTTTCC CAAACAACTT CCCTGCCTTT TTATTATTCT CCCCTGCAGC AGCAGCAACT	420
TTTCTTTT CACTCCCCC AGCAGCTTCA ACAATCTCCT TTATTCCCTT AGCAATCCCC	480
GTCACACTCG CCTCATCAGC AGCCTTCGCA GCACTATTAT CAGCCACAAC TTCTCCAATT	540
GCATCAGTAC CACTTGAAGC CCCCTCAGCT GTCTTTACAC AGCTTTTACC AGCTTATCCA	600
ACAACTCGCT AACTTCTTTA ATAGCCCCCT CAGCCTTCTC TTTCTCACCA CCACCACTCT	660

1009

TCACAGCAAA CTTTCCATCC TTAGCCATCC CCCTCAAAGC AATAGCAGCA GCAATCTGAT	720
CATCCTTCTT CATCTCATGA TTAAACTCCG CACCCCATC TTTATCCCCA ATAGCAGCAG	780
CAATCGGATT TTTAGCATCC TCAGGCTTCT TTCCCTCCTG ATCAGCCGCA CCAGCAGCCT	840
TAACAATCGC ACTTAATATC TGCTCCCCAC TAACAGCACT AACAGCACCA GCCGCCTTGC	900
TAGCAGCCTC ACTGTCCCCA GCAGCAGCAC CAGCCTTCCC AAACAACTTC CCTGCCTTTT	960
CATTGCTCTC CCCTTTAGCA GCAGCAACAG CTTTCAGCTT TTCACTACTC CCCCCAGCAG	1020
CTTCAACAAT CTCCTTTATC CCCTTAGCAA TCCCCGTCAC ACTCGCCTTA TCAGCAGCCT	1080
TCGCAGCATT ATTATTATCC ACAACTTTTC CAATTGCATC AGTACCATTT GAAGCCCCCT	1140
CAGCTGTCTT TACAGTTGTT ACCAGCTTAT CCAACAATC GCTAACTTCT TTAATAGCCC	1200
CCTCAGCCTT CCCTTTCTCA CCACCACTCT TCACAGCAAA CTTTCCATCC TTAGCCATCC	1260
CCCTCAAAGC AATAGCAGCA GCAATCTGAT CATCCTTCTT CATCCCCTCC TTATTAAACT	1320
CCGCACCATC ATCCGCATTA CCCTTCCCAA TAGCAGCAGC AATCGGATTT TTAGCCTCCT	1380
CAGGCTTCTT TCCCTCCTGC TCAGCCGCAC CAGCAGCTGC AGCCGTAACA ATCGCACTTA	1440
ATATCTGCTC CCCACTAACA GCACTAACAG CACCAGCCGC CTTGCTAGCA GCCTCACTGT	1500
CCCCATTAGC AGCATACCA GCTTTCCTAA ACAACTTCCC TGCCTTTTTA TTATTCTCCC	1560
TTGTAGCAGC AGCAACTTTC AGCTTTTCAC TCCCCCAGC AGCTTCAACA ATCTCCTTTA	1620
TCCCCTTAGC AATCCCCGTC AACTCTCCT TATCAGCAAC CTTGCGAGCA GCATCATTAG	1680
CCACAACCTC TCCAATTGCA TCAGTACCAC TTGAAGCCCC CTCAGCTGTC TTTACACAGC	1740
TTTTACCAGC TTATCCAACA ACTCGCTAGC TCCCTTAATA GCCCCCTCAG CCTTCCCTTT	1800
CTCATCACCA CTCTTCACAG CAACTTTCC ATCCTTAGCC ATCCCCCTCA AAGCAATAGC	1860
AGCAGCAATC TGATCATCCT TCTTCATCTC ATGATCAAAC TCCGCACCAT TCTCCGCATC	1920
ACCCTTCCCA ATAGCAGCAG CAATCGGATT TTTAGCATCC CCAGGCTTCT TTCCCTCCTG	1980
ATCACCAGCA GCCGCACCAG CAGCCTTAAC AATCGCACTT AATATCTGCT CCCCCTAAC	2040
AGCACCAGCC GCCTTGCTAG CAGCCTCACT GTCCCCAGCA TTACCAGCAT CAACTTTCCC	2100
AAACAACCTC CCTGCCTTTT TATTATTCTC CCCTGTAGCA GCAGCAACTT TCAGCTTTTT	2160
ACTCCCCCA GCAGCTTCAA CAATCTCCTT TATCCCCTTA GCAATCCCCT TCACACTCTC	2220
CTTATCAGCA GCCTTCGCAG CAGCATCATC AGCCACAAC TCTCCAATTG CAGCAGTACC	2280
ACTTGAAGCC TCCTCAGCTG TCTTTACAGC TGTTACCAGC TTATCCAACA ACTCGCTAAC	2340
TTCCCTTAATA GCCCCCTCAG CCTTCCCTTT CTCATTATTA TCCTTCTTCA CAGCAAACCT	2400
TCCATCCTTA GCCATCCCC TCAAAGCAAT AGCAGCAGCA ATCTGATCAT CCTTCTTCAT	2460

1010

CTCATCCTTA AACTCCGCAC CATTCTCATT ACCCTTCCCA ATAGCAGCAG CAATCGGATT	2520
TTTAGCCTCT GCAGGCTTCT TTCCCTCCTG CTCAGCCGCA CCAGCAGCCG TAACAATCGC	2580
ACTTAATATC TGCTCCCCAC TAACAGCACT AACAGCACCA GCCGCCTTGC TAGCAGCCTC	2640
ACTGTCCCCA GCATGAGCAG CATCACCAAC CTTCCCAAAC AACTTCCCTG CCTTTTCATT	2700
GCCCTCTTTA GCAGCAGCAA CTTTCAGCTT TTCACTCCCC CCAGCAGCTT CAACAATCTC	2760
CTTTATCCCC TTAGCAATCC CCTTCACACT ATCCTTATCA GCAGCCTTCG CAGCATCAGC	2820
CACAACCTCT CCAATTGCAT CAGTACCACT TGAAGCCCC TCAGCTGTCT TTACAGCTGT	2880
TAcCAGCTTA TCCAACAAC CGCTAGCTCC CTTAATAGCC CCCTCAGCCT TCCCTTTCTC	2940
ATCATCATTC TTCACAGCAA mCTTtCCATC CTTAGCCATC CCCCTCAAAG CAATAGCAGC	3000

(2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2991 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

GAGAAAAAAC ATGAATTTAG ACTATCATTG AGGGCCTTAT TTAATGGAGA AAGAATTGTT	60
GAAGAAACTC ATTTGTACCC AATTAAAGAA GGAGATAAGT TTATTGGTAT TTTTATGGC	120
TACAGAAAAC CAATAAAAAA GCCATTAATA AAGTATCAAA TAAACGGGGC TAGAAAAGCA	180
TATGCATTAG CAAGGGCATA TTATATGGAA TTTAGATTTA AAGCCGGAAG TGTTTTTTGC	240
TATTTTAAAG GGCTaTATCG ATTATTAGAT AAAAAAGAA CAAATAATCA TTACAACAAA	300
GTTTTATTTA GTATGTTTAC GGATTTAGAA CAACAAGTAT ATAAATTTTA TGGGAAAAAA	360
TACCCGGAAC AAGGACCGTT AATAAAATGG ATACTAAAAA ACCTAAAATA ATAACAATAG	420
CGTCAATCAA GGGCGGTGTT GGGAAAAGTA CGAGTTCAAT AATATTGCG ACATTATTAG	480
CTCAAAAATA TAAGTATTA TTAATAGACC TAGATACTCA AGCATCTACT ACCAGTTATT	540
TTTGTA AAAA ACTTGAAAAT CAAAAATTG ATCTTGTC AA TAAAAACATA TACAGAGTAT	600
TaAAAGATAC ATTAGATGTA AATAATGcAA TTGTAAATAT TaAAGAGaAT TTAGaTTTAA	660
TACCAAGTTA CATAACTTTG CATAAATTTT CAAATGAATT TATACCCCAT CAAGAGTTGA	720
GATTAAAAAGA TAGTTTAATC TTTTAAAGC AAGATTATGA TTATATAGTA GTAGATACTA	780
ATCCTAGTTT AGATTTTACT TTATCAAACG CTTTAATAAC TAGCAATTGT GTAATAGTTC	840

1011

CAATGACGGC	AGAAAAATGG	GCAATAGAAA	GTTTAGATTT	ATTAGAATTT	CATATTGAAA	900
ATTTAAAAAT	AAAAATACCA	ATTTTCTTC	TTGTGACAAG	GTTTAAAAAA	AACAATACTC	960
ATAAGAATT	ATTAAAAAT	GTTGAATCTA	GGGAAAGATT	TTTGGGATTT	ATTCATGAAA	1020
GAGAAGATTT	AAACAAAAAA	ATTGCGGGCA	ATAATGAATT	CAATATGGAT	AAAGACTATA	1080
TTAATGAATA	TAAAGAAGCA	TTATCAAAAT	TTTTTGAGAT	ATATTAAAAA	ATTTATTATA	1140
AAAAAATCC	AGATTCTGGA	CTTTTTTGAA	ATAAAGGAGA	TTTTTTATGA	AAATAGAATT	1200
AAATAAAAGA	ATTTTGGCAT	CAGGGATAGA	TCCCGATGGT	AAAAAAGAAG	TGATTACCAA	1260
TGAAGATAGA	ATTGCTCATT	ATAATGCTTT	GAAAGATAGA	TTAAAGGCTA	ATTTTAGAAA	1320
AGAAATATAT	CATAAATTGG	ATAGCATCAA	AATTTTGAAA	GAAATAAAGG	ATAATCAATA	1380
TTATAAAATT	GATGGATATA	AAAAATTTGA	CTATTTTATA	AAAGATTATA	AAATAGCTAG	1440
AAGTCAAGCT	TATAATTACT	TAAATTTAC	AACTGCGTTG	CAAGAAGGAA	TTCTTAAAGA	1500
AGATTATTTA	ATAGAAAATG	GCATTCATAA	TTCTCTTGAT	TTAATAAAGG	ATAAAGAAAG	1560
TCCAACATTA	AAAAAGTCTA	AACAAAATCC	AATAAAACCT	CTAAGATTTC	AACTTAAAAA	1620
TCAAGAAAGT	TATGATTTTT	ATAAAAGCAA	TGCTAAATTT	ACGGGATTCT	TGTTAGATAA	1680
ATTATTTATG	GATAAAAAAG	AAATAATTAA	AATAATTATG	AAAGAATATA	AACAATTAAA	1740
GGGATAATAT	GGAGGTTGTA	TGAACAATTT	AGCTAACAGA	ACGTTTAACA	TAGGAAATAT	1800
AAAAAACGAA	TTTTTAGAAA	TAGGATTTAG	CGAAGAGGCA	ATAGATTTTG	TTTTTCTTCA	1860
TAATGATAAT	TATAACTTTG	AGTTTTTAAA	AGAGAAATTG	ATTAATTTAG	AGAAGAATTT	1920
ACAAAAAGAT	ATATCTAATT	TAGATATCAA	AATAAATAAT	GTTAAAAACG	AACTTAATGC	1980
TAAAATAGAT	AGTGTAGAGA	AGAATTTACA	AAAAGATATA	TCTAGTTTAG	ATATCAAAAT	2040
AGATAGTGTA	GAAAAGAATT	TACAAAAAGA	TATATCTAGT	TTAAACACCA	AAATAGATAG	2100
TGTAGAAAAG	AATTTACAAA	AAGATATATC	TAGTTTAAAC	ACCAAAATAG	ATAGCGTAGA	2160
AAAGAGTTTG	CAAAAAGATA	TATCTAATTT	AAACACCAAA	ATAGATAGTG	TAGAAAAGAG	2220
TTTGAATCAA	AACTTAGCA	TGGGTAACAG	ACTAGTACAT	TTTATGATAA	TAACAGCAGC	2280
AATCTAGGT	CCAATTTTAA	ATGCCCTATT	TATGAGGTAT	TTACAATACA	TCAAATAATG	2340
ATGTATTGTA	TAATTTGATT	TTTAAAATGG	TACATTATAA	TATTGATGAA	GAGTATTATT	2400
AATTAACACT	TAATTTTGC	TTTTTCATAA	AGTAGAACTT	ATTTAAATTT	TTTAACAAGA	2460
TAACTTAAAT	AAGTCTTTT	ATTTTAACAA	ATACAAATTG	ATTTTAATTC	TAAATTGGAC	2520
TATACTCAAT	TATTGAAAAG	CTTTTAAAAA	TTATTTTAAT	AAGTGAATTC	GGTTAAACCC	2580
TAGCTTTATT	AAGTCTTTA	ACAAGAGAAT	TTAATAAAGC	TTTTATTAAAT	TATAATAATT	2640

1012

TCTGTAAAAA GTTGGCAAAA AACAAATTTAT AATAATTATTA TAAATATTAT AGGAGGGATA	2700
TGTTATTATA AATCCGATTT AGTTTGGGCT TAACTAAGTT CTTTGTGTTG AGAATATAGT	2760
TAAGCTCTTT TTTTATAAAA AATTGTTATA AAAAGTTGGT AAAAATAGTT TTTGTTATAT	2820
ATATGTATGT GAATAGCTAA AAAAGTGTAT TGCTATCAAA ACAATCCAAT TAAGTTGGGT	2880
TTAGCTAAGT TCTTAGACAA GAGAATTTAA ATAAGCCCaA CTATTTTTTTT TGTAAGATT	2940
TTTGTAAAAA AgTTGGCAAAA AATAGTTTTT GCTATATACn TATATTTATG n	2991

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2988 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

CTATTTGAAA ATTGCGAGCA TAATATGTGT TTTTTTATTT TAGCACAAGT TTTTLAGACT	60
TTCTAAAAAA GTTAAAAAAA AAGAAGATGC TGAGTAATTT GTATAGTTCT TTTAAGATTT	120
TCATTTAAGT AATAAATTAT ATTATCTTGA TATACTTCTA ATATTTACCC ATCAATAAAG	180
CTAGTGTGGC TTAACAAATA AAAACCAATA AATATTTAAA AAATGATTAA TTTAGAATAT	240
AATTTCTATA GCTAAAGCAA AAAATAAATA TAAATTTGGA CTAGTTTTAT TACATAAAAA	300
GATAAAATTA GTCATGCTTG TTGCAATAGA GCCTACTATC TATCCCGCGA GGTATATTTA	360
TTTATATTGC TTTTLAGTTT TTGTAAAGTG ACTTTTAATT ATTAAAATCT AAGGAGAAGA	420
GATTTATGAA CAAAAAATTT TCTATTTTCT TATTATCTAC AATATTAGCC TTCTTGTTAG	480
TATTAGGTTG TGATTTGTCA AGCAATAATG CTGAAAACAA AATGGATGAT ATTTTAAATT	540
TAGAAAAGAA ATACATGGAT AATTCAAATT ATAAATGTTT AAGTAAAAAT GAGGCTATAG	600
TTAAAAATTC TAAAAATTA TTAGGTGTAA ATAATACTAG AAGTCGTTCT TATTCTTCTA	660
GAGAGACTAA TGTTTCGGAT TCCTATAATA AAACCTATTC ATATTGCAAA AGCAACTGAT	720
TAATTTTATT ACAAAAAAAC AAGAGAATGC TCAACCCATA ATTAGGTGAC AATTAATTGA	780
ATATATGCAG GGATTATTAA AAGTTAGCTT CTGTGACATT ATACACTTGA ATATAATATT	840
ATAAAATAAT AGAATATATG GGTGTTAATA AAGCTTATAA GCATAGAATA TATCATATAA	900
AGAAGAATTT CTATCCCCTT AAAGGAAGTT GATAGTTTAG CTCTTTGTAA TGTCCAACCT	960
GACTTAGACT CTGCGTATAA TGATTTTTTT AGAAAAATTT AAAAGGGAAA TAGAACACAA	1020

1013

GGATTTCCCTA AATATAAAAG TAAGAAAAAT AGGGAACTT ATAGAACTAA TAATCAAAAA	1080
AACTCAATAG GAATAAAAAA TGGTTATATA AAGCTACCTA AAATAGAGTT TATAAAGTTA	1140
TGTCTATAAA TATTATATTT CAATAACAGT TGAGTGCTTA GATACTAAAA ATAATAATGA	1200
AACTAAAGGT GATAAAAAAG AGGCAGTTGG TATTGATATG AGCATGAAAC ATTTTTTAGT	1260
AAGTAGTGAA GGTGAGAAGA TTAATCATCC TAAATATTTA TTAAAAAATG AAAATAAACT	1320
TAAAAAATAC CAAAGAAAAC TATCAAAAAA GCAAAAAGGT TCTATTAATA GAGATAAGTC	1380
TTAAGGTTTA GACTTGCAAT TATATCTCCA TCATGCAAAG TTGTTACAAC TACTGAAAGC	1440
CCACCTAGTA TCACTTAATT TTAGAGCCAT ATTTTAAATA TGACAACTAC TACATACATA	1500
TAAATCAAAA TGGTATGGAT CTGCTTTGTA TAAAGTAGAT AGATATTTTC CATCAAGTAA	1560
ACTATGTAAA TTGTCTTGCA AACTCAGACC ATCCTAAATC ATTAATACTT TTTCCAAACA	1620
TTCTTTTCG CATGCCTTTT TTCATTCTTA GAATTCGAAC TGTAATCAGA CCTTTATATT	1680
CTTTATCAAT TATCATATTT TAGATTTAAA TTGTATATAG CAAAAAGGTC CTATATGGGC	1740
TATTCGGTTT GCAGTAAATA AATAGGGATT GGAATTAAAT CCCTAACCTA ATTGAATAAT	1800
ATCATACTTT CTCAAGAGG ATTCCCTTCG GCCACTTTTT TTCCTCGTTC TTCCATTACT	1860
TTTTTATATT TTTCAGCTTG TTCTCTTCTT TTTTTATTTA ATTCTGTCTGA TTCTCTTTTC	1920
TCTTTTATA ATTTTCTTG AACTACTAGT GGCTTAACTG TTTAGATTG GGATCGTCTT	1980
AGTTATAATT TTGGTACTTC TAATTTTCT GCTACCACCT TTAATTCTGC CTCTAGATTT	2040
GCTCAAATTT TAGGGATTGA TTCTAATTCA TCTCCTTTTA AAGATTTTTT TCTTCTACTT	2100
TCTTTCCCTT ATGTGCTTTT AAATCAAATC TTTTGAATT ATCCATAGCT TCTGTTGCTT	2160
TTCATATACT GTTGATAAT CTAGTGTCAT TTTATTTGGA TCCATTTTAT TTTTAGATGA	2220
TAACTTTCT AACTTTTTTT ATTATCTTTA TCTTCTTTT TTAAATCACA CGAAAATAGT	2280
AAAAATAATA GCAAGTAATG GCTAGGCATA TACTTATCTA ATTTAGAGAT TAGCTCCTAT	2340
ATTCAAGCGG CTATTATCCT TATTCTTCTG GCATAGAAGT TGAAAATTTA AATTTTAATA	2400
AATTGTATTT TTATTTTAAT GAGAATAAGC AGAAACATTC CATTCTTAAT TGAATTCATT	2460
AGAAAGTTTC CTTCTATTGC TAATATCATT AATATAATAA AATAATTATC AAAACATTA	2520
GCAAAATCCCC CTTTATCTCT ATGATACTCC TTCACATCTA TATGATTTCT ATCTTTACTT	2580
TCTACATTAG GCTGATTATC TCTACCATAT TTAATATAGC TAAGCGGCTT TTAACTTTA	2640
CCCATATTTT TCAGTTTGAA TAAAAACCTT TTAACATACT CTTCTATTTG GGATACATCT	2700
CCTTTTCAAT AAAAATTAAT ATGCGCTGAT TTTAATACAT TTACGAAAAA AGTTAATGTA	2760
TCGAGTTTTT CATTACTAAA TCTAAGATTG CTTTCTAAC TCAGTTTTAA ATTAATACTT	2820

1014

TCATAAGCTT TACAAGCTTT AGTCACTCCT CATATAAAAT CCAAAATTCA ATTGTTTTAT 2880
ATAAGTAAGT ATCAAGTAAA TTAAATTGG ATAGTAAAAT ATTAAATAGG GGAAAAACA 2940
AGCTTAATAT TGAGTGATAA ATAAATTTTT CTCTTATTAA ATAGTATA 2988

(2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2970 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

AGAGTTTTTT CGTCTTTTAA AGTACTTGTT GATTTTCTGG TAACATTCTT TTTTAGGATA 60
CTTTAGCTTA TAGTAAATTT CAGTtCCACA ATTTACACCC ATGTGTTGGT AGTAATTCGT 120
TGTGACTTTT AATACTTTTT CTAATTTATA AAGATAATTT TgCaTTGTTC TCAGTGTAGT 180
GGGAGCCAAA CCATTTCTTT TTAGATTTTT ATTATAGTAA TAGAGTATGT TTTGTTGTGT 240
ATATTTCTTA TCTTTTTTGT TTAGAAAATC TACTGTTGAT GTAAGATATA TTAAGTTGTG 300
TTGGTGTGTTG TTGTGGCAAG TGGGATTTTT TGTGGTGATT AAAAAATCTT TCATTTTTTA 360
CTCCTTATTT TGTATTAAAC AATTACTATT ATAATGCAAA ATTTTGATTT AAAAGTAAAT 420
ACTTTTCTAA AAAAATATTA AATTTTAATT ATTAATCTTA TTAATTAAAT ACATTTTGTG 480
TAATTTGGTA AAAAGATTTA TTGATTTTAA TCACAAATTA GACTATACTG CAAATAGCGT 540
AGGAAAATAT CTCATATTTT TTACCTACCT TATTTTGTAG TTTTCTAAAA TCATAGTGGG 600
AACTTGGCGA AATTCCTTTTT AAAGGGAATT TGGTTAAGTC CCACTTCTTT TGTGTAAAAT 660
TTTTTGTAAG AAAGTTGGCA AAAATAGTTT TTGCTATATA ATTATTTATT ACAAATAAG 720
GAGGAAAAAG ATGGAAAATC TTTCAAACAA TAATAATCCA CAAGAAAATA TTCAAGGAGA 780
AATTAAATTC AGAAAAGATA TGAGCACCTT AATCAGAAAC TTGCCGCGTA TTGACAAAAG 840
TCTTAAAGGG TATGGGTATA AGTATCAAGA TTTCAATGAC ATAGTAGAAG TAATTTATAG 900
TGTATTGAT AAGCATAATT TGGATCTTTT TTTTACGCAA GCCCCAATTT CTGTAGAGGG 960
GCAATATGGC ATAGTTGATT ATATTAGGAC TACATTCTAC AGTACAAGCA CTGTGTACAA 1020
ATACTCATTT GATACGCGAA TTCATACAGA TAAATTACAA TGGAACAGTG AAAATGGGTC 1080
TAAAAATATG AATACGATGC CACAATTGTG TGGATCAGCT ATTACTTATT TCAAAAGGTA 1140
CGCTTTAGTA GGGCATCTTT GCATAAGAAG CGAAATGGAT ACTGATGCAG CACCTATTTA 1200

1015

CAATAATTAT GAAAACAGAA ATTCTATGCC TAGCAAACAA TCTAGTGTTA ATCAAAAGCA	1260
AGAACAAAA AGAGAGCAAA AACAAGAGAT TAATCAAAAT CAAAAAATA ACACTATTCA	1320
AAACCAGAAA AGAGACATTA AGCAAGAACA AAAAAAGAT AGGTTTTATT ATTACGGTGT	1380
TTTTAAAGAA GCGTTGTCTA ATATAAAGA TTGGGTAAAT AGCCCTACAA TAAAAGATAA	1440
TATAAATCA ATTATTCAAA AAATAAGCTT TATTCAGAAT ATAGACCCCA ATAATGTTGA	1500
TGATATCAAG AAAATTGAAT CTGATTAAAT CTCGTATTTT GAGAAAAATA GTGATTTTAA	1560
AAGTATAAAC TATTGGGCGG AGATTATAAA AACTATTTT AAGAAAAATA ATAGATTAAA	1620
GGATTTACAA GATTTTGAAA AGTTTGTGTC GTTAAAGAGG ACTGCTTATG GCCCTAGTCC	1680
ATTAATATTC TTTAGTGTCT TAAAAGAATA TGAACGGTTT GATTGCATAT TTGCAGCATA	1740
GCGAATTCTT ATATGGTGAA GGGGGCACAT GGGGGCTGCG ATATTATTGC TGAGCTTGGC	1800
AGGTACTACT TGCACTAGTT GCAAACTAT CTATACCGCC ACCAAGAGCC CCCTTAACCA	1860
CCTCTTTGAA GGTGCTTTTT TGTTGTTTCTAG AATTATCCCC AGTACACTTA TCAAGTTCAC	1920
TCTTTATATG ATTAAGTGCA CCTTTTATTT TGTCTTCGTC ATATCCTAAA AATTTATCAA	1980
ATTCTCCAGC ACCAGTTAAA GCGGTTTTTA ACCAGTCAAG ATGTGTTTTT TGGTCTTCAG	2040
ATAGCTTTTC TCTAAGCAGG TCTTCTTTAG ATTTTGGTTT TTCTTGTTT GCTTCTTTTT	2100
GGGTAAATC ACGTTTTTGT CTACTTTTGT TTTGGCTAGT ATTAGTATCA TTAGAATTAC	2160
AGCTGTTTAG CATTAGTAAA AATAACAAA ATAATATGTT GATAATTTTC ATTTTATTC	2220
CTTTTTTAT TATTAATATT CACTTAATCA ATTATTAATA CTAAATATTG GATAAACAAAT	2280
TATTATTTGA ATTGATATTC TTTAAGTGAG GTAGTAGCTA TTTAGAAATG AAAGCAAATA	2340
TTAGCCCGGC TATCATGTGTT ATAGACATTG CTCCCATAAT TCCTAATACC CATTTAAGCA	2400
TTTCTGAAAG AGACATTAAA TTCTTTTCCA CATTGTCTAT TTTAGCAGTA AGTTCATTTT	2460
TAACACTATC TATTTTTAAA TTAAATTTCT TTTCTACAGT ATCTATCTTA GTATCTAAAC	2520
TATCTATTTT TAGATTTAAA TTCTTTTCCA CATTGTCAAT CTTAGTATTA AGTTCGCTTT	2580
TAACAGCATC AATCTTAACA TTAAATTTCT TTTCTACAGT ATCTATTTTA GAAATAAGAT	2640
TATCAAATTT TATATCAAAT TGTTTTTCTA AATTTTCTAA ATCTCTATAT GTTAGTTCAT	2700
TGTGATAATA TCTTTTAGAT AAATCTTGTG CTATTAGTTG TTCCATGCCC AGTCTAATAA	2760
ATTCTTTATA TATTTGTTCT TGAGTTACAC CTGCAATATT TGTGACACT GTTTCCATAA	2820
AATTTTCCCT TATGGTCATA TTATACACTA TTTTATGATTA ATTGGCTTTA GAGATTTTTA	2880
TATGTAAAT AGAATTTCTT GCAAGAAAA CCTTTTGTGA ATTTACATTT TTAATTGGGA	2940
ATATTTATTA TAGACTTTTT CCGCTATTGG	2970

(2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2942 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

AGAATAGCTT GAAGTAAGGA TAAATGAAGT AGAAAATTTT GCCTGCTTAG TGCAAATTTG	60
TCTATTCCTA ATAGCAATAA CACTTCTGAA TGGAGTPTTG TTAATAAAG TTCTTCTTCT	120
CCCACAACTT GTGCTTGTA GCTTCTTGT TCACTCATTT TCACTTACCT TATACTTTTA	180
ACTTTGCTTT ATGTTAACTT GCAAAATAGT TTTTCTAGTA GCAAGTAGAC CGCCTAAAC	240
AAAATCAATG TATGAATGAG CTACATCGGT TGAGTCTTTA TCAACTTGTT CATTCCGTGT	300
AGGTAGCATA TACTTACTAG GTTTAAATTT AATAAGTTCT GAATTGAGTG GATAAATGAG	360
TATTTTATGT TTTAGCAAGT TTGAAGTTC AATGTAAACA TCTTCTCTAT TATTAATAGC	420
CTTAATAGTT TGAATTAAAA CATCTTCCCA TTTTTCACAA CTACTTGCTG CACCCTGTGC	480
TGCTGCGTAT GGTTTTACTA GTTTAAGTGA CGTTGCTGGG TCAACTATTA CCATCATCGG	540
TGTGGAATAT TCGTCGCCCA GTTCCAACCT TGAAAGTCCA GCCTCAATTT TTTCAATAT	600
TTTATCCATT TTATCTTTAT CACCCTAGC AACCTCTTCT TTTATCTGCT CGGGCATATT	660
AAGCAGCCCA TACATATTTG GAAGCAGGCG TTTTGTATTT TTTCCATCTT TTGAATCGA	720
AACAGTTCCT GTTAGTACAA AGTGATTAAT AAGTTTAATA ATTTCACTAC TTGCAAGCTT	780
ATACGCTTGA GCAAAAGGAA GTAAATTATT ATTAATGTCC CCAATATATG AATCTGAAGT	840
ATAAAATTTT TCAGAAGTCT GCTTTAAATG TCTGAATTTA TACTGTAATT TCAAATAATT	900
AAGTCTTACC ACTTCAGAAC TAAATCCAAT AGTTGAGATA GTATTAACCT CATTGGCAAT	960
TGTTGTAGGA TTAGCATTTA AAAACGCGTC CCATTTTACG GTTTTTTGAT ATCCCATTTG	1020
TAGATCAACA TCTTCAATTT GATCGGGCGA AAACCATTTA TACATAATAG GATCTTTAAC	1080
TTCTCCTATG ATATTTGCCA CAGCTTTTGC ATAATAATTT TCATCAAATA ATTCCATATT	1140
AAATCCTCCT AAATATTATT AATTTCTACT CATAGCTTTA TTCCCAAATA CAGCTACTTT	1200
TACTAAATAA ACCTCATTTG TAATTTGTTT CGCATCAGTC AATGCTGTTG CATTAATAGT	1260
TGCTTTATTT GGTGCTCCAG TCACCTTTTC AAGAGCACCG TCTTTATTAA AAACAAGTTT	1320
GTCTTTTACT TTAACCGTAG AATCTTTTGC CACTAAATAT CCCTCAAAAT TATTGGTAAT	1380

1017

TGGCACAATA GTAGCTGTTT TACTAACTC ATCTATGTCA ATGCATATTC CATATAAGTC	1440
TTCACCTCCA CCAGCCTCAA CATGTGGCTC ATAGTGACTT TGATTATCTT GAGCCTCTTG	1500
AATAACTCTT TTTACTCCAC GCTTGACGG ATACCCCAA AATGGATGAT TTTCCAATTT	1560
ATCAAACCTA CTAGTTCTAG TGCCTCCAGA AGCAAAAAAT TtCaCATTTT TGTCTCTAAA	1620
TTCATTAGAA TTGCTAAGCA AACTAGCGTC ATGTTGGGGA TTTTtCATAA ACTTTTCCAG	1680
TTTACTTCTT TtCTCTkGAT ACTCTTTTAC TAATTGCGTT GTATCTCCCA TTTATTTACC	1740
TCCTTTTATT CGCCCAAAGT TTAACCACCA TCAGGTATTA CTATCTTCTC AAGGCCTCTA	1800
TTTCCAAAAA TTGCAACTTT TATCAAATTA ATAGAATACT CTGCTTAGG ATATCTATTT	1860
TGATCTtGAT TTCCAtCTTC GGGTGCAAAA TTGATtGTAA ATGAATCAGA TAGAGCATAT	1920
ATGTTAATTA CGGTTGGTGG CCCACCTCCA GCCTTGATAA TAACACCGTT ATTATTTATG	1980
TCTAGGATTT CTCCTATTTT TATACTTGGA TTCCTTGTA CAAGGTACCC TTCAAAATTG	2040
TTAGTAATFG GCAATACATA CGCGGTACAA CTAAACTCAC ATACATCTAC ACATATCCCA	2100
TACATATCAG TATCAGCTCC AACTTCyACA TATATAGAGT TCTCTTTTGG AACAAGTTTA	2160
ACCCACGCT TGTATGAAA ACTATTTGCT GGGTCGTAAA GGTATTCCTC TATTTTGTCT	2220
GTATAACTTG AACATGCAAA TGAATATGCA TCAACTCGCT CATTCCTAGA TTTAAAACAA	2280
CTACTCAAAC CGCCAAAAAC CTtATTTTCA ATTGAACTCA TAGATTTTAC ATATTTCTTG	2340
AATTTCAAAA GGATATCATC AAGCTCGTTA ATGCTCTCA AATAGGGATC TTCCCCTTGT	2400
GCATCCTCAG CTtGTCTTGc TTGCCGTTTA GCTCTAGGAG CAGCGGAAAC TTGTGCCCTT	2460
AAATCTACCT GTGGGTCTC AACAGCCTCA AGATTTTCTA CTtGCATGTT GCCTTTTAAA	2520
GCCATAATTT ATTACCCTTT TATTGCTCTA TTCCCAAATA CACTAGCAAG CACTATAAAT	2580
AAATCTTCAG TTAATTTGTG TGCCTTTGAA AGTGCTATTG CATTAAACAGA TTTTGTAGCC	2640
CCAGTGACCT TTTCAAGTTC CCCATGTTGG TTAAATTTTA ATTTATCTCC TGGATTTACA	2700
CCATTTTGTC CTtCTTCTT AAGCGTTAAA TACCCAGTAA AGTTATTTGT AATTGGTATA	2760
ACAGTTGCCA TACCGCTAAA CTCATCTATA TCGGAACACA CTCCATATAA ATCGTCTCCA	2820
CCACCAGCCT CAACTTCTAG TTCGGTTGTT CCATCTCCAA AACTAAGCTT AACACCCCGT	2880
TTATACGGAT ACCCTTTAGC AGGGTAATTC TCTATTTTGT CTTTACTGCT AGTGCAAACC	2940
CC	2942

(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2892 base pairs

(B) TYPE: nucleic acid

1018

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

GGGCTATAAA TGTCATTTAT TATTTCTCA GTGCTTTTTC CAGTTTTTAT TCCGTATTCT	60
TGCGCTGCTT TATAAGAGCT ATACATTTGA CTTTTTTGTT CTTGCGTTGC TTGTTGCGTT	120
TCATAAAGTT TATTTATTGA CTTTTTTAAA TCTTCACTAA GATTATCATA AAAATTTGAA	180
ATTTTCATTAG TATGCATATT AATTATAGAT AGTATATAAA TAAACAATAT TTTGAGCAAT	240
AGTTTTTGGC ATTTTTTAAA TGAAAGTTT GATAGAAAAC ATTTCTATAT TCATAACAAT	300
GAAATCTACA AAAAAATAAC AGCCAGTGAA CTTTTCTACT AGCTGTTACT TTGTATACGC	360
AAATTTAGTT ACACCTAAAA GCATCCAATA TAATTACTGA CTGTCACTGA TGTATCCTTT	420
AATTTCTTCA AATTTAGAAC TATCTTTAAG ATATTTTTTA ACTTCTTCTA ATTTTGATTT	480
TAATTTTCT AAATCTTCTT TAATTTGCT AACATTTACA CTTTCTTTTA ACTTAGGCTC	540
TTCGTAACCA GTATATGGTT TATTGCCTTC ATTTAATTTA GTTCTTAGCG CGTCCCTAGC	600
ATCACTCAAT TCTTTCAATA ATTTTCCTAA TCCTTCGTCT TCTGATTCTT CTTCTAACCC	660
CTCCCAAGTT TCGCGTATAG AATTATTGCC ATTGGTAAAA TCATCATACA CAGGCCAGT	720
AATTCTATCT ATAACGCCTT GTGGGCCTAC AGTCGTTTGC CATTTTATAA CATCAATATT	780
TTCATTTGATC TCATCTATTT TAGCTATAAG TGTTTAAATT TGGTTATCAA CTTGCCTTTT	840
TTCTTCCTCT TCTTGTGTC GTTTTTGTTG TTCTGCCTCT TCTCTTCTC TTTTTCTTT	900
TTCTGCTTTA GCTTTTCTTT GTTGCTCTTC TTGATGTCTT TTTGTTCTT TTTGTTGTT	960
TTCTTCTTTA GCTTTAGCTA ATTCTTGTTC GTTTGTTCG TCTATTATTT CTTTTCTTT	1020
AATGTTTTCT TCTGATTCT CTGTTTTTT TTTATTTTCT TCAACTTTAG CTTCAGCTTC	1080
TTCTACTTTT TTTCTTGTG GACCATCACT TTGTCTATT GCTTTTAATA CTAATGCATT	1140
ATTGTGAATA TTTCCGGCA ATACTGGTGG CGGATTTATT CCACTGCCAT TAGGATCATC	1200
GCCCTGCATT AATCTTCTT TTTCTTCTTC TTGTAATTTT TTTGCTACTT CATCTACTTT	1260
TGTACCACTT GAAGCAATTT TATCCTTTAC TGGATCTAAA ATCTTATTTA CAAATCCTTT	1320
AATTTCCCT TCTGAATTT GTTTTATATC TTTACCAGTT GCAAAATCT TGCAAGAAAT	1380
TATCAGCGCA AAAACAGCAC AAATAATCAA TGTTTTTTTA TTCATAATTA TTCTCTCCTA	1440
TATTTCTAAA TTCTATTTTA AATTTTTTT AAGCACTTCT AGTGGTATTG CATATTCAGC	1500
TGTTTTATCT CCCCCACAC CGTTATTAAT TTTATCTCCT AAAACGCAA TATGTTTCTCAGC	1560

1019

ACCATTAATA CTTTCTATTT TTGTTATGAT CTCCTTGTTT TGGATACCAT TTGCACTACT	1620
TTGTTTCGTAC TTATATCCAT AATACAAACT AGTTTTAAAT GATCCGCCTT TAGTCATTGC	1680
TTTTATAAAG TTATTAACCT CTGATTCTTT TAATGAAAAG AATGTAGCCG AATGTCCCCC	1740
AGCGTTTAAA CCCGTATCAA TACCATTTTC TTCTTTTCTT ACAACTAAAT CTCCTAGGTC	1800
TGTCCAGTTA CTATTATTAT CTTTATTTTT AATTTTTACA GTAAATTTAG AGAATTCAT	1860
TTTTTTAAGT TTTAACTCAC CATFACTTTG CTCATCATAT AAAGTATGGT TTATCTCACC	1920
ACTACTTTGC TCATCATATG AAGTATGAAT TTTGCAAGCA CCTATAAGTA TAAAAACAGC	1980
ACAAACAATA AACATTTTCA TTTTCTTATT CATAAATTC TCCATAAGTC CTAATCATAC	2040
CACAACAGCT AATAATTGCA ATATTTCAAA GATTTAAATA TATAATTTTG TTACATTCAG	2100
CTATTACATA TTAACAAAAC TCAAATGTAA TTTTAACCAA CTCCCAAAAA TCTCTCCATT	2160
GCAATGCCC GGCTCATTAC AAAAGACTAC AAAACACATA CAAATTAAAT TTCAAAGTCT	2220
TTGCTATATA TCACTTAAAG TATCATGTCT TTCTTAAGTC CACCCCTTAA AAATTGCCTC	2280
TTCTGTTTAT CACAGCCACT CCACAACCCA AATTTGCGAT GCAATGAGAA CACCATAAAT	2340
TTGACTAAAA TTTTAGGGTT TTGATAAAAT ATAAATTACA TTTTATTAA ATTTTATTA	2400
CTTTTACTTA ATTTAAAAGT AACACTTCAA AGGAGAGGAT TTTATGGATA CTAATAATTA	2460
TTTTAATTTA AATAATTTG ATACAGATTT GATGCACAAA TTCTTAAAAG ACTATCAAAA	2520
TGTATTAAAT GAAAACAAAA TTCTTAAAAA TTCACTAAAA ATTTCTTCTA AGCCTACTAA	2580
AAAAGCTTCA AAACCAACTC CAAAGTTTTA TTTGAATCAA AAAATTATCA AAATAATTGA	2640
AAAATGTGTT AAAACATTAA AATAAATTGA CCCAATTTCT GGTGTTT TAAATCTACT	2700
GGCAATAAGT GGCTGCAGAG GTGCCGAGCT GCAAAAAGTA AAAATGCAAG ATATTACTCC	2760
CTTTTAAAGC AAAACTGGAG AAACTTTTTA CAATATAAAA GTAAATGTAG CTAAAAAAG	2820
AAATGTCACT TGCATTAGAG AAATGTGCAT AAAATCTGTA GAATTTGATG CTATTCAAAA	2880
AGCTCACGAA AA	2892

(2) INFORMATION FOR SEQ ID NO: 46:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2849 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

GCTAGAAAAG CATATGCATT AGCAAGGGCA TATTATATGG AATTTAGATT TAAAGCCGGA	60
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AGTGTTTTTT GCTATTTTAA AGGGCTATAT CGTTTATTGG ATAAAAAAG AACAAATAAT 120
CATTACAACA AAGTTTATT TAGTATGTTT ACGGATTTAG AACACAAGT ATATAAATTT 180
TATGGGAAAA AATACCCGGA ACAAGGACCG TTAATAAAAT GGATAATAAA AAACCTAAAA 240
TAATAACAAT AGCGTCATTA AGGGCGGTGT TGGCAAAGCA CAAGTGCAAT TATATTTACA 300
ACTCTATTGT CTCAaGATtG GAAAGTGCTT TtAATTGATA TGGATACACA GGCATCAGTA 360
ACTAGTTATT TTTACAAAAA AATAATAGAA GATAATTTTA ATTTATTGGA AAAAAATATA 420
TATGAAGTTT TGAAGGGGAA TGTATTAAAT GATAATTCAG TTATAAATAT TAGTAATAAT 480
TTAGACTTGA TACCTAGTTA TATAAGTTTA CACAAATTTA ATAAAGAGGC TATAACATTT 540
AAGGAAATTA AACTTCAAAA ACAGCTATTA AATTTACAAT CCAATTATGA TTACATAATA 600
ATTGATACAA ATCCCAGCCT AGATTATACG CTAACCAATG CTTTAGTATG TAGTGATTAT 660
ATAATAGTTC CAATAACAGC AGAGAAATGG GCTGTTGAAA GTTTAGAACT TTTAAAGTTC 720
TCAATTAGTG ATTTAGCCAT TGATATTCCA ATTTTTTTTAA TAATAACTAG ATTTAAAAAA 780
AATAATACCC ATAAGGCACT ATTTAGTTCG CTTAAAGACA ATAAGAATTT TTTGGGGTTA 840
ATTTATGAAA GAGAAGATTT AAATAAAAAG ATAGCAAAAA ATGATCTATT TAATTTAAAT 900
AGAGATTATA TGCTAGAGTA CAAAAATATA TTAAGTAAAT TTATAACAAT AATCATGTCC 960
AGGTAAGTGG ACATGATTGC CATTTTAAAT GAAAGGAGTC CATATATGGA GATAATATTG 1020
AACAAAAGAA ACCTAGAAGT GCTAAATGAA GCCGAAGAAC ATTACAAGAA GTTAAaGCAA 1080
AGATTAAAT CTAGTTTTCA ACAAGAAAT TATTATAAGA TGGAAATTAT TAAGATATTA 1140
AAAGAAATAA AAGATAACGA ATATTATAAA TTAGATGGAT ACAGAACATT TGAAGATTTT 1200
ATCAAAGATT ATCATTTAGC AAGGAGTCAA GCATATGACT ATTTGAAAAT AGCAAATGCA 1260
ATTAAAGATG GCATTTTAGA AGAAGCTTAT GTAATAGAAA ATGGTGTTAC AAAAACTCTT 1320
GAGTTCCTAA GAAATCGCC AAATGTTTTG AAAAAATCTA AACAAAATCC AATAAAACCC 1380
TTAAGATTC AACTTAAGAG TCAAGAAAGT TACGACTTTT ATAAAAGTAA TGCTAAATTT 1440
ACTGGATATC TTTTAGACAA ATTATTTAAT AATGAAAAGG AAATGATTAA AAAAAATTATG 1500
AAGGAATATA AACAACTGAa AGGATaGTAA GAAGTTTTAT GACTAATTTA GCGTACAGAA 1560
CATATAACAT AGAAAGCATA AAAAATGAAT TTTTAAACAT AGGGTTTAGT GAGGAGGCAA 1620
TAGATTTTGT TTTCTTCAT AATGATAATT TCAATTTTGA ATTTTAAaA GAGAAAAATAA 1680
TCGATTTAGA AAAGAATTTG AGAAAAGATA TATCTAATTT AGATATAAAA ATAGATACTG 1740
TAGAAAAAAG TTTAAATCTA AAAATArATA CTATAGAAAA AAGTTTAAAT CTAAAAATAG 1800

1021

ATTTTGTAGA AAAGAGTTTA AATGCCAAAA TAGATAGTTT AGATACCAAG ATAAATAATG	1860
TAGAAAAAAC TTTACAAAAA GATATATCCA GTTTAGATAC TAAAATAGAT AGTGTAAAAA	1920
ACGAACTTAA TTCTAAAATA GATAGTATAG AAAAAACCTT GCAAAAGGAT ATATCTAGTC	1980
TAGATAATAA AATAGATGTT TTAAAAAATG AACTTAATGC AAGCAATAGA ACAATACAAG	2040
TAATTCCTAAT AATGGGAATA ACACCTGCTC CAATTATCTA TTCTATATTT AATAAGTATT	2100
TCTTTAATTG AGAATGATTA AAATTTTTTTA AAATATTAAG GGAGTATATA GCGTATTTTT	2160
TAAATAGAAT ACTATAATCT TGATTTAAAT TCTTTAAAGa AACATTTTAT TTTTACTTTC	2220
TTTTTAAATTT AGAACTTATT TGAATTTTTTT AACAAGAAAA TCTAAATAAG TTCTTTTATT	2280
TTAACAAATA CAAATTGATT TTAATTCTAA ATTAACTAT ATTCAATTGT TGAAAAGCGT	2340
TTATTTATTA TAATAATTC TGTA AAAAGC CTGACAAAA TAGTTTTTGT TATATATATG	2400
TATGTGTATA GCTAAATAAG TATATTGCTA TCAAAAAAAT CCAATTAAGT TGGGTTTAGC	2460
TAAGTTCTCT AACAAGAGAA TTTAAATAAG CCCAACTAAT TTTTGTAAA ATTTTGTGA	2520
AAAAAGTTGG CAAAAATAGT TTTTGCTATA TACTTATATT TATTACTATA AAAGGAGTAA	2580
AAAGATGGAA AATCTTTCAA ACAATAATAA TCCACAAGAA AATATTCAAG GAGAGCTCAA	2640
AATGATAAGT ATTAATCAAC AAAGTTTAC TGGTTGTGAA ATATTGAGG AAAAATCTTC	2700
TCCATTAA GAAAAAGTA AATTAAGTAA GATAGGCAAG AAATGCCAG GaATAAGTAG	2760
TCAAGAATGT TTTAGATTTA ATCGCAATAT TGATTTTAGT GTGCAAAGAA ACAAGTTAGA	2820
TAAATACGGT GCTAGTGAAG TAGGCAATA	2849

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2682 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

AGTTGCGTAT CTTGACATAA AAAGTGAATT TGATACTGAT GCAGCACCTA TTTACAATAA	60
TCACGAAAAC GAAAATTCTA TGTCTAACAA GCAAGTTAGT GTTAATCAAA AACAAGAACA	120
AAAAAAGGAC ATAAATCAAG AAAAAATCA ACTGAACACC TTTAATAAAA ACTTAAATC	180
TGGCAAGGCT TATTGCTATG AAATTTT TAG AGACGCACTG TTTAATATAA AAAATTGGGT	240
AAATGAAGGT GAAGAAAAA ATAATATAAA TGCTCTTATT CGGGCATTAT GTACTGATAA	300
TGATGATGCT TTAGAAGATC TTTTGA AAA GAATGCTGAG CTTAAGAGTA TAGAATATTG	360

1022

GGTAAATTTT TTAAAAAAT ATTTCAATAA AACTAATAGA TTTGATGATC TAAATAAGCT	420
TAAAGTATTT ATGTCTGATA ATCGGGATGT TTATAAAACA AAAGTATTAA AATTCTTTTG	480
TATGTTGAAA AAAGAAAGAC AATTTAATTA TATATTTGCA GCATAGCAAT ATTAAAGCCC	540
CCTATTTGGG GGCTGCTATA GGTATAATAA TTAAGGTTTT TATTTTGTGAT TGAGAAATGT	600
TTTTAGTTTT GCCAATTAGC TGTAAGACCA GCATAATGAT TATCTTCTTT TAAAAGTTCA	660
yCTTTAAgGT ACTGATAAAT TTCTTCATTA GAATTTCTAT TAGaCATATC ATTAGCGACG	720
CCTCTAAAAT aTTGCyCTAy TAAGTTGTCC ACCTCCCCAT ATTTCAATTAT TTTTATTACA	780
ATCTTGTGGA GTGTTTTTTT TACAATCAAT AGCTCCTTTA ATATAAGTAT CAAAAGTTTC	840
ATTTTGTGCT TTTGATTTTA AGAAGTTGTA AACCTTGGTA AAAGCACCAG CTAATTCTTT	900
TTGTTTTTGA ATATCTTCAG AAAGCCAATC AAAGAAGTCA TTACATTTAC TTTTGTTTCC	960
ATTCATGCAC CCTTGATTTT CATTGTTTAA TTTTCAATT GTGTATTTAA ACACATTGAT	1020
TAATGAAGTA AACATTTTTT CTTCGTCGGA TGTAAAGTG ATTTTCTCTT GTTGTGGCAG	1080
TTCTTCTTGG CTAAATCAC GTTTTTTCCT GCTTTTGTGTT TGTTGGGCAT TGTTTTTTAA	1140
AGTGTCAATTA TCATTGGAAT TACAGCTATT TAGTAGTAGC AAAGATATAC AAAATAATAT	1200
GTGATGATT TTCATTGTTA CTCCTTTTTT TATTATTAAT ATTCACTTAA TCAATTATTA	1260
ATACTAAATA TGGGATAAAC AATTATTATT TGAATGATA TGTTTTAAGT GAGGTAGTAG	1320
CTATTTAGAA ATGAAAGCAA ATATTAGCCC GGCTATCATT GTGATAGACA TTGCTCCCAT	1380
GATTCCTAAT ACCCATTTAA GCATTTCTGT AAGAGACATT AAATCTTTT CTACATTATC	1440
TATTTTAGCA TCTAAATTAG ATATGTCTTT TTGTAAATTC TTTTCTACAT TGTCTATTTT	1500
AGTATTAAGT TCGCTTTTAA CAGTATCAAT CTTAACATTT AAATCTTCT CTACakTATC	1560
AATCTTAGTA TCTAAATTAG ATATATCyTT TTGTAAATTC TTTTCTACak TATCwATCTT	1620
AGTATCTAAA yTAgatmTAT cTTTTwGtaA ATTCTTTTCy ACATTtTCTA TCTTGGTATT	1680
AAGTTCAC TT AACAGCAT CAATCTTAAC ATTTAAATTC TTTTCTACAG TATCTATTTT	1740
AGAAACAAGA TTATCAAATT TTATATCAAA TTGTTTTTCT AAATTTTCTA AATCTCTATA	1800
TGTTAGTTCA TTGTGATAAT ATCTTTTAGA TAAATCTTGT GCTATTAATT GTCCATGCC	1860
CAGTCTAATA AATTCTTTAT ATATTTGTTC TTGAGTTACA CTTGCAATAT TTGTTGACAC	1920
TGTTTCCATA AAATTTTCCC TTATGGTCAT ATTATATACT ATTTTAGATT AATTGGCTTT	1980
AGAGATTTTT ATATGTAAAG TAGAATTTCT TGCAAGAAAA ACCTTTTTGT AATTACATT	2040
TTTAACTTCA GATATCAGTT TTAAATTTTT TACTGTAGAT TTTTACAAA AACAGTATTG	2100

1023

CAAAAACCTCT	TAGATTACTT	TTTCCTTTCT	TTGTATACTA	CAATAACTCC	AAAACCCACT	2160
AAATGGTTTA	GTGATTTAAC	CTCAAGAATA	TTTTTCGGCAC	CTATTTGGTT	AATAAAATTT	2220
TCTAACCTTA	TCCCTATAAT	FTCGAATAGA	GTTTTGTCTT	TATCTTCTTT	TTTTATAGGA	2280
AAGTTAATGk	TATGCTTATG	ATCATCACCG	CCTTGATCTA	AAGCaTTAAA	GTTTTAACTT	2340
TaTAATTTCA	TCyTTTtAAT	TcATATGAAA	TTAAATTACC	AATACTGATA	ATAAACATAA	2400
aTAACATTAA	TAAATTAATT	TTTTGcACAT	tGTGTTCTT	AATAAATAGA	ATATTAACAA	2460
TATTATATCT	TTATTAAGAT	TTGCCCTAAA	ATATAAAATT	TTATTAAAT	ATAGCAGTAA	2520
TAAACGACTT	TAAGAATATA	AATGGGAATT	TCTTGCAAGA	AAAACCTTTT	TGTAATTTAC	2580
ATTTTAAATT	GAGAATATTT	ATTATAGACT	TTTTCCGCTA	TTGGTTTGT	TTTTTTAATG	2640
TACTCTAAAT	ATATGTTGAG	GGTACTCTGA	GCTCAGATTT	TT		2682

(2) INFORMATION FOR SEQ ID NO: 48:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2532 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

CGGCATnACC	AGTAAAGTTC	AACACTAGAA	TATTGCCTTA	AATGCACGTA	TAAATCCTAA	60
TTTTAAATTA	GCACACTCTA	TATCTAATTC	ACTTATAACT	TTCTAGCGT	TAACTTCTGA	120
TTTAAAGTT	TGTGATAAAA	GGTGTCTTAA	AGTATCTTCA	CTAATTGTTA	CTCTAGAGTC	180
TTGGTTAACA	ACACTTCTC	CACTTTCCCA	TTTTTTCCTC	ATCCTCCACA	CATTTACCCT	240
AGAAACCCCC	AATTTATCCG	CTATTTCCCT	ATCATCTAAC	AATCCTTCTC	TAAAATATGC	300
AACATAATCA	TCAAAAGACC	TTTTGGCTCT	TTTCAAGAAA	ATTCTCTTAA	AATAACAAAA	360
TTAACAAATT	GTTACTCTAA	ATAGTAAAGC	AATTTGTTAA	TTCAATTAAC	ATAAATTATT	420
AATTTCTTTA	TACCTATTAA	CAACTGCCCT	ATATTTACAA	TATTTATTAA	TATAAAAACC	480
AAACATTTCA	AATATCCAAA	AAGGAGCATT	TATATGAATC	AAAAACAAAT	ATTTTTATTAT	540
TTTTTATTAT	TTTTAAAAGT	AACAATAAGT	TTTCTTATG	ATCAATCTCA	ATACAAGGGA	600
TATATGGAAA	AATATTATCA	TAAGAAAGGC	AAAACAGATA	CGCACATATC	CTTTTTTCAA	660
ACTCTTAGTG	CTGATGAAGG	GGGTTTTTCT	ACTATCTTTA	TAGGAGAAGA	TGAACAATTA	720
AGTCGTCTTA	GTTTTACCAC	TTTAAAGGAT	ATTAAAGACG	GCAAAGAAAC	CTCTTATATG	780
GGTTTTAACT	TAGAATACCA	TTACAAAGCA	AAGTTTAACA	ATCCATACCC	TATGTTAAAT	840

GATATACGTG CAAACATTAG TAAAGTGAAA GTTAAATTTT TTTTGTATAA TGGCCCCGAA	900
AAAATAATAA GAGAATTAAA TCAAAAATTT GTAAATAATA GAGTTATGTG GGAAATTTGG	960
AATAATTCAT ATAATAAGCT TTCAGAATAT ATTAGGATTA ATCTAAGAAC CTCTGATCCG	1020
GGCATAGAAA ATTTACTGCC AAAATTTATTA AAACATAAAA CCGTAACAAT AACAAATTGAA	1080
ATTCTTGAAA GTGAAGATCC TGAGAAATTA ACTAGTTCTA TAACTTTTGA TCTTGATAGC	1140
TTTCAAAAAC TATACAAGAA ATATAGTACG TATTTTAAAT AATATAACAA GACTCGCTGT	1200
GAGTCTTGTT ATATTATAAT TTATGATTGT AAAAAAATTT TTTCTATTCT TTTTATTAG	1260
AATCTTTAGA TTCTTTCTCT AACTTTTTAA GCTCTTCAAG CTCTTCTTCA ATCTTTTTAA	1320
GCGAGCTTAC TATTATTTCT TTAGCTATAT CGCTAGTACT ATTACCACTA GAAATATTTT	1380
TAAAGCCCCA ACCCCGAGCA TGCCGCAAGG nTTCTATTCC AACTTTCCCT TGATTTTTAG	1440
CCCTTTCTCC ATCAGTTATT CCAATGTCAG ATTCAACTTG ACCCTTAAGT TCTTCAAATT	1500
TTTTTTGAGA CTCTTCTAAT TCTTTTTTTC TTTTCTCTAT TTTTTCATTT AAAGCTTTCT	1560
CAAGGATTTT TAATTCTTTT TCAAACTTTT CTTTATCTTT TAGTTTTTCC TTTAATTCTT	1620
CTATTTCTTT TTCATAATCA GAATATGTTT TAAGAGAAAC ACTTTTAGGA TCCGACTTCT	1680
CTATCTTATC CTFTAATTCT TTTATTTTTT GTTCAATTTT TTCTTTTAAT TTTTGATCTT	1740
CAGCAACACC TTGAACCACT TGATCTTCGC CCTGCTCCTG AGGCTCATCA GCTTGCATAG	1800
ATTCTTCATC CTTTGGTTGA ACTTTTGCTT CTGGTTTTTT AAAATCTCCA AAAAATCTTT	1860
CTTTTTTTGT ATCTAAAAAT CCCTTAACTT TTCCTTTTAA ATCTTGTTCT AACTTTTTTT	1920
TTACATCTTC ACCACTTGCG TAATCTTGC AAGAACTAT CAGCGCAAAA ATAGCACAAA	1980
TAATAAACAT TTTCTTATTC ATAAGTTGCT CCATAAGTCT TAAATCTAAC GCAACACCGA	2040
ATAATTACAA TTTTCAAAG ATTTAAATAT ATAATTTTGT TACATTCAGC TATTACATAT	2100
TAACAAAACG CAAATATAAT TTTAACCAAC TCCCCAAAAT CTCTCCATTG CAAATGCACC	2160
ACTCATTACA AAAGACTACA AAATCCATAC AACTTAAATT TCAAAGTCTT TGCTATATAT	2220
TAGATAAAGT ATACTGTCTT TCTTATCCGA CACCCTCAA AAATGCCTAT TCTGTTTATC	2280
ACAGCCACTC CACAACCCAA ATTTTCGCATG CAATGAGAAC ACCCAAATTT TGACTAAAAT	2340
TTTAGGTTTT TGATAAAATA TAAATTACAT TTTTATTAAA TTTTATTAC TTTTACTTAA	2400
TTTAAAAGTA AACTTCTAA GGAGAGGATT TTATAGATAT GAATAATTAT TTTAATTTAA	2460
ATAATTTCAA TATGGATTTT ATGCTCAAAC TATTTCAAGA TTATCAAAAT GTGGTAAATG	2520
AAAATAAAAT TC	2532

1025

(2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2528 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

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nAGGATCCCC AGCTCCcTA ATAGCCCCCa TCAGCCTTCC CTTTCTCACC ACCATCCTTC      60
ACAGCAAAC T TCCATCCTT AGCCATCCCC CTCAAAGCAA TAGCAGCAGC AATCTGATCA      120
TCCTTCTTCA TCTCATCCTT AAATCCGCA CCATTCTCCT CATTACCCTT CCCAATAGCA      180
GCAGCAATCG GATTTGTAGC ATCCCAGGC TTCTTTCCCT CCTGATCAGC CGCATCAGCA      240
GCCTTAACAA TCGCACTTAA TATCTGCTCC CCACTAACAG CACTAACAGC ACCAGCCGCC      300
TTGCTAGCAG CCTCACTGTC CCCAGCATTA GCACCAGCAC CAGCCTTCCC AAACAACCTTC      360
CCTGCCCCCTT TATTACTCTC CCCTGTAGCA GCAGCAACTT TCAGCTTTTC ACTCCCCCA      420
GCAGCTTCAA CAATCTCCTT TATCCCCTTA GCAATCCCCG TCACACTCGC CTTATCAGCA      480
ACCTTTGCAG CACCAGCATT AGCCACAAC TCTCCAATTG CATCAGTACC ACTTGAAGCC      540
CCCTCAGCTG TCTTTACAGC TTTTACCAGC TTATCCAACA ACTCAGCAGC TCCCTTAATA      600
GCCCCCTCAG CCTTCCCTTT CTCACCACCA cTctTCACAG CAAACTTTCC ATCCTTAGCC      660
ATCCCCCTCA AAGCAATAGC AGCAGCAATC TGATCATCCT TCTTCATCcn TCATsmTTAA      720
ACTCCGCACC ATTCTCckCA TyACCCTTCC CAATAGCAGC AGCAATCGGA TTTkTAGCAT      780
CCCCAGGCTT CTTTCCCTCC TGATCAGCCG CAcCAGCAGC CTTAACAATC GCACTTAATA      840
TCTGCTCCCC ACTAACAGCA CTAACAGCAC CAGCCGCCTT GCTAGCAGCC TCACTGTCCC      900
CAGCATTAGC ACCAGACCA GCCTTCCCAA ACAACTTCCC TGCCCCTTTA TTACTCTCCC      960
CTGTAGCAGC AGCAACTTTC AGCTTTTCAC TCCCCCAGC AGCTTCAACA ATCTCCTTTA      1020
TCCCCCTTAGC AATCCCCGTC AACTCGCCT TATCAGCAAC CTTTGCAGCA CCAGCATTAG      1080
CCACAACCTT TCCAATTGCA TCAGTACCAC TTGAAGCCCC CTCAGCTGTC TTTACAGCTT      1140
TTACCAGCTT ATCCAACAAC TCAGCAGCTC CCTTAATAGC CCCCTCAGCC TTCCCTTTCT      1200
CACCACCACC ACTCTTCACA GCAAACTTTC CATCCTTAGC CATCCCCCTC AAAGCAATAG      1260
CAGCAGCAAT CTGATCATCC TTCTTCATCC CATCATGATT AAATCCGCA CCATTCTCCG      1320
CATCACCTT CCCAATAGCA GCAGCAATCG GATTTTTAGC ATCCCCAGGC TTCTTTCCCT      1380
CCTGATCACC AGCAGCCGCA CCAGCAGCCT TAACAATCGC ACTTAATATC TGCTCCCCAC      1440

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1026

TAACAGCACT AACAGCACCA GCCGCCTTGC TAGCAGCCTC ACTGTCCCCA GCATGAGCAG	1500
CATCAACTTT CCCAAACAAC TTCCCTGCCT TTTCATTGCC CTCTTTAGCA GCAGCAACTT	1560
TCAGCTTTTT ACTCCCCCA GCAGCTTCAA CAATCTCCTT TATCCCCTTA GCAATCCCCT	1620
TCACACTCGC CTTATCAGCA ACCTTCGCAG CATTATCATC AGCCACAAC TCTCCAATTG	1680
CAGCAGTACC ACTTGAAGCC CCCTCAGCTG TCTTTACAGC TTTTACCAGC TTATCCAACA	1740
ACTCGCCAGC TCCCTTAATA GCCCCCTCAG CCTTCCCCTT CTCATCATT CTTACAGCAA	1800
ACTTTCCATC CTTAGCCATC CCCCTCAAAG CAATAGCAGC AGCAATCTGA TCATCCTTCT	1860
TCATCTCATC CTTAAACTCC GCACCATCCT CATTACCCTT CCCAATAGCA GCAGCAATCG	1920
GATTTTTTAGC CTCCCCAGGC TTCTCTCCAT CCTGCGCAGC CTCACCAGCA GCCTTAACAA	1980
TCGCACTTAA TATCTGCTCC CCACTAACAG CACTAACAGC ACCAGCCGCC TTGCTAGCAG	2040
CCTCACTGTC CCCAGCATT CCAGCACCAG CCTTCCCAA CAACTTCCCT GCCTTTTCAT	2100
TATTCTCCCC TTCAGCAGCA GCAACTTTCA GCTTTTCACT CCCCCAGCA GCTTCAACAA	2160
TCTCCTTTAT TCCCTTAGCA ATCCCCGTCA CACTCGCCTT ATCAGCAACT TGGCTTTTAC	2220
AATTAATAAA AACAAAGAAA GTTGTTAATA AAATTGCACT TGAAATTTTT TTCATATTTT	2280
TTTGTTTAAT GATTGTTTTG AACATTTAAA AAATGTTTTT GTTAAGAGGC TTTTATCTT	2340
TGTTTAAGTT AAAGTTAAAT AATAATAACT AGTTTTTTTA ATTGGATTTG TGAATTTTGC	2400
CTACTTCCGT ATCACATATA ATAAAGTTG ATGACATATA TAGTATTTTT ATTGCTTGAG	2460
AGTTTAAACA AGTGTAGGTG AGAGAATTTT TCATTTCTTT TATTATAAAG AATAAAGAA	2520
ATGAAAAA	2528

(2) INFORMATION FOR SEQ ID NO: 50:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2496 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

TGCAGGTCGA CTCTAGAGGA TCCCTGCCTC TTyaAGTATG CTAGCCAAAA TATraCGAGT	60
AAwTTCTTTG TCTGATACTT TAAATCTTT GTcATATATA TTTTtTkcAA TTTTAAATAC	120
TATAGArTCA TCAGGcTcTC ATAAAGyATC TCTCTAAGAG TTTTtTGAAT TATmTCTTTT	180
TCTtTrgAtA TTTGyTCTTT TTCAACTGmT ATTAYATTc TTGTyTTTAG GTATCTTTCT	240

1027

TTTCTTATAA GATAGCTAAA TAAATAAAC CATTCTTGCT CTTTATATTC TTCTTTtTCT	300
TTAATTTTAG AAAATCAAA TTCAATATAT CTTTTTCTC CATAAAGTAC TTTCGATTTA	360
TCATATAATC TCCATACCTT TCCATTTGAA AGTATCCCAT AATGTTTTTG ATATTGATTT	420
AGATATCTGT ATAGCTGATC TTCTGCTTCT TTTACCTTAT CTTTAGCATC AAAACTAAAT	480
GATGGACGCT TAACTTCTGC TATAAGCAAG ATATCTTCAG TTGGAATAGA TTCATTATTT	540
TTTTTAGCTT CTTCTAATTT TTTATFAAAA GCTACTTTAT CTTTATCATT TTCAAAAAGT	600
AGTATATCTA CTCTGGATTT TACTCCTTCT ATTTGCCAC CTTTTGTG TTCTACTGAA	660
TAAGCTAATT CTTCAAATAT AGACTTTAGC AAAGACTCTA TATTTGCTTC TGTTGAATTG	720
TCATCTATAG CTGAATTTT ATTTTTTAAA AAAATAAAAA AGTTTTTTGA TTTAACAATA	780
TTTTCTTTTT TTATAAGCC TTTTGACAGT TCTTTATAAA GAGATACATT TGGATCATTT	840
GT'TTTTATAA TGAATCGGCT TTCATTGTTC ATATTTACAA CCATTATGTT ATTTATAAAT	900
CCTTTTATAG CCTTCTTGAT ACTCGAAATG TACTCTAAGA TTAGTTTTTT TAAAATTAAA	960
AAACTAATC TTAGAGTAAG TCGGCCAAAA CTGTGTTTTAA TATTTATTTG ACTATCAATA	1020
CTCTATCTTT AGAATAAGCT TGTTAAAAAT TATTTCTCAC TTTTCTCAA TTAATTAAAG	1080
TTATTAATTT ATTTTTTATA AGGCATCCTT AATTAAAGAG CATTTAAAAA ACACTTTTTT	1140
AAAACCGAAT TTTTCTTAAA CATTCCCCAA TTTGTGAAGC ATAAACAAAA AAATGTTTTT	1200
ATCCTTTTCA TTTTCAAAAT TACAATTATA GAGTCTTTTG TTAATTTCTT CTTTAAAAAC	1260
ATCTTGCTCA GAATCATGCA AGCAACAAAG ATGCAAAAAA TTTTAAAAG AACTTATCAG	1320
GTCAAAAACA ACACAAATAA TAACCCAGTT TTTATTCATA ATTATCCTCT CTCAAAATTA	1380
AAAAATAAAT CAAAGTCTTT GATTTACAAT TTTTATTAA GCAGTGAAGG GGGAAAAACA	1440
AATTGTCCTA AATATTTAAC AAAAAATGGA AATAGACTTA ATAACTTGG TTTTCTCTCA	1500
GGAAGGATTT CTAATTACAA CATCAAATTC TTCCTGAATA TCTGGAAACT CAATTCCATA	1560
GTAAAAAAT TTATAGTAGC CGCTTAATTT TCTAATTATA TCTATTTTTT CTTTATCTTT	1620
ACTAGAAGTT TTATTGCCA AAATATTTTC AATTAAACTA ATTAAAGCTG TAATATCACT	1680
AAATTTTATA TTTAAAGATT TGTCAAAAGA TAATGAATAA AGTTTAATTA AAGAAAATAT	1740
TATTCCTAAA TTATCTGTAT CTTCACTTTT CTCATATTCT TTATATATAT TTTTAGATCT	1800
TTCTATATCT TCTTTAGCAG TATCGTTAAT ACCTCTAATT TTTTGATAGC TATATCTAA	1860
AATAATTGTA ATTTCTTTAA TTCTCTTTTT AAATAAGAA AATCCACCTT CAAATTTCTT	1920
TTTTTTAATA TCAAAAATTT AATCTTTGGC ATATCCTAGT AAAGGATTTT CTACTTTTAT	1980
ATGATGTTCA ACAAAGCTTA ATGGTGTTCC AAAAAATAAA TATTTTAATA ATCTAACTTA	2040

1028

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TTTTTTTGAG ATAGTTTTTT ATAAACTTG CCCAAGCAAT CTATACTCTT AAGTTCGGGT      2100
TTTCTCAATC ACCTATAACT TTATTGCTA ATTAATTTTT TATAAAGCT ATCCTTAAAT      2160
TTTTCAAAAT ATACTATATG AACTACTGCT TAAAAAGCAA AGACTATAAA ATAAGTAGTT      2220
CATCAGAAAG TTTTGTATGG TATTACTACT ATTAATAGAA TTTAAAAAAT CGAGCTTACC      2280
AATGTATTTA AATAAACTAG AAAGCAAACC ACAATACATG ATTAAATGA TATGGGCAAT      2340
AAACTTAAAA AGTTTAACGA TAATTTTGAA ATTCTTATTA GAATCTAATT AAAAATGTAA      2400
ATTTATATAA ATTTTATAAA TAAAGAGTCA AAGAAAACGC TTTATACTAG AAAGTCTTTA      2460
TAAAGATAAT AAAATATATT TTTTAGAACT TTCTTC                                2496

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(2) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2487 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

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ATTTATTTAC ACGAAACCCT GACTTTTTGA GAAGATTTTT GAATTTATTA GAAATATGGA      60
TAATGCTAAT TTGGTTGTCT TTAACTTAT GTTTGGATTT TTGAAAAAAA TAAGTACGTC      120
TTGTATCAAG ATTTTCTCA TTAAATGAT TTTTGTGTGC TGTTGGATA GCCTCGAACT      180
CTTCTGAGTT GATAACAATT TCTCTAATAC AAGTTACATT TCTTTTTTTT GCCACATTTA      240
CTTTTATGTT GTATAAAGTT TTCCATTTT TGCTTAAAAA AGTTGAAATA TCTTGCATTT      300
TTACTTTTTG CAGTTCGGTG CCCCTGCAGC CACTTATTGC GAGTAAATGT AAAAACCAAC      360
CAGATATTGG ATCAGCTTGT TTAAGAGTTT TGATGCATTT TTCAATTAGT TTGCCAATTT      420
TTGGGGTCAA ATAAAATTTA GGAGTTGGCT TTGAAGCTTT TTTAGTAGGC TTAGAAGAAA      480
TTTTTAGTGA ATTTTAAAGA ATTTGTTTT CATTTATTAG TTTTGTATGA TCTTGAATA      540
ATTTAAGCAT AAAATCTATG TTGAAATTAT TTAAATTAAG ATAATTATTC ATGTCCATAA      600
AATCCCCTCC TTATAAGTGT TACTTTTAAA TTAAGTAAAA GTAATAAAAA TTGATTAAAA      660
ATGTAATTTA TATTTTACCA AAAACAAAAA AATTTAGTCA AATTGTGTGG CTTCTCATTG      720
CATGCAAAAT TTGGATTGTA GGATAGCTGT GATAACAGA AGAGGCAATT TTTAAGGGGT      780
GCACTTAAGA AAGATACTAT ACTTTAAGTG ATATATAGCA AAGACTTTGA AATTTAAGTT      840
GTATGTGTTT TGTAGTCTTT TATAATGAGC AGGCCATTTG CAATGGAGAG ATTTTAGGGA      900

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1029

GTTGATTAAA ATTATATTTG CGTTTTGTGA ATATGTAATA GCTGAATGTA ACAAATTAT	960
ATATTTAAAT CTTTGAAAAA TTGTAATTGT TTGGGGTTGT GGTAACCTTA AGGCTTATGG	1020
AGTGGATTAT GAATAAAAAA ATGAAAATAT TTATTATTTG TGCTGTATTT GTGCTGATAA	1080
GTTCTTGCAA GATTGATGCA ACTGGTAAAG ATGCAACTGG TAAAGATGCA ACTGGTAAAG	1140
ATGCAACTGG TAAAGATGCA ACTGGTAAAA ATGCAGAACA AAATATAAAA GGGAAAGTTC	1200
AAGGATTTTT AGAAAAGATT TTAGATCCAG TAAAGGATAA AATTGCTTCA AATGGTCCAA	1260
TAGCAGATGA ATTGGCAAAA AAATTACAAG AAGAAGAAAA GGTAAATAAC GGGGAAGAAG	1320
AAAATGATAA AGCTGTCTTT TTAGGAGAAG AATCAAAAGA GGATGAAGAA GAAAATGAGC	1380
AAGCTGTAA TTTAGAAGAA AAAAATGCGG AAGAGGATAA GAAAGTTGTT AATTTAGAAG	1440
AGAAAGAATT AGAAGTTAAA AAAGAGACTG AAGAAGATGA AGATAAGAA GAAATAGAGA	1500
AACAAAAACA AGAAGTGGA AAAGCACAAG AAAGAAAACA ACGACAAGAA GAAAAGAAAC	1560
GAAAAAACA AGAACAGCAA GAAGAAAAGA AACGAAAACG ACAAGAACAA AGAAAAGAAA	1620
GGAGAGCTAA AAACAAAATT AAAAACTTG CGGATAAAAT AGATGAGATA AGTTGGAATA	1680
TTGATGGTAT AGAAAGTCAA ACAAGTGTA AACCAGAAAGC AGTTATAGAT AAAATTACGG	1740
GGCCTGTATA TGATTATTTT ACCGATGACA ACAAAAAAGC TATATATAAA ACATGGGGAG	1800
ATTTAGAAGA TGAAGAAGGC GAAGGATTGG GAAAATTATT GAAAGAATTG AGTGATACTA	1860
GAGATGAGTT AAGAACCAAA TTAAATAAAG ATAATAAAAA ATATTATGCC CATGAAAATG	1920
AGCCTCCTCT AAAAGAAAAT GTAGATGTCA GCGAAATTAA AGAAGATTTA GAAAAAGTAA	1980
AATCAGGATT AGAAAAGGTT AAAGAATATC TTAAAGACAA TTCTAAATTT GAAGAAATTA	2040
AAGGATACAT CAGTTACAGT CAGTAATTAT ATTGGATGCT TTTAGATGTA ACTAAATTTT	2100
ACGTACACAA AATAACAGCT AGTAGAAAAG TTCACTGGCT GTTATTTTTT TGTAGATTTT	2160
ATTGTTATGA ATATAGAAAT GTTTTCTATC AAAACTTTCA TTTAAAAAGT GCAAAAACTA	2220
TTGCTAAAAA TGTTGTTTAT TTATATACTC TCTAGAGCTA TGACGTATAC AAATGAGATT	2280
TCAGATTTTG ATGATAATTT ATATAAGAAA ACAAAAAAAG AAATAGATAA ACTTATAAAC	2340
AAGCTCTATT TAACTAGCCn AATAACTCTA AAGCAAAAAA GACAAATnTA CAGTGCTGTT	2400
GAAAGAATGC AAAAATACGT AATAAAAACC GGAAAAAGTG TTCTTTTAGA ATCGGAAAAA	2460
GAATTTGTGA AAGACACTTT GAAAAGA	2487

(2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2462 base pairs

(B) TYPE: nucleic acid

1030

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

AGGAGATAAG TTTATTGGTA TTTTATTATGG CTATAGAAAC CCAATCAAAA cCTTTAATAA	60
AGTATAaAAAT AAATGGAAct AGAAAaGCAT ATGCATTAGC AAGAGCaTAT TATATGGAAT	120
TTAGATTTTAA AGCCgGAAGT GTTTTTTGCT ATTTTAAAGG GCTATATCGT TTATTGGATA	180
AAAAAGAAC AAtAATCaTT ACAACAAAGT TTTATTTAGT ATGTTTGCaG ATTTAGaACA	240
ACAAGTATAT AAATTTTATG GGAAAaMATA CCCGGAGCaA GGACCGTTAA TAAAATGGAT	300
AATAAAAAAC CTAAAATAAT AACAATAGCG TCAATCAAGG GCGGTGTTGG TAAAAGCACA	360
AGTGCCTTAT TTTATGGCAA TATTTTAGCT AAAGAAAGAC ATAAAGTATT GATAATTGAT	420
AGTGATCCAC AGGCCAGTAT TACTAGTTAC TTTTGTTTA AATTAAAAGA ACAAATGTG	480
AATGTCGAAA ATTACAATCT TTATGAAGTT TTTAAACAAA GAAAATATAT AGAAAATTGC	540
ATTTTACAG TATCTAATTG TTTAGATATA ATTCCCAGTT CCTTAGAATT ATCTGTTTTT	600
AATTCAGAAA GCATACCATT ACAAGACAAC CTTTtagAAA AAAGACTTTT GACTATTAAA	660
TCTAAATATG ATTATGTGAT AATCGATACA AATCCCAGCT TAGGACATCT TTTAAACAAT	720
GCTTTAGTAA TTACCAATTA TTTAATAATA CCAATTAATT CCGATTTATG GGCAGTTGAA	780
AGTATAGATC TAATATTAGA TGCAATAAAT AAAGTTTATA GAAATGATAT TACACCTTAT	840
TTTTTAGTGA CGGGGGCACT AGAGAGACAA AACATAGATA AGGAAATAAT ATTtAATTTG	900
GAGAATAGAT ATAAAGAAAA TCTAATAGGA GTTATTCCTA AAAGAGATGA TATCAAAAAA	960
GTGCTGTTTT ATAGAAAAGA ATTTTCTTCA AAAACAGACT ATTATCAAGA ATATAAAAAA	1020
TCTTTAGATA AAATGTTAAA AATAAAATAA CAAATAAAAT ATATCCAGTA ATGGACAAAT	1080
AAGGAGTTTG CATGAGCATT AAAAATAAAA TGATAATAAC CAAAAGAATA GATATAAAGG	1140
AAAATATGTC TAAAATGGAG TCATTAGAAG AAATTCATAA AGAAGAATAT TTGAGATTAA	1200
AAGACAAATT AAAAActCTA ACAACGGATG ATATTTATAA TAAAATAGAA ACAGCAAAAA	1260
TATTAAATGC GATTAATCAA AAAAACTGT ATATTTTAGA CGGATATAAA AATTTTATA	1320
GCTTTTTAGC TGATTTTAAA ATCGCTAAAT CTCAAGCATA TAAATATATA AAAATAGTAT	1380
CGGGCGTAGA AAAAGGTATT ATTGACTATA ATTTTATTGC TAATAATGGC ATTGAAAAAA	1440
CAATTAAACA ATTGGAAAGT AACAATGTTA TTAAAAATC TAGGCAAAAT CCAATAAAGC	1500
CTTTAAGGTT TCAACTTAAA AAGCAAGAAA GTTATGATTT TTATAAAAAA AATGGGAAGT	1560

1031

TTACTGGGTT TTTATTGGAA GAACTTCTTG AAAGTCAAAC AGATTTGATT AATAAGCTTT	1620
TAAAAAATA TAAACAATTA AAAGGATATT AAGAGGATTT TATGAGAAAT TTGGTGCACA	1680
GAACATATGA TATAGAAAGC ATAAAAATG AATTTTAAA CATAGGATTT AGTGAAGAGG	1740
CAATAGATTT TGTTTTTCTT CATAATGATA ATTACAATA TGAGGTTTTA AAAGAGAAAA	1800
TAATTGATGT AGAAAAGAAT TTGCAAAAAG ACATATCTAG TTTAGATACT AAGATAGATA	1860
ATGTAGAAAA GAATTTAAAT GTTAAGATAG ATAATGTAGA GAAGAATTTA AATATTAAAA	1920
TAGATAGTGT TAAAAATGAA CTTAATTCTA AAATAGATAG TTTAGATACT AAGATAGATA	1980
ATGTAGAAAA AACTTTGCAA AAAGATATAT CTAGCTTGAA TACTAAAATA GATAGTGTAG	2040
AAAAAACCTT ACAAAGGAT ATATTTAGCC TAGATAATAA AATAAATGTT TAAAAAACG	2100
AACTTACTGC AAGTAATAGA ACAATACAAG TAATTTAAT AATGGGAATA ACGCTkGCTC	2160
CAATTATTTA TTCTATATTC AATAAGCaTT TTTTAAATTA AGAaTGATTA rAaTTTATA	2220
AaGTAATAAG TTAGTATATA GCTTtAAAGT AGAACTTATT TGAATTTTTT AACAGAGAA	2280
TTTAAATAGG TTCTTTTATT TTAACAAATA CAAAATAATT TTAATTCTAA ATTGAACTGA	2340
ATTTAATTGT TTAGTGAGTT TATCTAAAAT AAATGAGCT AAGCCAGCGG CTTTCTTAAG	2400
CTCTTTAACA TGAGAATTTA ATAAAGCTTT TATTTATTAT AATAATTTCT GTAAAAAGCn	2460
TG	2462

(2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2447 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

AACCCcAAAA AAGGGCTCCC AATATTAAtw GAGAGATTTA TATTTTTCrA ATGTTGTGCT	60
AGCTTTTATy TCATTATTAT TGAATATAGG AGTAACTAAT GAGAAATAAA AACATATTTA	120
AATTATTTTT TGCAkCAATG TTATTTGTAA TGGCTTGTA AGCATATGTA GAAGAAAAGA	180
AAGAAATAGA TTCATTAATG GAGGATGTTT TAGCTCTTGT AAATGATTCT TCTGGAGGCA	240
AATTTAAAGA TTATAAGAC AAAATAAATG AATTAAAAGA AAATTTAAAA GATATAGGCA	300
ATGCrGAGCT TAAAGAAAA CTATTAAATT TGCAAAATTC CTTTCAGGAT AAATTAGCGG	360
CCAAATTAGC AGCGTTAAAA GCAGCTAAAA ATACCATTGA AAACATTACT GACAAGGATC	420
AGGATATTTT AAAAAGAAAA ATATGGTCAG AAGCAAAATT AGTTGGAGTA ACTGTACCAC	480

TTCTTGGAAG CAATACTTCT GGTAATGGGG ATAAAATGTC TAAAAACGCT GTAGAACAGA	540
TAGACAAAGT AATAAAGTTC CTCGAAGAnG GACTAATTA ATTAGCAAAT ATTCCTGTTG	600
AAAATGTTAA AATCTAGATA TTAAATCTGC GTCAATCTAA TATCTAGATT TTCTTTTGT	660
TGCAAAAGCC GATTTGATCA TAAATTAGAA TTTCTTGCAA GAAAAACCTT TTGTAATTT	720
ACATTTTTAA CTTCGAATAT TGATGATATA CTTTTTCCGC TATTGGTTTT GCTTTTTTAA	780
TGTACTCTAA ATATATCTTG ATGTTATGTT TTACCGCAGt ATAGAGTGTT CGTCTTTTAG	840
TGTTGATAAG TCTGGATAAG GATATTCTGG ATAATTGGGG TCATTAACCT TCACTTTTGT	900
TTTAGCTAAA AATGTTACAA GATACATAAC ATATTCTGAA AGTTGTGTTT CATATTTAGC	960
TAAAGATTTT AGCGTTGGAA TAATTGGCGG TTTTGGTTCT TCTGGTAGGT TAGCAATAGT	1020
GGTGCAACAT AACAACAAAA CAATTAGTAA ACAATGCAAT CTTTAAAGCA TTTTCACTCC	1080
TTTTAAGCAT TTTGATGTAT TCTTTCATAA TTTTGTGCG TTTGCTTTA AGTGAAGTGA	1140
TAATTTTTTT ATTTTTGTCA TAAGAGATAG CCTCTATTAT CTCAATATTG TATTTTAAAA	1200
TGTCTTTTAT TTCTTCAAAT ATTTTAGTTG AyTCAGCTGT TTCCATAGAT TTTAGTGTGC	1260
TTATATATGT TTTATAGAAA AAATCTATTA CTTTACTAAA AGTATTAATG TAATTATGAT	1320
CTATGTTTGT ATCAGTTTTA GCTATGTTAG TTAAGCTAGA TAGTAAATTA AGTCCCAATT	1380
CAATAGTGTT CTTTTGCATT ATTTGCTCTC TCTTTGTAGA TAGGTTTTCC GTCTTTATTG	1440
AATTTTAGAT CATTGGATAT TTTTAGATTT TTATCATTAG AATTAACCAA ATCAATAACC	1500
GTATTGATTT TTGCATTTAA AGGAGCGAGT GCCGCATTTA TTGCTGGGGT TAATGCACTC	1560
TCAAGTCTTT CCATATTTGC TGTATAGATT AATTTATAAT GAGAATACAG CTCATAAACC	1620
AAAAAGAATC CTTTATGTGC AATTTCATCA AATTCATCTT CAAATTTAGA AAATATATCA	1680
ATAAGGGTTG ATAAAGACGT AAGTCCAAGC TCAACATTAT CTTTGGATAA TTTCATAAGT	1740
TAATCTCTTT TTTTAATGTG ATTTTGGCCA TTACCATTAC CATTCCTAAA AATCTTGCCT	1800
ATTACAATAG TCAATATGTC TTTTAGTAAA GGCTTGAGAA GAATTAATAC TCCTAAAACC	1860
AACACTGTTA CAAAAATCAT TACGGCTATA AGTTTAATTT CGTTTAAATT GATAAGAAGT	1920
TCTGTTAATT TAATAGTATC CATTTTTTAA TCCTTTATTT TAATTTTTTA TTTGTATATA	1980
CATTATATAT CAAAATCGTA ATTTTGTCTA AAAAAGCTTA CAGTTTTTAA AGATCTGGGA	2040
CTGAATCTCC ATACATGTAG GCTCTTTTTT GGATATACCA TCCGTTATAA ATGGGAGTTC	2100
TGGTGAATAG TCCGCGAGGG CCCGTAATTT CATAAACCCA ATTGTATGTA ATTTCATCAG	2160
AATACATAAG TTTTAATGAT TTTTCTGCA TCCTATTATC ATTGATTTTT ACTTGAATCT	2220

1033

CAATATCAAG ATAAATGGGA TCATTATCGT AATTTTGTGTA AAAAAAAGA GTTACATCAT	2280
CATTGTCTTC CATATTAATA GATATCGCTT TATTCTCATA GTCAGAAGGA TAAAGTGTAG	2340
TACTTCTAGT TATGCTGCCA TAAGTAAAT TTGATGGTAC TCCAAGTATA TGTTTAGGAA	2400
CnGGTGT TTTT TTGAATAGTA TCTGATGAAG GCATTATCAA AAGATCA	2447

(2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2401 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

TATTATTATA TTTAGGGAGA GAATTTATAA AATAAGCAT AATTACTAGA ATACTGTTTT	60
TTTCTATGAA TGATTGTAAT GCGGATCTTA ATATTAATAA TTATAAAACC AAAACTAAAG	120
ATGGGTTTTA TGCTTTAATT TAATTAATTT TAAGGAAAAA CTAATTACCA TATTAATCCC	180
AAATATATAA TTATTGACAA AAGTTGTATC AAGGGATATT GCCTAATATA GCAGAAGTAT	240
ATTCTGTTAT TAAATATCTC CTAAGGAGGA TTTTATTTTT AAAATAATAG AAAATAGTGC	300
ACTTATTTTA ATAGATATAC AAAATGATTT TTTAGAATCA GGCACTTTGC CAGTATCTAA	360
CAGTAATGAA ATAATTTCTT TGATTAACCA ACTTCAAAAT TATTTCAAAA ACATTATGTC	420
CACCAAGGAT TGGCATTGTA AAAATCATGT AAGCTTTTCT AACAATAAAA ATGGGGGTAT	480
TTGGCCTGAG CACTGCGTCA AAAATACTTG GGGATCAGAA TTTCCTAATG ATCTAAATAC	540
GAAAAGAATA AAAAAAGTTT TTTTAAAGG AACCGATCAA TATTACGATA GTTACAGTGG	600
ATTTTATGAT GATTGCATTA AAAAAAACA AACGGGCCCT CAGCTTTATC TGAAAAACAA	660
TTCAATCAAT ACATTATTTA TAACGGGACT AGCATTGGAT TTTTGTGTAA AAGAAACAAT	720
ACTTGATGCA ATTAACCTGG GATTTCGAGT TTATCTAATA ACAGATGCTA CAAGAAGCAT	780
AACATCTACT CCTGAATTAA TAATTCAGGA ACTTAAAAAG CTTAATGTAT TAACCTGCTT	840
CTCCAAGGAC ATCTTCGACA GCCAAAGTAA GCTTAATATA TAAAAAATCA TTCAATAGTA	900
TTTAATTAGA AAACACTAT TTATAATTAA AACTATCATG GAATGATAGT TTTTtagact	960
ATATAAGAAA AGTTTATTCA CCAAAGAATG GCCTTTATAT TAAATTAAAG CCGCCTTTTC	1020
CTTGGTTTTT ACTTCTTAGT AAGAATAATT TTAAGATTCA TAGTTACATT TATATCTCTA	1080
TCATATAAAG CTCTGCAATT AACACAAGTC AACTTAATAT TACTTATCCT TTGTGTAATA	1140
CCACTTCGAA TGCCCTATTT AAATATAATA AAAGAATGAT AAAGAACTCA AATACTTCCC	1200

- 1034

CCATGCATCA TATAAAAATA TCCATCTCAA AATGTTAAAA ACAACGCCAC CGACATAATT	1260
CTCTAATACC CAATGTACAG TCTATAGATA CAATAAAATC TTTTAAGAAT TTAATTCCAA	1320
TAACACCTGT TTAAACCGGC TCACAATATA AAAAATTTTT ATTTTTTAGT GATAAACTTT	1380
ACTTATCTGA AAAATGCTT TATTATGTAA GAGTGTATAA AAAACCATCC GAAGTTGAGG	1440
AGGCAGAAGT GAAGGTTAAT AAATCCCTAC AAATACAAAG TAAATATCAA CACAAACTAA	1500
TTGCTTTAAT TGCGACACTT GAGTATATTA ATAAAAACAA AAAAAAATAC AACCAATCAG	1560
ACATCCTTTA TTGTTTTAAC AGTAACTTAA GCGCAACGG GCAAAAAGAA GTTCAATCA	1620
AAACGCTTAG AAACACTTC TATAAAGTAG AAAAGCTAAA TATTACTATT AACTACTATA	1680
GACATCTAGG TATTAATATG GGCAGTAAA TCTACTATGC TCTTAGGCAT TCTAAAAAAG	1740
ACTGCTATAA TCTACTAAAC CAACACTTTA GGAATAAAAA AACAGAAAGA TTTCAAAGAC	1800
GTGTTAATGT ATATATTAAA ATAAATTACG ATAAAAAGGA CAATGTAAAA AATGGGGAGT	1860
GTCTTAATAA TAAATATAAA AAAGAAGAAA GAGAAACCGA AAGAAAAAAA AGGATTAATA	1920
AGCTTAACT AAAAAAATAT GCAAAAAAAT GTAATTTTCA TAATGAAATT TCCTCTTTTA	1980
TTATTAATCT TAACTTAAAA AAAGAAACAA CAATCAAGCT TTTTAAATTT ATAATCAAAG	2040
AAAAATATTA TTTCAAAAAA GAAAACAAAT GTAATTTACA AAAAAACTG CAAAACAAAA	2100
AAAGAGATTT AATTTCAATA TTAAGAAAAA CCCAAAAAAT TTAATAAAAA GAAGGTTGCG	2160
ACAAAAAAA GATAAAACC CAAATACAAA ACACATATCA AAAATATAAA AACAAACCCC	2220
ATTTTCATATT AGAAAGCAAT AAATATAAGG ATTTGATCA AATTATAAAA AAGATAAAGG	2280
ACGATACTAA TAAAACCGAA CCCCAAAAAC ATAAAGACAA TATAGAAACC AATATATATA	2340
ACATACTTTT AGATCAATTA CATAGAAAAA CCAACACAAC AAATTTAAGG TCGGGGATCC	2400
G	2401

(2) INFORMATION FOR SEQ ID NO: 55:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2324 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

CAATATGACA TCCTGAGGAC CTTTATGGA GACTTGTAAG GCTTTTATT TCTAATGTTT	60
TAGCTTTTAT AAAAACACCA ACCATGACAC ATATTGAATT TTTAAATCTA TAAACATTAT	120

1035

TTCCTTAAAT TTCTAAAAGT TTTT TAGGCT CTGTATTTAA AAAATCACT TCACCAAGAA	180
TAACCTTTTC ATCATTTAAT AATAATGTTT TCTTGCTAAG AAAATTTATA AATCTATTTA	240
AAATGCTTAA TTAAGCTTAT TTGTTTTCAA ATAATTCTCA TATCCTTTTA TTA AAAACAA	300
AATGTATTCT TCTCCCTTTT TATTTTTTAG CACCTCAAAA TCATTAAGCA AAACCTCAAA	360
ATCTTCTTTG GTTAGCGAAT AAAGACTAGC TACAATAAAG TTATTTTCAT TTTCTTTTTC	420
TTTGAAAAAT TCATCTTTAG TGTCTAATTT TAGAATTTTA TTA ACTTTTT CT TTGCTAAA	480
TTTAAATGC TCTAAGTAAA GCAAATTAGA GAAATTTAAA GGATCATTTT TAGCTATTAA	540
CAAGGAAGTG TTTTTACTA AAGTTAAGTA TATCGGATTA GCTAAAATTT CTTCTTCTTC	600
GGGTTGAGGC ATAGGGCATT GATATAAGCA TGATTTTACA ATATCAGTGC TTAAAGCAAA	660
TCTTCTTATT AAATAGTCAA AAACAAATGA ATTAAAAATA GATATAATAA ATAATTTTTT	720
ATAAATAGAT ATTGGTGTTT TCTCATAATT TATATATATT GTAGAAACAC AATAACAATT	780
TCTAGGAGAT AAAGTACTAA TCATGGTCT TATATCTGTA TTTCTTGCAA TCCTTCTATA	840
TAATATTTTT TCTATTGAT ACTGATTGTC TTTAGTTGAT ACTTTTTGAA AGTCATCTTT	900
ATCTATCCAT AGTAATTTAG AGCTTCTTTT TGCATCTTTG TCTTCAAAAA ATCTTGAATT	960
AACTGATGA ATATTAGCTC CAGAATAAAG AAATATAAAA TTTTCATTAT TATATTCTTT	1020
ACATAGTGTT TTATACTTTG TTAAATTTAG CCCTACTCCA AAATTAATAT ATTCTTCACT	1080
AAGAGTACTA AATTGCTAA ACATTTTGTT AATTAAGATA AGCTCTTTAC TATCTTTAAA	1140
TTCAATAATT GATTCTTGAA TAGGAGACAG TTTTTTAATT TGCTCTATAT CTAATTTAAT	1200
TCCTTTATAA GGATCATCTT TATTATTTTC TAAGTTACTG GTTATTTCTT TTA AAATATT	1260
ATCATTACTC TGAATCATAA ATTTTGCTTT AAAATTCGAT GTAGGAGTTT TAGTATTGCT	1320
TATTTGAAAT ATTGCAAATT TAAAAAGTGT TGCCACATCT TTAAATCTTT TTGATTTTG	1380
AAATTGATAA ATATAGTTAA GCTTATAGTT AGTAAATATA TATTTTCTTA GTATCCTAGC	1440
ACTAGATTCA CTCAAAGAG CTGAAGGAAC TAAATAGGTT AAATTTCCGT TTTCTTTTAT	1500
TAATTTCAAA TTAAATGCTA CAAAATATCT AAAAAGATTT GGATCACCAC CACTAGCAAA	1560
ATTTTTAAAA TCGCTTTTAT AAAGATTGTT GATAGTACCC ATACTATTTT TTTCTTCATT	1620
GTATTCAATA TTCAAAGGAT GATTATCTCT GCCAAGTATT TCTTGCTTTA TTTTATTTTG	1680
TTCTTTTATG CTTAGCTTTC TATAACTGGG AATATGTTTT GAGAAAAACT CTGCTTCATT	1740
AACTTAGTT TTTTCCCATG GAGGATTTC AATTACAATA TCAAATCCTT CTTGAATATC	1800
TGGAACTCA ATTCCATAAT GGAAAAATTT ATAGTGGCTA CTTAATTTTC TAATTTTCTC	1860
CATTTTTTCA TTATCTTCAC TAGAAATTTT ATTGCCTAAA ATATTCTCAA TTAACTAAT	1920

1036

TACAAC TGCA ATATCACTAA ATTCTATATT TAAAGATT TG TCAAAAAGATA ATGAATAAAG	1980
TTTAATTAAA GAAAATATTA TTCTTAAATT ATCTATATAT TTACTTTCTT CATATTCTTT	2040
GTATATCTTT TTAGATCTTT CTATATCTTC CTTAGTGGTA TCGTTAATAC CTTTAATTTT	2100
TTGATAACCA TCTTCTAAAA TAGTTGTAAT TTCCTTAATT CTTTTTTTAA ATAAAGAAAA	2160
TCCACTTTCA AATTTCTTTT TTGCAATATC AAAAAATTCA TCTTTAGTAT ATCCCAAGAG	2220
AGCATTTTCT GTTTTTATAT GATGCTCAAT AAAGCTTAGT GCGTTCCAA AAATAAAGGT	2280
ATTAATCCAC AAACCTAGCA TAGTAATTTT AACCGAAATA GGAT	2324

(2) INFORMATION FOR SEQ ID NO: 56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2148 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

TnAAATCTAG GATACCCCGA cAAATATTAT TTTCCAGTAA TTATGAATAT TTGCTCGTAC	60
GACAATGTAA AGAAATTGCC TTATGACGAG CTTTGTAGAGG TCAATAGACT TGCTGAGATT	120
AAATTAGAAA AAGAATTGTA TGAATTAATT TTAAGCAAGT GAGGGCTTAG TGAGCGACAA	180
ATTCACCATT AAATTTAAAG GGATTCTTGA TCATGCTGCA ACAAAAAAGG CCATTGAACA	240
AGATATTTCT AAAATGGAAA AATATCTTAA ACCCAGAAAC TCCAGTTTGG GAAGCACTAA	300
AGATATTGTA AAAATAAATT TGTCGrACAA GAAAAAGAA CTTAGyArAC AATCTAAATT	360
TGAAAGCTTA AGAGAGCGTG TTGAGAAATA TAGACTTACA CAACTAAAA ArCTTATAAA	420
ACAGGGCATG GGrTTTGAGA AAGCTAGAAA AGAGGCTTTC AGAAGATCTT TAATGTCTGA	480
TAGAGACAAA AGGCrTCTTG AGTATAAAGA ACTTGCAAAA GAATCAAAAG CAAAAAGTAA	540
AATGTTAGCG GCCTCTCAAG GAAAAGGACT TGTTGCCAAA ATTGCAATAG GTAGTGCCCT	600
ArGGAATATC ATTAGCAACG CTATGAGTAA AGTTGGAGGA GGCCTTTTAG GTTTTGCTAA	660
AAAAGCrGTT GAAGAAGACA CCAAAACAAA AAGAACAAA CTTCTCAATA GTGCATTTTTT	720
TACAGATAAC GAACGAAATA TGATTATGGG AAATAAAGAC AAGAATACTA AGGGAATTCT	780
TGACGGAATG AArGGwTTTG AGCGmGACTT AGAAAAAGAA GArTTcTtAm ATCAAGCAAG	840
TGyCTTTAAG GGTACTyTAA GGGACyTAGA TATGTTAAAT GAACTAATT TGAAAAACGC	900
aGTAGAATTT GCAGCTATGC TTAAATCCAG TGGTGCTATG AGCAGCGAAG ATGCAGTAAA	960

1037

GGCTGTTAAT AGTGTTCCTTG GGGGTGATGG AAGTGAGCTT TTTGATCTAT TAAAGAAGTC	1020
aGGTGTGGGA GACAAATATA TAGAAGATGC CAAAAGGCGy TGGCAArGCG GGCwsArGT	1080
AGATCTAGAG TCyAGAATTA CCAAGATGAT GGAAATGTTT GAGGATTTTA AATCTTTTCGG	1140
CCTTACAAAA AAAGTCAATA ATGCTGAGAG TATTCAAAGT AATTGGCCT CAGCTGAGCA	1200
AACTCTTCAA AACTTAACCA CTAAGTCTT GGACCCATTA CTTGACCTCA TTAATAAGAT	1260
AACTAATTAC TTTAAAGACT TTGCGTTTGA AACACACATT ATTAATCCCA TAATTAATGG	1320
CATTAAAAGT ATTTTAAATC TTAATTATTT CTTTGCAAAA TTAATTCGA TGCTACCTGG	1380
ATGGATGGGC GGAGATGAGG GTGCGGCTCT AAAAAACTA CAAGAAGAAA TTCAAATCA	1440
AGACAATGCT AACAGCACAC CATAATTTTT ACAAAAGTA ATTACTTATG ACAAGTAACA	1500
AAAAAATTGC TAACAATGCA GCTAACAAAA TAGATATTAA TAATAAAAT ACTAACAATC	1560
ATGATATTGA AAAGAAAAAA ATCAAGGAAA AAATyAATGA TATTGAAAAG AAAGAAATCA	1620
GGGAGATTAC TCGAATAATA AGAGATGTAA TAACCCAAAT ATTTGCCCTT TTCGGAGCAG	1680
ATAATTTTTT AGTGTATTTT CCTAGAATGG ATCTAAAAGG TTTTGGATAT ATTCCTCAAT	1740
TGTTTTTTAT AAAACCAAAA AATGAACTCA TAACACGCAC TTATAATACT AGTTGTTCTA	1800
AAAGACCACT TATCAATTAT TATGATAGAA AAGCGGAATA TGTAAGCTAC AATCCGGTAA	1860
TGACTGGTGA ACATATCTCA TTAAACGGkG GAATACTAAC ATCCTTATAT AAGGATATGm	1920
TTCTTTTACT yAAAATGACT GTTTTGGCA ATACTATGCT ACGTTTGTGAC GCGCATCTTG	1980
TAAAAGAACA ACTAGCCAAT AGAATACAAG CACAAGTCCC TTTTAGTATm TATAGTCCAA	2040
CTTTTGGACT TAAAGAATTA GCTGTAATTA CAAGTCTTTC GTTTAAAGAT ACTCCTTTCA	2100
TTGACGAGTT GAAGGTAGT CTGTCAATAG AAATAGTAAA AACATTTCG	2148

(2) INFORMATION FOR SEQ ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2123 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

ACATATTATT TTGTTTATTT TTAATAATGC TAAACGGCTG TAATTCTAAT GATAATGACA	60
CTTTAAAAAA CAATGCCCAA CAAACAAAAA GCCGGAGAAA ACGTGATTTA ACCCAAAAAG	120
AAGTAACACA AGAAAAACCT AAATCTAAAG AAGAACTACT TAGAGAAAAG CTAAATGATG	180
ATCAAAAAAC ACAACTTGAC TGGTTAAAAA CCGCTTTAAC TGATGCTGGA GAATTTGATA	240

AATTTTTAGA AAACAATGAA GATAAAATAA AATCTGCACT TGATCATATA AAAAGTGAAC	300
TTGATAAATG CAATGGAAAA GAAAATGGGG ATGTTTCAGAA AAATACATTT AAACAAGTAG	360
TTCAGGGAGC TCTTAAAGGG GGAATAGATG GCTTTGGTGC AAGCAATGCA ACTACTACAT	420
GCAACGGTTC CTAATAGCTA TTAGCCCCCT ATTTGGGGGC TTTAATCTTG CTATGCTGCA	480
AATATCTCAT CAAACCGTTC GTATTCTTTT AAGATACTAA AGAATATTAA TGGACTAGGG	540
CCATAAATAG GCCTCTTAAG CCCCATAAAC CTTTCAAAAT CTTGTAAATC CTTTAATCTA	600
TTATTTTTCT TGAAATAGTT TTTTATAATC TCGGCCCAAT AGTTTATGCT TTTAAATCA	660
CTATTTTTCT CAAAATACGA GATTAAATCA GATTCAATTT TCTTGATATC ATCAAAATTA	720
TTGGGGTCTA TATTCTGAAT AAAGCTTATT TTTTGAATAA TTGAGTTTAT ATTATCTTTT	780
GTTGTAGGGC TATTTACCCA GTCTTTTATA TTAGACAAAG CTTCTTTAAA AACACCGTAA	840
TAATAAAGCC TATCTTTTTT TTGTTCTTGC TTAATATCTC TTTTCTGGTT TTGAATAGTG	900
TTATTTTTTT GAATTTGATT AATCTCTTGT TTTTGTCTC TTTTTGTTC TTGCTTTTGA	960
TTAACACTAA CTTGCTTGCT AGGCATAGAA TTTTCGTTTT CGTGGTTATT GTAAATAGGA	1020
GCTGCATCAG TATCTATTTT ACTTTCTATA CCAAGAGCTG CAACTAAAGC ATACCTTTTG	1080
ACATAAGTAA TGCCTGAACC AAACATCTGA TACACTGTAT TTGTAACTTT AGACCCATTT	1140
TCATTGTTCC ATTGTAAATT TTCTGTAGGA ATTGCGGTAT CAAAAGAAAA TTCATATCCA	1200
GTACTGTAC TGTAGAATGT AGTCCTAATA TAATCAACTA TGCCATATTG ACCCTCTATA	1260
GAAATTGGAT ATTGCTCAAT ATCAAGCTCC AAATTGTGCT TTTTAATAAC ATTTTTAATT	1320
TCTCTAACTA TTTCATTGAA ATTTTGATAT TTATATCCAT ATCCTTTAAG ACTTTTGTC	1380
ATCCCTGGTA AATTCATTTT TAGGGTTTTT ATATCTTTT GGAAGCTTAT TTTTGCTTGA	1440
ATATTATTTT GTATTTCTTG ATTATTGTTT GAAAGATTTT CCATCTTTTT ACTCCTATGG	1500
TTATTTATAA AAATAAGTAT ATAGCAAAAA CTATTTTTCG CAACTTTTTT ACAAAAAATT	1560
TTACAAAAAA ATAGGGCTTA GCTAAATCTT CTATTATCTA CTAAAGAAAT TAGTTAAGCC	1620
CGTGCTAAAA ATTTTTTTGC AAATTACCAT AGGTAGTCAA AACTGAAAAA TGTTTAAATA	1680
ACTACGCTGT TTGTAGTGTA GCCCAATTTT AAATTAAAAT CAATTTATAT TTCACTGAA	1740
TTAAAAATTT CTATATTAAT TTAACAAAAT TAATAATTAA AATTTAATAT TTTTTTAGAA	1800
AAGTATTTAC TTTTAAATCA AAATTTTGCA TTATAATAAT TAATTATTAA TTACCATAGG	1860
AGAAAAACA TGAAAGGTTT TTCAAATACC ACAAAAAATC CCACTTGCCA CAACAAACAC	1920
CAACACAAGT TAATATATCT AGCTTCAACA CTAGATTTtC TAAACAAAAA AGaTAAGAAA	1980

1039

TACACACAAC AAAACATACT CTATTACTAT AATGrrAATC TAAAAAGAAA TGGkCTAGCT 2040
CCCACTACTC TAAGrACmAT GgCAAAATTA TCTTTACAAA TTAGAAAAAG TATTAAGT 2100
CACAACATAAT TACTAACCCn AAA 2123

(2) INFORMATION FOR SEQ ID NO: 58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2093 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

AAAAAGTGC GCCGTGCGGC GGTGnAACGA CTCAATAGTT ACTAATAATC CATTTCTAAA 60
CTTAGAAATG CAAATTAATA ATATTTTCTA AAGTATTTTT TGTTCCTCA TAATATGTTT 120
CTTTTACAGA AGGTTCTAAA AGTTCATTTA TAAGAACTTT TACACTATTG TAGTAATGAA 180
TTTTTCCCTT TATGTAAAAA GAATATTCCT TATAAAGCAG TTCTTCTACA TCTTTAAATG 240
TATTTCTATT TTTTAGAAAC TGATTTTCTA TAATCGAAAT ATTAAAGCTT TTATTTCTAA 300
AATCTTTAAT ATCATTAAATG GTTTCATTA AAATACTTAA ACTTCTACA GAGAATCTTT 360
CTACTTGAAC TGAATTATT ATATAATCTG TAACATTCAA AGAATTTTTT AAAATAAAAC 420
CCAAGTTGGG TGGGGTGTCA AGTAAGATAT AATCAAAATT ATAATTTGTA ATATTTCTAT 480
TCAAAATATT TTCTAAAAGA AGATCTTTAT AATTAAAAT TTCTGAATTA AAATTTCTA 540
AAATAGGATG AGATGGAATT ATAGAAATAA AATCATTAAT TTTATTAATA CACTGTCCAA 600
AATAAACATC TTTTTTTAAT AAGCTGTAAG AATTGCATTT ATCAATGTTG AAAATATATT 660
TACTAAAATA AGAACTTAAA GAATCTGTG GATCTAAGTC AATCAATAGA ACTTTTTTGC 720
TTAAATCTTT TAATATATAA GAAAAAGTA TTGTAAATGT GGTTTACCT ACACCTCCTT 780
TAGGGCTTGC AATTGTTATA ATGTTTGATT CTTTCTATC CATTTGTTA TTATTCCTTC 840
CTCTTTTATT TTTTATTGT AAAATTCGTA AACTGTTTTT TCCATGTTTT TTATATTTTC 900
TAATGTAAAT TTATAGTATT TTGTTGTTT TTTTCTTTT CTTAGTAATG TCCATAGGGA 960
CTGAACGTAA CACTTAATAG ATCCTTTTTT AAATACATAT TCTATGTAAT ATGCCTTTTT 1020
TACTACATAT TTTATATTAT TATTGCCTAT GATAAAAAAA GGTTTCTCGA GATTATCCCA 1080
ACCGTATTTT ATGCCTAAAA ATTTTTCATC TTCTTTTATT GGAAATAGAT TGAAAAAATT 1140
CCATCCTCCA GTATCATTAAT ATTTTGGAA GGTTATCCTA AGACCTTTC TAGTAATTTT 1200
AAATTTGATT AAATGCTTAA ATATTATTGA ATAATATGTT TTTTATTCT CTTTTCTTC 1260

1040

TATTTTATAA AAGAAGATTC TTTTTTTTGT TTCTTTTTTA AGATTTCTAA ATCTTTCTGT	1320
AAAGTTGTTC AAATTTTTTT CCTTTTATAA TTAGCTAGTA AATCAAATAG AAATGTTTTA	1380
TTTTGATTTA TTTTCCATTT ATTGATGTAA GTGTCTTTAA ATTCTCCTAC AATTTTGAAG	1440
AAATCTGTTT CGTAGTGAGC ATTTTGTCTC ATGAAGTGAA TTTTATTTTT ATATTTTTTT	1500
AGCTTTTTTA AGTAAACTC TTTTATATCT TTGTTTGAT AGTCGTATTT TAAATGCTTG	1560
TTGAAATCTT TGTAATTTAT AAATAACAAT GGGGTTATTA TCAAGGCTGG TGGTGGGCA	1620
CCAACCGCAA TTAATGCATA TGCCCTCTCT GATTCATTTA CAATCAATTT TGCACCCGAA	1680
GATGAACATC AAGATCAAGC TAAACATCCC AAACAAGAGT ATTCTATTAA TTTGATAAAA	1740
GTTGCAATTT TTGGCAATAG AGGCCTTGAG AAAACAGTAA CACCTGAAGC TGGTGGTTAA	1800
GCCTTGGGCA ATAAAAGGAG TTAAACAAAT GGCAGACACA ACGCAATTAT TAAAAGATTA	1860
TCAAGATAAA CGAgTAAACT TGAAAAGTTT ATGAAAAATC CCCAGTATGA CGCTGGTTTG	1920
CTTAGCAATT CtGTAGAGTT TAGAGATAAA AACATACAAT TTTTGCCTC TGGAGGCACT	1980
AGAACCAGCA AATTtGACAA aTTAGAAAAT CATCCATTTT CtGGGTATCC ATACmAGCGg	2040
GGaTAAAAAG AGTTATTCAA GAGGAAAAAG CTGATCAAAT TCACTATGGA ACC	2093

(2) INFORMATION FOR SEQ ID NO: 59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2019 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

GTCTTAGTCA TATTTTCATT AAGTCTTTTT GCTTATTCTT AGCAACCTCT AGCAAACCTTT	60
TAGTACTACT CATTGAAGCT TTAGCATCAG CCATAAATTG GTGGTAGCCA GCATAGTAGT	120
AGCTCTCATG CCTTGAAGCA TTGCTATTAC TTAATGCCTC TTCTAAAGCC CGATCTGCTT	180
TTCTTTGTGC ATACTCAAAA TCGTTCTTAG CTCTTTTAA AGCAGCAATA GCATCATTGC	240
AATGAGTATC AGCAGAAGCA TGATTACTCT TAACCTTAGC AATAGCTTCT TCTAGGCTAG	300
GCAATAAGGC TAAGTTAGCT TTAGTAGATC CCACACCTCT TCTAGTCTGC TCTAAATAAG	360
ATTAGCTGT ACTAAGTAAG CTTTTTATCT TATCAAGGCT TGCTTTTACT TTTGCTAAAT	420
CTTCATTTAT TCTATTGTAC TCTTCTTAG AAGATTCAAT TTCCGTCATA ATGTTTCTAG	480
CTTCACTAGC TTCATTATCT TGGATATTAA CTTGTAGAGT ATGGTTGCTG CTACTATTAT	540

1041

CATTTTGCAT ATCGGGTTGC ATGTCTGCCA TCAAAGGTTT TTTGCCTGTA TCTTGGTCCA	600
TATAAGTATT ATCTACACTT CTAGGCTTAC GACCACTTCT CTTGCTGTCA TCGTTACTCT	660
TTAGAGTATT AAAAGACCCA TTATTGCTTT TTAGTTTGTC TATAACCTGA TCGGCGTTGT	720
ATGTAATCTT CTTGTATAAT TTACAAGAGA TAACACTGGA AAATAAAATA GTTAGAATAA	780
ATAATTTATT AATTAAATTC ACCTTATTAC TTCTCTTTAG AATCTGATAT TCTTATATTA	840
AAAAATATAT TGCATTTATA ATTTATAAAA TGATTAATAA TGCATAAGCC AAACATATAA	900
TCTGAAAGAA TTAAAGTAGT GTTTGTAAAG GCAAGATAGG AGTGAGATAG TTAATTTAGG	960
TAAGCTGATA TAAGTTTTTC TAGTAAATAG AGTTTCATAT ATGATTAGAG ATATTAATAA	1020
AACTAAAGCC TAACTGGAA GTTTTAAAGC TTAAATATAT TTTCTATTTT TTTTCTGCAA	1080
GAATTTCCAT ATTGAAGAAA ACTAATAGCA TTTTCCATAT ATTTAATGCA TTCAGTAGCA	1140
AGATCTATAG CTCTTTTTGC TAAATCTTGT ATATTGCGTT TGTAAAAATT ACTGCCTAAC	1200
CAGTATGAAT TGCCATTTTC ATTGTTTAAT CTTTATAAAA TAGAATCTGC TAGTTTATCT	1260
CGAGCCACAT CTAGCATATC TTTAGCAGAC CCCCAAGAAT TAGTTGCTTG CTCCATAAAA	1320
GAACGCATTT CTTCTAATTT TACCCATAGT GTGGCTTTGA CAGACTTAT TTTTCTATTT	1380
AAAGGAGATG TGCTTAGATT AGAAAATAAT AAATCTGACA TTTTTTGATG AAATCTTTA	1440
AACTCAAGGA GTGTATTGTT TAAGTTATTT TCAGAATTAG CACGATTAAT AAACGTCTCT	1500
GCATTTTTTAA TTTCTGAAAG AGATGTTTGC TCATACTCTT CTTGTGCAAA TTCATCTAAT	1560
TTAGCTTTTAA TTTCTTCTTC TGAAGGAATA GCAGGAGTTT TACTTGTGT AGTAAGGCTA	1620
TTTTTAAAT TACTTTGTTC AATTGGATCA TGTGTGGAG TAGCTGATTT ATTTTCTTCC	1680
ATCTTTACAT TATTTTGAGC ATGCGAGTCA TTTTGCATTA TTGCTGGACT TGAATTTGGT	1740
AGGGATTCTT TATTATTTGC ACCAGGATCA TCTGACATAT GTTGATTAGA ACCTACTTGT	1800
AAGATTGGAT CATAAGTTTT TTTATTTGAT GATGTAACGT CTTTAGGAGA TTCAATTTCC	1860
TTACTATTTT TATCTACTGA AGTATTAGTA GTATTTTAT TTTCTTGATG ATCTTTTAAT	1920
GCTAATGCAA ACTGTTCTAT AGATTTTTTA GATAGAAAAC CAGAACAAC TTCAAATAA	1980
AAAAGAGAAC TAAATACTAA ATTAGGTATA ATAAAAAT	2019

(2) INFORMATION FOR SEQ ID NO: 60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1907 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

AGAAAAACAA AATCTATTGC TTCTTCACTA AATCCTATCT TTAAAAATTC ATTTTTTATA	60
CTTCTATAT TGTATGTTCT GTAAGTCAAA CTATTCATAA AATTTCATA TTATCCTTTT	120
AATCTTTTAT ATTCTTTCAT AAGTTTTTTA ATTATTTCTT TTCCATCACT AAATAATTTA	180
TCTAACATAA ATCCTGTAAA TTTAGCATT ATTTTATAAA AATCATAGCT TTCTTGCTT	240
TTAAGCTGAA ATCTTAAGGG CTTTATCGGG TTTTGTTTTG ATTTTTTTAT TGTTTTGCTC	300
TCTTTATTTT TTAATACAAT TAACGTTTCC AGTATACCAT TTTTATTATAG AAATCTTCT	360
TGTATAATCC CATCTTCTAT TGCATTAGCA ATTTTAAAGT AATTATAGAC CTGTGCTCTT	420
GCAAGTCTAT AATCTTTAGA AAAAGCTTCA AAACTTTAT AACCATCAAA CCTATAATAA	480
TGATTGTCTT TAATTTCTTT TAAAATTTTT AAAGTTTCTA ACTTACAATA GATTTCTTTT	540
TTAGAATTAA TTTTAACTT TTCTTTTAAA GAATTATAAT GATTTAATAC ACTATCAGTA	600
ATAATATAAT TTTCATTATC ACTTAAATCT CTTTTATTAA CCTTAATATC CAATTTAAAC	660
TCCTTTTACA TTAAACTGTC TAATTATTAG ACTTTATATT TTTTTTAAAA AAATTTCTAA	720
AATATTTTCA TATCTTTTTA TATAATCTTT ATTTAAATCA AAATTATTAT TTTCTGCAT	780
TCGTCTATTT AAGTCTTCTC TTTCAGATAT TGTTCTTAAA AATCTATCTT TTGTTTTTAA	840
TATTTCAAAT AATGTTTTAT GwGTTCTAKT TwwwtTaAAT CTTGTTATTA TCAAAAATAT	900
AGGTAAAAAT AAATTTAATT TTCTTACAAA GAAATTAAAT AAATCTAAAC TTTCCACTGC	960
CCACTTTTCA GCCGTCATTG GAATTATTAC ATAGTCACTA CATAAAAGAG CATTTTTTAA	1020
CGTAACATCT AAACGGGAT TTGTATCGAT TACTATATAG TCATATTTAT AATACAAAGT	1080
TCCCAGGCTG GTTTTTAACA AAAAATCTTT ATGTTTCGATT TTATCTTCAC TAAAATTATG	1140
TAGCGTAAGA TAGCTAGGTA TAAGATCAAG ATTATTATCT ACATTTATAA TGGTACTATC	1200
GATATCTACA TTTTCTTTCA AAATCTCATA AATATTAAAT TTGGTAAAAT TAATACCTAG	1260
TTTTTCTATT TTTTCGTAAA AATAACTAGT AATAGATGCT TGAGTATCCA TATCAATTAA	1320
AAGAACTTTA TTATTTTTTG ATAATAAAGT AGCCAAAATT ATCGCACTTG TGCTTTTACC	1380
TACACCGCCC TTAATTGACG CTATTGTTAT TATTTTAGGT TTTTATTAT CCATTTTATT	1440
AGTGGTCCTT GTTCCGGGTA TTTCTTCCCA TAAAATTTAT ATACTTGTTG TTCTAAATCT	1500
GTAAACATAC TAAATAACAC TTTGTTGTAG TGATTGTTTG TTCTTTTTTT ATCTAATAAA	1560
CGATATAATC CCTTGAAATA GCAAAAAACA CTTCTGCTT TAAATCTAAA TTCCATATAA	1620
TATGCCCTTG CTAATGCATA TGCTTTTCTA GCCCCGTTTA TTTGATACTT TATTAACGGC	1680

1043

TTTTTAATCG GCTTTCTATA GCCATAAAAA ATACCAATAA ATTTATCTCC TTCTTTAATT	1740
GGGTACAAAT GAGTTTCTTC AACAAATTCTT TCTCCATTAA ATAAGGCCCT CAATGATAAT	1800
CTAAATTCGT GTTTTTTCTC ATAAACTCCA AATTTATAAA TATCCATCAT TATTTTGTGA	1860
TGGTACATTG CTTTACCATT TTCTTTTCA ATTAAAATAA AGCGTTC	1907

(2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1907 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

GAAAAGATAT ACGTAGAAAT AGAAAGACGT ATTGAAAACC ACAATTTTTT GTTTTACAAA	60
GATGAATCTT TAGTACAACT ACAAGACGCA CTTTCTAGTG CAACAACCTC TTTAAGTGCA	120
CTTACTCAAG GCAATAATGA TAGAGGAAGT GGCATTTTAT CTTCTTTTTT AAGAAAACAA	180
AATTCAAACA ATCATAGTAA AGATATTTCT AATTACGTA GTCTTAATGA CTCATTGGCA	240
CAGGAACCTG CTAGGTTAAA AAGCAATCTA AATAATGAGG GAATGTTTTA TACAGCTACT	300
CCGAGTGCTA GTTTAGAGGT TATTAAATAC GATCTTAGCT ATTTAAAGGA GGCTTTAGCA	360
TTAATTAAGG CAAAAATTGG TGCAGATACT AAAGAACCCC TAACTAGAAG TTTTAATGAG	420
CAGGCTAAAG GACTAGGGAA TGATGGTAAA GGAGATAGGA GCAATTATTA CGATTTTCTA	480
AAAGGTGTAC AAGAACAAGT TGAGAACTCT TGTAATTTAA AACTTACAAA GTATTTTGGA	540
CTTGATATGA AGTTTAATTC GCTGATTATG TTAAGTGAAG AACAAAAAGT GGAAAGAGAT	600
ATAAAGCTAA TTGAGCTTaC AGTAAATATA ACCAGCTTAT ACAAAGTAGC TCCTTgATAA	660
TGAGGAGTTA GCGATTtAAA AGAGAAATaT TCTCATTTtG AGAAAAGGAG TTAAAAAGTG	720
ACTGAGAAAAG AAGAAAAAGA AGACCTGCAG GCACmAGATA AAGArGAGCa GCAAAaTTAaG	780
GctGATACTA AAGTTATAAG TGCGCAGGAA TTTGAAGAGT ACATGCGTTT TAAAGAGCAG	840
GCAAATAGTA AATCTAAAGA GACAAGTCGA GATTTAAGTA TAAATGAACG AATAACAAAA	900
GAACCTGCAG AAGTTGAAGA GCGGGAGCGT ATTGAAAAGC AATTGTTACT AGAGGCTGAG	960
CGAATTAATG AAATTGATAC ACTTGCAAAA GCACATCTTA GCAATCATTT TAACAAAGAG	1020
GTGCTACTTG CAAAAGGATA TACATTAAAA GACATTATGC AAGCACAACG TAGAGAACTT	1080
GTACGCAAGT TCGTTCCAAT TGAGCAAATT AAAGCTATTG CCAAAGTATC AGACATAAGT	1140
CATATmGATG GrGAGATATT AGAGCAACTT GTTCTTTAG CAAAAGTGAA TATTAAATTA	1200

1044

AGAAAAAATG CGAGTAGCAA TTCTTCTTCT GTTGACTCTA TTAAGGGGAA TATTGCTATT	1260
AAATCAGAAG AAAGAGCAAG TTTGCTTAAT TCTAATTTTG TACCTATTAA TTTCACAGAA	1320
TTTGTACAAG CGATAAGTAA TACTTACAAG CAAAGACGAA TTCAATTTTA TGAAAATCTA	1380
AAAAGACATA AAAGAACAAG TATTGCTTAA AGGAGTTTTT AATGAGCGAT GGTATTACAA	1440
AAATAAAGA AGAGTTTGAT AAAAAAGTTG CAGAAATTAA AGCATTAAATG AAAAATCCTC	1500
AGCAAGATrC TGGTTTGCTT AGTAATTCTr TAGATTTTAG AGATAAAAAT CTAATTTACT	1560
CCAATTCGGA TGGAGTTTTT ACTAGTAGTA AAGACAAAAT AGAAAATTAT CCTGCTAAAG	1620
GGTATCCATA CAAGCGTGGA GTCAAGCTTA GTTTTAGTGC AGATGGTACA ACAGAACTAG	1680
AAGTTGAGGC TGGTGGTGGG GATGACTTGT ACGGAATATG CACTGATATA nATGAGTTTA	1740
CTGGCATGGC AACTGTAGTT CCAATTACAA ATAACCTCAC AGGGTATTTA ACATTTAAAnA	1800
AAAAATGGACA AAATGGTGTG AATCCGGGTG ATAAGCTGCA TTTTAATGCA CnAGGAGAGC	1860
TTGAAAAGAA TGGGGGAAAT GATAAATCTG TTAATGCTAT AGCnCTT	1907

(2) INFORMATION FOR SEQ ID NO: 62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1902 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

CGGGCATTTA AGCTCTTTTC TACATTGTCT ATTTTGATAT TCAAACCATC TATTTTAA	60
TTTAAATTCT TTTCCACATT GTCTATTTTG GCATCTAAAT TAGATATGTC TTTTGC	120
TTCTTCTCTA TATCAATTAT TTTCTCTTTT AAAAATTCAA AGTTGTAATT ATCATTATGC	180
AGAAAAACAA AATCTATTGC TTCCTtGCTA AACCTTATAT TTAAAAATTC GTTTTTTATA	240
CTTCTATGT TATATGTTTT GTATGCTAAA TTGTTCATAG ATTATCCTTT TAATTGTTTA	300
TACATTTTAA AAAGTTTACT AATCAAATCT TTTTGATTTT CAAAAATCTC TTGCATCATA	360
AAACTTGTA AATTAGCATT GCTTTTGTA AAATCATAAC TTTCTTGAGT TTTAAGTTGA	420
AATCTCAATG GTTTTATTGA GTTTTGTTTA GATTTTTC AACTGGACT TTCTTTATCT	480
TTCAATACAC TTAATATTAA TCTAAATCCA TTATCTAATA CATATTGTTT CTCAATAACT	540
CCTGCTTCTA TTGCATTGGC AATTTTAA TAGTTATACG CTTGAGTTTT TGCAACATCA	600
TAATCCTTTA TAAAGCATC GAACTTTTG TATCCATCAA GTTTATAGTA TTCATTATCT	660

1045

TTAATTTCTT TTAAGATTTT CATACATTCT ACTCTATTAG AAACCTCTTC TCTAAGGTTT	720
ACATACAATT TCTTTTTCAT AGTATTATAA CGATCTGTTT CAACACCATT TTTACTAACA	780
TTAGAAGAAT CTACAAGTAA TGCATTCCCC TCAGAATCAA TATCCCTTTT ATTGATTATT	840
AATTTTGTAT TATTTTTCAT AACAAGCCTC CTTAATTATA AGTTCAACGC GTCGAACCTA	900
TAATTATAAT TATTTTAATT TTGCATAAAA ATTCATTAAT GAATTTTAT ACTCTTTTAT	960
ATAATCCATT TGAAATCAA AAGAAGAATT ACTAGCAATT CTTCTATTTA AATCTTCTCT	1020
TTCTGATATC ATTCCTAAAA AATTTTCTTT GGAGTTCAGC ATTTCCAACA ATTGCTTATG	1080
TGTATTATTT TTTTAAATC TCGTTATTAT AAAATAAGTA GGCAATTCTA CACCTATTTT	1140
TTCCATAAAA AATTTCAAAA GGTCAAACT TTCAATTGTC CATTTTCTG CTGTCAAGGG	1200
GACAATTACA TTGTTACAAC AAATAAAGC ATTAGTTAAA GTAAATCCA AACTTGGGGG	1260
AGTATCAATT ATAATAAAT TATATCCAAC ATCTATATGT TTAAGCTCTT TTTTAATCT	1320
AAATTCATCA AAAGTGTGCT TATAACCAA AGCATTTATA CTATGTAAAG TCAAATAACT	1380
AGGTATTAAA TCTAAATTAT TCGCTACATT AACGATTGAT CGATTAATAT CTAATTTTC	1440
TATTAAACT TCATATATAT TATTTTCT TAAATCTATA CTGGATTTT GTATATCATC	1500
ATAATAATA CTAGTGGTGG ATGCTTGAGT ATCTATATCT ATTAATAATA CCTTATATTT	1560
TTGAGCCAAT AAGGTTGCAA ATATAATTGC ACTTGTGCTT TTACCAACAC CGCCCTTGAT	1620
TGACGCTATT GTTATTATTT TAGGTTTTTT ATTATCCATT TTATTAACGG TCCTGTTC	1680
GGGTATTTT TCCCATAAAA TTTATACACT TGTGTCTTA AATCCGTAAA CATACTAAAT	1740
AAAACCTTGT TGTAATGATT ATTTGTCTT TTTTATCTA ATAATCGATA TAATCCCTTG	1800
AAATAGCAAA AGACACTTCC GGCTTTAAAT CTAAATCCA TATAATATGC CCTTGCTAAT	1860
GCATATGCTT TTCTAGCCCC GATATTGAA CTTATTAATG GC	1902

(2) INFORMATION FOR SEQ ID NO: 63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1761 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

AACnGGCCCC GGAAGTTAAA GCCTGTGGG nCCCATGCTC TAGTGGATGA CCGTTCTTTT	60
AGAGCCTAAA AAGCTATCAT GGGATGAAAC AAGAAGCTAT TTCTATAATC TTTGATTTAG	120
AAATAGCAGT TCACATAAAG ACGCTTGATA TTAATTTAAA TTTAATCTAT AATATAAATG	180

GCCTAGTATG AATGTAAAT AATTTACGTT TGAGCTGCCT TATGGAATCA TTTACAATTG	240
AAGGGCTTAA AGAAGTTCTT TAGCAAGAGA GTTTCCTTAA GCCCTAATAA TATTTGAACA	300
ATCTTTTTCT AGGTAAATTG ATCTTCAATA GGATTTTTTA AACGACAGTT GGAATCCGTT	360
TATTCCAATG TCAAAATTGG GTTCAACCCC CGCAAGTGCA ATGCCGAGCC TTTTTTTAAG	420
GTCTGCGTTG TATCTATTAG CAAATTTAAA TGGAATAATA ATTCCAGTTA TGTAGGATGC	480
TACAATTGTG AGCCCTCCTA TTCCTGATAA TACTCCTCCG GTTATTACTG TTGCTGTGCT	540
TTCTGTAACG CCTCCAATAC CTCCTACGAT CATGTGTCCA GCCATTATAA GTATTCCTTC	600
CAAGCACTTG AGAGCCAAGT AGTGCACCAC CACCAATATA ATCTCCTTGA ACAAAGATC	660
CTATCCCTAA AGACAAAAAG ATATTCAAAA GTAATGGTGC TAGTATGGTT GCTTTTTCGC	720
TTTCATATTT CATTACAGTC GCGATATCTC CACTCCAACA CCTTTTTCAA GTTTATCTTG	780
TGCAAAGATT TGCAATTGTTA AACTAAAAAT TAATATTAAT GTGAAAATTT TTTTCATATT	840
AATATTACCT CCTAATAATT AAGTTTGTAT AAACAAATGT TAGCACAATT TTTAGATTTT	900
ATTTATGGAG TTGAATCTTT TCTTAAAGAT ATTGTTTGAA TTTCTTTGCT GTTCTAAGCA	960
GATTTTAATG TAAAGTTTTC ATTAACTCT TTTAAATTTG AAATTATGCT ATCTATTTTT	1020
TTTGTATGCC AATTGTATAA TGAATTGTTT TGATGACTTT TTCGAGATGT TCAACTTCTT	1080
TTGAGGGCAT TTCTCTGCCT TTTCTATAAG TTAAGTAACT TTTTAGAGTT TGCCAACTCC	1140
CAATAGTATA GTTATACACC TCTTTGAAA CATTAATAAA TCTAGAAGTT TGGTTATAGT	1200
AAAGTTCATT TGTTTCTTCT TTATAAAAAA CTTTTTCTAT GATTGAGTTT TGTTTTAGGG	1260
TTTCATCTAA AAATGAAAAA CATTTTCCAA TGTTGATATT TATTGTTGGA ACAACTTTTA	1320
CTAAATGAGA ATTAATGAGA TCTGTTCCAA GTTTGCCAAG TGTACAAAT ATGTCAGAAT	1380
TATCTACGAA AATAATTTTA GGAAAGTCTA TTTGTAGGTG TTCGTAGAAT CTATCTCGAT	1440
AGATATTTGA ATAAAGAATT GCGTAAATAT AGCCAAGTAT TTCTTCTGCA GTAAATTTTT	1500
TATTGTATTT AACATCAAGA AAATGTCTAA ATTTATTTTT AAAGTTTCT TTTTAACTC	1560
TCTCAGGTGT TTCGCTATCT TCTTGATAT AAATGGGAA AACATATCCT AGTGAATAA	1620
TGCTTAATTC TGATATTTTA GAAGTAACGA AAGCATGAGA AAAACGATCA GTTTTGATA	1680
GTCTTGTTGT TATTAGTGCT ATATTATTTT GAATTTCTAA GATATGTTTC ATTATTTTAT	1740
AACCAGGCCT AATTATGACC C	1761

(2) INFORMATION FOR SEQ ID NO: 64:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1717 base pairs

1047

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

GCATCATTTTC TGAGACTGTT GTTTTTGTAG ATAAAAATTT TCCCAAATAA TATTTAAGCA	60
ATACAAGATT TAGTAAAGCG TATATTTTTA TTTTPTGATT TAATTTTCAGT TATTTTTAGG	120
ATTTTTATTA TTTTAATCAT ATTTTCTTTA TCAATATTTA ATGTTAATAA AATTGAAATA	180
ATTTCTTTAC ATAAAAAGTC ACATTTATTG AAATGCTTTA TTACTTGATA CTTTCTTATT	240
TCGTTAATTT TTCTTTCTTC TTTTATATTA TTATTACAAT TCTCCAATTG TACACTACCC	300
ATTTTTGTAT CAGAATTTTT ATTAAAATAG TTGGCAACTC TATTTTGAAA TCTTTTTTCT	360
TTTTTTTCTT TAAAGTGTG GTTTATCTTA TGGTAACAAT CTTTTTTAGG ATAATTAAGC	420
TTATAATAAA TTTCTGTACC CGAATTTACC CCCATATGTT GATAGTAATT TGTGTGACT	480
TTTATTTCTT TTTGTAGTCT ATAAATATAC TTTTGCATAG TTCTTAGTGT AGAAATAGTT	540
TGCCCCGTTTT TTATAGATTT TCATTGAAAT AATATAATAT GGTTTTTGGG GTATATTTTA	600
GATTTTGGT ATTTAAATAG CTTGTAGAAA TAAGAACTAT CAATTTATAT TTATATTGGT	660
TATAATTTAG AATATTACTA GATTAATATA TCTAGACTTT ATTTTCTATT TAATATACAA	720
TTAATTAGGA AGCATTATGT GCTCCAAATG GATGATAACC AGATAAAGGG CTTTAAGTGG	780
CTTAAGGAAG ATAAGTTACT TAAAGCCCTT ATCGCATTTA TACTAATTTT CCTAATTTAC	840
GTTTTATTTT GTTTAGAGCG TTATATTATT AATTTTAAAT CATAAAATGG AGGATTAGTT	900
TTGTAATTGT ATATATTTTT AGCTTTAATT GTTCTTTATT AGGCCTTTAA TACTCTAAAG	960
TATTATGCTA TTTTCGCAAAA ATAATTTTCT GGATTATATT AGCTTACATA TTAGGATGAG	1020
AATTATAAAT TTTAGTGCAA CAACCTTCTA CAGGGTAAAG GAGTGTATAA AGGCCTCTAA	1080
AGCTTTCATT TTCTTTATTT GTGGAACATT TGAAGATTAC TTTTGGATT TTTCTAATAT	1140
TTCAAGATAT TCTAACAGGG TTTTAGAATC AACTTCATGT TGATTAGTTT TAGCTAGAGC	1200
CTTATTAAAC TTGCTTCTTA TTAAGGAATA AGCATAATTT TTATTTGCAC TATGGAATAA	1260
TTTTTTATTC ATATGATCTA GTGTTTGTAC AAGAATGATT AACTTATTCT TAGCAAATTA	1320
AATTTGCTTT GTTATTCTTG CCAATGTATT GTTAATTACT CCATCCATAA TGAATTAGCC	1380
CCCTATTATA TTAAATTTAT ATTATAAATA TAGCACAGTA TTTTTTTAAA TTTTTTTAGC	1440
GTAAACAAT ATATTTCTAA AGTTTTGCAT AAGCTTATTT TATAATGTAT TTATAATTAA	1500
GTAGTAGTGA TTTTTTGTA AAATTGTTTT AATTCCTCAT AGAATAATAC GTAGTAGTCT	1560

1048

TTTATTTTTA ATAAACTCT TtCTAAGGAG CAATTAAC TT TATAATAAAT TATAGATTTA 1620
 GGATTTTCT TAAAATAAAG TTTGACTATG ACGGTTATTT CTTTTCTAA TTTGCGTTTT 1680
 ATTTATATAT TTTTGTGTT TAATTGTTCT TTATTAG 1717

(2) INFORMATION FOR SEQ ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1566 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

AGnCACGTAA AATAACTTCA GTTCATATTA TCATATAATA AATAAAACAT TAAGTACAAT 60
 AACCTAACAT TTAAAAGGA TGTACATTTT AATACAGAAA CTGAAGCTGT TCAACTACAA 120
 TTATTGCACT TGAAATTTT TATATTTAAA TAATAATACA AATAATTATA TTAACAAATA 180
 TCAATTAAAT TTATTTTAC ATCATATAAT AGTGCTATAT ATTGTATAAT ATGCTATATA 240
 CTTGAACTA AAGGGGGGC ATATTAGTTA AGATAATATT CTTATATTTT TTATTAAGGA 300
 GACTAATATG AAAAAAATAT CAAGTGCAAT TTTTACAATA ACTTTTCTTG TCCTTATCAA 360
 CTGTAAAAGC GATACTAGAA AAGCTATTAA TTCAATACAA ATCCAAAAAT TACTTCCTT 420
 TGATGGGTTG ATTGATGGCT TTCTACGCCT TAATTCAAAT CCCAAAAAAT CTGAGAGGTA 480
 AAAGATTGTT TTAACAGCAT GGCTAAAACA TTAAATAAGG CCAAAGACAA ACTTGCTAAA 540
 TTCATTAGTG AAAAAGGTGG CAAGACAACC GAAGGAAAGA ATACTGATAC TGCTAAAGAA 600
 GATAATAGCA CAGTAAACCC TATTGATGAT GAAATAAGTA AAATTAACGA TATGATGGGA 660
 AAAATGATAG ATGCTGCTAA TACCATTGTT GAAAATGTAG CCGAAACCGT AACTGAAGCT 720
 aTGGGAGAAG TTGTCGAGGT TAAGAGTATT GGTAAATGTAG CAACCAAAGC CGATGTAAAA 780
 AGTGTTGTTG AGATTGCTAA AGGAATAAAG AAGATTATTG AAGCTGCTGG TATTGCCGAT 840
 AAATTAAG CTGAAGCCGA TAAATCTACA AAGCCAATCA GCGAAGAAAG TAACAACAAG 900
 TAAGCGGGCA AGATGTTCTC TGGGAAGCAG GGTGATCAAG GTGGTCGAGT TTTCGATGAA 960
 GTCATTCCAC CTGAGATTGG AAGAGGAGCT AATCCATTG ATATTAAAAA GGCTACTAAA 1020
 GCTATTGAAA GTGTTAGTGG AGAGCAGATA TTAGGATCTA TTGTTGTGCT GCTACTAAAA 1080
 CCGTTAAAAG TGGTGGTGAG GAGCCAAAGG GGAAGAATGC GGATGAAGCT ACAAATCCGA 1140
 TTGAAGCTGC CATTGGAGGA AATGACGATT CGGATGCTAC TGCATTCAAG GGAATATGG 1200

1049

AAAAAGATAA TCAGATTGCT GCTGCTATTG TTTTGAGAGG AATGGCTAAG AACGGGGAAT	1260
TTGCTGTGAA AATGGGTCGA AAACCAAGTG GTGATGGTGA TAATATTAGA GTTCTTGTTA	1320
ATAATGCTGC TAATAAAACT GTTGATGCTT TATCTAAGTT AGCACTAGAA GCTATTAATG	1380
AAAGCTTAAAC AAAAATAGCC AAGACTATAC ATTGAAAAAA TAAAGTAAGA ATCAGCATTT	1440
TTAATAAATA ATATTATTTA TTAAAAAATG CTGATTCTTA CTCAACATCT TACGTCAGTA	1500
GTTTACTAAA CTGCATAATC ATTACATATA CACCAACATA TCTAAATTTG CAAACAATCA	1560
TCTTAG	1566

(2) INFORMATION FOR SEQ ID NO: 66:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1552 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

CTGTTTTGTA AACCAAAAGT GGATTATAAT AATTGGGCCT ACTAGCTTGA ATTCTAGAGT	60
CAAGCAAAC TACACTAATT GTATCTTGCG GCAATTTTGT ATTCCTCCTT TAAAATTTCA	120
ATTGCTTTTA CACTAGCATT AAATGCTATA GATGCACTGT ATGCATGGTT GCTATATTTT	180
GTGCCTAAAT TAATAAGCCC AACTGTTTGC ATATTAGATA TTGGATAAAT GTAAAAGTTA	240
ACTTTACTAA TATATTCGGG TTGGGATTGA CTTTCTAAAG TATACTTATG GGCTTTATTG	300
TGTAGAAAAT TGCTAAGCAT ACCATAAAGC ATTAACATAC GTGAATTAGC GTCAAAATCT	360
TGAGCGTTTA ACACTATAGC AATAATATAT ATTTGAAAAT TTAACTGAA TTCCAAAGCA	420
TTTTCATAAA ATGCACCGG TCTAGAATTA TGATCAAATA GATTTTCTGT ACCATCAAAT	480
TTCAATGCTA TTATATTTGA GCTAGCAGCT GTGATTTTTG AAAGGTACGG GTGATTGTAA	540
GTATTTATGA TATCGCACTC AAAATTATTT TCAGTTGCAT ACGCCTTAAA CCCTTTGAAT	600
ATTTGAGTTA AATGGTTTAA AACCATATCT AAAGTAAAA TCATTCAAGT GTTACCCTTAT	660
AAGTAATCTC GGATAACATT TTGGCTGTAT CAACAAGTGG AATTGCTGCG GTGTTACTAC	720
CCTTTTAAA CTTACTTTTG ATTGATTAG CTTTAAAGG TGGAGAGACT TGTGCTGATA	780
ATAGATAATT TCCATAGTAC CTTATAAAG CTTGTCCAAT AGCCTCCATT CCCGATTTGG	840
GGTCAAGATT AAACCTAGAA TTTATATAAC TATTATTGAT ATATTCTCTA AATTCAGAAC	900
TACCAGCAAT TTTGGTTAAA TGTTTTCTTG CTGGTAAATT GCTACCCCT TTTTCATGCA	960
TTCTAGCAAT CCCTGCACGA CCACCAAACC ACCCAATTTC CAATTCCATT TTAACTCTA	1020

1050

GTTCGTCCAT ATAACTCCT TTAAAACCAA AGTAAATAT CCGATTGAAG AGTCAATACT	1080
AAATATTTCA AAGTAAATTA AATCCGAAAT TGATATGCGG TCTTTTAGTT CATAGTTAAG	1140
GTCCTGATAT GTGTAAAGTT TGAATATCC TTGAATATCA GACATATCAG AGTCATAAAG	1200
CACTGCAAGT TCTTGTGGCC TTATGTCAAT AATAACTCCT GCAAATTCAG TGTACTTATT	1260
TTTATCAAAA ACTCTCTGAT AAGAAGAATC GTTTTCAAGT TTAACAACAG TGCCTTTATA	1320
AAACCTTAAA GGTTGAGGAT CCTTAAATAC GTTGATCATG cGGAAAGACA TATCTGAAAG	1380
TCTTTTCTA ACACCATTCa TTAGACAACC CCCACACAAG ATGGCGTTGA AGTTTCTCTT	1440
TTTAGTTTTT CTAAAAAgCa TCAAGTTGTG AACAAAAATT CyTGkTTGAG CCACAACCCC	1500
CCTCGsCGGC TTCTTCGGCT CCACTGGCTA CTAGGnTAAT AATCAAGTTC CA	1552

(2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1484 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

AGTCATTACC GGATTGTAGC TTACATATTC CGCTTTTCTA TCATAATAAT TGATAACTGG	60
TCTTTTAGAA CAACTAGTAT TATAAGTGCG TGTATGAGT TCATTTTTTG GTTTTATAAA	120
AAACAATTGA GGAATATATC CAAAACCTTT TAGATCCATT CTAGGAAATA AACTAAAAA	180
ATTATCTGCT CCAAAAAGAG CAAATATTTG GGTATTACA TCTCTTATTA TTCGAGTAAT	240
TTCCCTGATT TCTTTCTTTT CAATATCATT AATTTTTCCT TTGATTTTTT TCTTTTCAAT	300
ATCATGATTG TTAGTAATTT TATTATTAAT ATCTATTTTG TTAGCTGCAT TGTTAGCAAT	360
TTTTTTGTTA CTGTGCATAA GTAATTACCT TTTACCAAAA TTATGGAGTG TTGTTAGCAT	420
TGTCTTGATT CTCAGCCTGT TCTTGCAGTT TTTTAAAGc TTCGCCGCA TCTCCGCCGA	480
ACATTGTAGG TAGAACCGAT TTTAATTTGG CAAAGAAATA ATTAAGATTA AAAATACTTT	540
TAATGCCATT AATTATGGGA TTGATAATAT CTTTGGTAAA ATCAAAATTT TTAATTTTAG	600
CGGTGATCCA GTTAATGATA TTAAGTAATG GGTCCAAAAC AGTAGTGGTC AAATTTGAAA	660
GAGTTTGCTC AGCTGAGGCC AAATTACTTT GAATACTCTC AGCATTATTG ACTTTTTTTG	720
TAAGGCCGAA AGATTTAAAA TCCTCGAACA TTTCCATCAT CTTGGTAATT CTGGAATCTA	780
GATCTACCTC AGCCCCGCCT TGCCAAGCCC TTTTGGCATC TTCTATATAT TTGTCTCCAA	840

1051

CACCTGACTT CTTTAATAGA TTA AAAAGCT CACTTCCATC ACCCCAAGA AACTATTAA	900
CAGCCTTTAC TGCATCTTCG CTGCTCATAG CACCACTGGA TTTAAGCATA GCTGCAAATT	960
CTA yGCGTTT TTCAAATTAG TTTCATTAA CATATCTArG TCCCTTA rAG TACCCTTAAA	1020
GrCACTTGCT TGATTTAAGA ATTCTTCTTT TTCTAGGTCG CGCTCAAATC CCTTCATTCC	1080
GCCAATAATC TTTAAAAGAC TCTCTTCTC TTTTGGATCA CCATAAACG CTTTATTGAG	1140
AAGTTGTGTT CTTTTGT TTT TGGTGTCTT TC AACCGAT TTTT TAGCAA AACCTAAAAG	1200
GCCTCCTCCA ACTTTACTCA TAGCGTTGCT AATGATATTC CCTAGGGCAC TACCTATAGC	1260
AATTTTGGCA ACAAGTCCTT TTCCTTGAGA GGCCGCTAAC ATTTTACTTT TTGCTTTTGA	1320
TTCTTTTGCA AGTTCTTTAT ACTCAAGACG CCTTTTGTCT CTATCAGACA TTAAAGATCT	1380
TCTGAAAGCC TCTTTTCTAG CTTTCTCAA CCCCATGCCC TGTTTTATAA GTTTTTTAGT	1440
TTGTGTAAGT CTATATTTCT CAACACGCTG GGTACCGAGC TChA	1484

(2) INFORMATION FOR SEQ ID NO: 68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1452 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

CTGCTTATTA ATTCCAATAA GTGCTTATAA GTGTTGTTTT TCTTAAAATT AGTTACCATT	60
GGGAAATCG GTATTTTCAA TTTTAATCTT TTTAGAGCAA ATTCTAATAA TTGCATGCTT	120
TCTACCGACC ATTTTGTAGC AGTCATTGGA ATTATTATAT AATTACTTAC AACTAATACG	180
TTTGTTAAAA TAATTCCCAA ACTAGGACTA GTATCTATTA TTATGTAGTC GTATTTATGT	240
TTTAATAATT TTAAACTATC TTTTAATCTT GTTTCCTTAA ACGGGATGTT ATCGTCATAA	300
AAAAGGTATA AATATATATA ACTGGGCAAT ATGTATAAAT TATTGTTTAA TCTAAAGGTG	360
GAAGAATTTA TGTTTTTTTT ATCTGCTAAT ACTTCGTAAA TGTTTTGTTT TGAAACATCT	420
ACCCCTTGTT CTCCAAGAG ATCTGAAAA TAGCTAGTGG TTGATGCTTG TGGATCGGCG	480
TCAATTAGAA GAACTTTATA TTTTTTAGAC AAGAGTGTG AAAAAATAAT AGCACTTG TG	540
CTTTTGCCAA CACCTCCTTT AATTGAGCAA ATGGCAACTA TTTTAGTGTT TTCTCTATCC	600
ATTTATTTAT AATTCCTCCA TCAGGCAATT CTTTGCAATA AAATTCATAC ACTTTTTTTT	660
CCAATCTGTT TAACATGTCA ATAAATGTTT GAAAATATTT TTTATTAATT TTTTCTTTTT	720
TGATTAACCT AGCAAGACTT CTAAATAAC AAAACACACT GCCTTTTTTA AATTAAATT	780

1052

CTATATAATA TACTTTGGAA AATGTATATG ATTTTAAAGT GCCATTGATT TTGTATTTTA	840
TAACAATGTT TTTTATAGGT TTTCTGTATC CATAGAAAAT TCCTATAAAT TTATCATTTT	900
CTTTTGTAGA GAATAAATTA AGTCCTTCTA ATTTTCCTTG ATTAAATAAT TTTCTAAAAA	960
GAATTAAAAA TTTGTTTTTT TTATATCTGT TTATTTCAAA TTTGTATAGA TCCATTAGCA	1020
TTTTAGTGTG ATATATTGCT CTTTCGTTGA GAATTTCTTT TTTGATGAAA ATTTCTGGCT	1080
TTCTACTTTT TTTTATTATT TCTTTTTTTT TGTTTTTAAG TTTTCTAGT ACACTTTTCA	1140
TTTCAAACTC TTAATTTATA TAGCTATTTT TATAAATATT TTGTGATTCT ATTAGTTTGA	1200
TAATTTCAAT ATAGTATTGA TTATTAAATA TTTTTTTGTA TTCAAGTTTA TTTTGTGTGT	1260
TTAAGTATTC TTTAATTTTC GACCTTAAAT TTGTTGTGTT GGTTTTCTA TGTAAATGAT	1320
CTAAAAGTAT GTTATATATA TTGGTTTCTA TATTGCTTTT ATGTTTTTGG GGTTCGGTTT	1380
TATTAGTATC GTCCTTTATC TTTTTTATAA TTTGATCGAA ATCCGGGGAT CCTCTAGAGT	1440
CGACCTGCAG GC	1452

(2) INFORMATION FOR SEQ ID NO.: 69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

CCCAGCCGGA AGGGCCGAGC GCAGAAGTGG TCCTGCAACT TTATCCGCCT CCATCCAGTC	60
TATTAATTGT TGCCGGGAAG CTAGAGTAAG TAGTTCGCCA GTTAATAGTT TCGCAACGT	120
TGTTGCCATT GCTACAGGCA TCGTGGTGTC ACGCTCGTCG TTTGGTATGG CTTCAATCAG	180
CTCCGGTTCC CAACGATCAA GGCGAGTTAC ATGATCCCCC ATGTTGTGCA AAAAAGCGGT	240
TAGCTCTTCG GTCCTCCGAT CGTTGTCAGA AGTAAGTTGG CCGCAGTGTT ATCACTCATG	300
GTTATGGCAG CACTGCATAA TTCTCTTACT GTCATGCCAT CCGTAAGATG CTTTCTGTG	360
ACTGGTGAGT ACTCAACCAA GTCATTCTGA GAATAGTGTA TGCGGCGACC GAGTTGCTCT	420
TGCCCCGGCT CAATACGGGA TAATACGCGG CCACATAGCA GAACTTTAAA AGTGCTCATC	480
ATTGGA AAC GTTCTTCGGG GCGAAAATC TCAAGGATCT TACCGCTGTT GAGATCCAGT	540
TCGATGTAAC CCACTCGTGC ACCCAACTGA TCTTCAGCAT CTTTACTTT CACCAGCGTT	600
TCTGGGTGAG CAAAAACAGG AAGGCAAAAT GCCGCAAAAA AGGGAATAAG GGCGACACGG	660

1053

AAATGTTGAA TACTCATACT CTTCTTTTTT CAATATTATT GAAGCATTTA TCAGGGTTAT	720
TGTCTCATGA GCGGATACAT ATTTGAATGT ATTTAGAAAA ATAAACAAAT AGGGGTTCG	780
CGCACATTTT CCCGAAAAGT GCCACCTGAC GTCTAAGAAA CCATTATTAT CATGACATTA	840
ACCTATAAAA ATAGGCGTAT CACGAGGCC TTTCTGCTCG CGCGTTTCGG TGATGACGGT	900
GAAAACCTCT GACACATGCA GCTCCCGGAG ACGGTCACAG CTTGTCTGTA AGCGGATGCC	960
GGGAGCAGAC AAGCCCGTCA GGGCGCGTCA GCGGGTGTG GCGGGTGTG GGGCTGGCTT	1020
AACTATGCGG CATCAGAGCA GATTGTACTG AGAGTGCACC ATATGCGGTG TGAAATACCG	1080
CACAGATGCG TAAGGAGAAA ATACCGCATC AGGCGCCATT CGCCATTCAG GctGCGCAAC	1140
TGTTGGGAAG GGCGATCGGT GCGGGCCTCT TCGCTATTAC GCCAGCTGGC GAAAGGGGA	1200
TGTGCTGCAA GGCGATTAAG TTGGGTAACG CCAGGGTTTT CCCAGTCACG ACGTTGTAA	1260
ACGACGGCCA GTGCCAAGCT TGCATGCCTG CAGGTCGACT CTAGAGGATC CCCaGatGGG	1320
GTTATTATTG TTA CTGTAA TGA CTATCTT GCAGAACGTG ATTCCAATTG GATGAAAGCC	1380
GGTTTTTGAA TCTGTGGGG TGTTAGCGTn GGGGTGTTC TAATCn	1426

(2) INFORMATION FOR SEQ ID NO: 70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1425 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

TTTTGTTGn AATTGCCACn ATAAAAGGGA TTCTTTTTTG GGTTTTATGG GCGGTATTCT	60
TCATTAtAAA nTTmTCTAT ACAGCAAATA TGGAAAGACT TGAGAGTGCA TTAACCCAG	120
CAATAAATGC GGCACCTCGCT CCATTAAATG AAAAAATCAA TCAATGCATT GACTTAGTTA	180
ATTCTGATGA AAAAAATCTC AAAATATCTA ATGATCTGAA ATTCAATCAG GAAGGAAAAC	240
CTATCTATAA GGAAAGAAyA AATAATGCAA AATAACACTA TTGGTTTAGG ACTTAATTTA	300
CTATCCAGCT TAACTAACAT AGCTAAACT GATACAAACA TAGATCATAA TTACATTAAT	360
ACTTTTAGTA AAGTAATAGA TTTTTTCTAC AAAACATATA TAAGCACACT AAAATCTATG	420
GAAACAGCTG AGTCAACTAA AATATTTGAA GAAATACAAG ACATTTTAAA ATACAACATT	480
GAGATAATAG AGGCTATCTC TACTGATAAA AGCAAAGAA TTATCACTTC ACTTAAAGCA	540
ACACGTAACA AAATCATGAA AGAATATATC AAAATACTTA AAAGAGGTGA AAATGCTTAA	600
AAGATTGcAT TGTCTACTAA TTGCTTTGCT GCTATGTTGC ACCACTATTG CTAACCTACC	660

1054

AGAAGAGCCA AAACCGCCAA TTATTCAAAC ACTAAAATCT TTAGCTAAAT ATGAAACACA	720
ACTTTCAGAG TATGTTATGT ACCTTGTAAC ATTTTITAGCT AAAACAAAAG TCAAAGTTAA	780
TGACCCAAAT TATCCAGAAT ATCCTTATCC AGACTTATCA ACACTAAAAG ACGAACACTC	840
CATAACTGCA GTAAACACA ATATCAACAT ATATTTAGAG TACATTAAAA AAACAAAACC	900
AATAGCGGAA AAAGTCTATA ATAAATATTC CCAATTAAAA ATGTAAATTA CAAAAAGGTT	960
TTTCTTGCAA GAAATTCTAC TTTATAATTA AATTGGCTTT TACAACAGAA GAAAATCTAG	1020
ATATTAAATT TACTTTAATC TAATATCTAG ATTTTAACAT TTTCAACATG AATATTTACT	1080
AATTAATTAG TGCCCTCTTC GAGGAACTTT ATTACTTTGT CTATCTGTTC TACAGCGTTT	1140
TTAGACATTT TATCCCCATT ACCAGAAGTA TTGCTTCAA GAAGTGGTAC AGTTACTCCA	1200
ACTAATTTTG CTCTGACCA TATTTTCTT TTTGAAATAT CCTGATCCTT GTCAGTAATG	1260
TTTTCAATGG TATTTTITAGC TGCTTTTAAC GCTGCTAATT TGGCCGCTAA TTTATCCTGA	1320
AAGGAATTTT GCAAATTTAA TAGTTTTTCT TTAAGCTCTG CATTGCCTAT ATCTTTTAA	1380
TTTTCTTTTA ATTCATTTAT TTTGTCTTTA TAATCTTTAA ATTTG	1425

(2) INFORMATION FOR SEQ ID NO: 71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1423 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

CAGGTCGACT CTAGAGGATC CCCTAAAATA ATTAACCCTG TCAATAAAGC GAGAGTGGAC	60
ATTGATTGGA TGATCTATTA CAGAAACCCC ATTAATATAC ACCTTTTAA ATACAATCTC	120
TGTGTTATTT ATAACCTGTA TATTAAAACC TAAATCCATG TATCCGTCGT GATCATACCT	180
CAAAGTAAAA GATCCAAATT TGGTTTTTAA TTTAAGAATT AAACCGAAAT CATATCTATT	240
ACTATCATTT AAAATAACAA CTTCTTCAGA TATTTCACTA GGAAAAATAA ACCTGCTGGG	300
AATTAATAAA AAAGAAATTA ACAATATTAT TACTTTCATA CCTTTTATTA TTATACTATT	360
CTAAAGAAGA AATAAATAGA ATAAAAAATT TTAATTTCTC TTTTTTAAAA CTATTATTTT	420
TAGGTCAAAG ATTATAGAAT AGAAATAGTT TATTGCTTTA TCTAATGATA GCAGCTTATA	480
GGATCTTTTT TAAGATCGGT CTATCATCAA GAATATAAAT CACAAAAGCT TTTTAAAAGC	540
TATCTAAATT CTTTATTCAA GGCAATAATT TATGTAAAAA TAATTAAAAA AACCTCCATT	600

1055

TTTGAGCAAA CATTTATACG AATTGATTTG GAAAGTCAAA TGCACAATTC TAACACTGAT	660
TGATAAAAAT ACTTTTTAAG TTTTTTATAT TCAAAATATA AAAAATTAT TTATAAAGA	720
TTTTTCAATA TCGATTTTTT TGTGATTTTA TTATTATTGG TATAAAATCA CATAGGGCCT	780
AACCATAAAT ACTCTTAAAG CAAGAATACT TATCTTAAGC CCTATAAATA GACATCGACC	840
AAAGTTAAGG ATGCTTATAG TTAATAGCAC CACTTACCAA GATTATACGC TATTATAGTG	900
TTAAAATCAA TACATTATTC TCAAATAATA TACATATTTA TTTATAAATT ATCTTTTAA	960
AAATTTACTT CACTTTATTG ATTATTTTTC TAACACTTTC TGATTAAAGT CAATATTTTA	1020
CAAAGTATTT AAATTCGGGT ATTTGATAAA AATAGTGAAT TTAAATACTT TATTTTCCAA	1080
AAACTATAAT TTTATATTCT GCACACAAAA TTATCTATAT TAAATTTTTA ATTATATTTT	1140
TTACACTCCT TATATTCTTT CATAATTTCA TTAAGCAATT CTTCTTTATC TTTAAGTAAT	1200
TTTTCTAGCA AAAAAGTAGT AAATCTTGCT TTTGATTTGT AATATATGTA TGCATCTTCT	1260
GTTTTAAGCT GAAATCTTAA TGGCCTGATA AAATTTTCGAT TGGATTTTTT AACTTTCCCC	1320
CCTTCTTTAT CCTTTAAAAA AAATAAGAA TTCTGTATAC CGTTTTCGAT TATGTATTTT	1380
TCCTGAACTA ACCCTTCTTC TATTGCATTT GCCATTCTTA AAT	1423

(2) INFORMATION FOR SEQ ID NO: 72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1405 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

TATTTATnAA TATTGAGAAT ATTATCTAAT AAAATATTAA AGATGTAAAA ATTAGTTACA	60
AAAAATTGCT GTAGTGACAT AAATAATAAA ATTGAACTGC TAGAATTTTA TACAAAAAAT	120
AACAAAAACT TTATAAAGTT GATAATTATA AAAAATTTTA AGATTTTCTT GAAAAGTTTA	180
TCATATATAT AAAAAAGAC AAGCACCATT ATTAATGTTT ATTAGTATAA AACCCCAAAA	240
TAATACAAAT TTAATCCCAA CAATATAGAT AGGATCTTAT TTTTtagata AAGTTTTTTA	300
AAACTTTAAA AAATATATTA AAATTATATA AATATAAAAA GCCTATAATA CCGCACTTTT	360
ATTATCAAAA ATTGCTTATT TAATCTCATA AAAGCATCTT ATTGTTCTAT CAAGCTTATG	420
TATTCTCTAT TATAAGAGCA CAATTAATTA TACCAATTGG GGAGAATATT TTTATGAAAA	480
ACAAAATGAT TTTCTGTATC TGTGTTTTTT TACTTTTAAAG CTGCTGTGCT GCAACCATGA	540
CACTGAAACA AAAATTGTTG ATAAAACAAA AACCTAATAT ATTAATGAGA TAAAAATTTA	600

1056

ATAGCAGCAA GTAAAGAAAT CATCGAGAAA CGAACACTGC AACAACTGA GCCAACAGAT	660
CAAGAACCTG TAGATAATAA AACTGGGAG GAAGTTTTTG ATATAAATAA AAAAATTAT	720
GACTTTATAA ATAGTTTTTT AACAAATGCT GAGTTCAATA TATTTGCAAC AATATTAAAT	780
AAACCAAAAC AATCACCAAG CAAGATGTTA AATAACATAG CAATTTTAGA GCTTAATCTG	840
GAAGAGACAA TTAATTACTT AGACTCAAAA AAAGATGTCT TAGATAAGGT AAACACCTTA	900
GATTTGGAAA AGATCAAAA CTCTCTTGAA TAATTACTCT CTATAAGGAA TTTTTTCAA	960
TAAGCATAAG AAAAATTTA TTAGATCATC AAAATAATAC CGGTTCTATA AAAAAGGATT	1020
ATTCTAAATT AGATTCTTAT CTTAATACAA TACTTAATCA GTTTAATGAA AAAATTAAAG	1080
AGGTTGGAAA TTGAAAAAA ATTATATTAT CAATAACTGT TTCAGCATTA TAAATTAAAA	1140
TTTATTAATG CAGGGGCTTA AAGTAAATTA AACCTTTAGA TATAAGGGGC TAATAAACTT	1200
TTTTATTAGC CCCTGTTAAC ATTCTTTTAA TCAAAAATAT TGAATTTTAA TTACAAAAAC	1260
AAAAAACA TTAGATTGTG AAAACAATAA AGATCTTATA TAAACAGATA TCAATGAGCT	1320
TAAATCTAT GTAAGTAAAC TTGCCGATGA TTAAACAAC TATCTGCAGA AGCAAGAAAT	1380
CTGCATTAT AGTGCAACA TATAG	1405

(2) INFORMATION FOR SEQ ID NO: 73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1398 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

CnTCAACTTC AGCTCTGTAG TACTATCTGC ACTAAACTA AGCTTGACTC CACGCTTGTA	60
TGGATACCTT TTAGCAGGAT AATTTCTAT TTWATCTTTA CTACTAGTAA AAATCCATC	120
CGAATTGGAG TAAATTAGAT TTTTATCTCT AAAATCTACA GAATTACTAA GCAAACCAGC	180
ATCTTGCTGA GGATTTTCA TTAATGCTTT AATTTCTGCA ACTTTTTTAT CAAAATCTTC	240
TTTTATTTTT GTAATACCAT CGCTCATTA AAACCTCTT AAGCAATACT TGTTCTTTTA	300
TGTCTTTTTA GATTCTCATA AAATTGAGCT CGTCTTTGCT TGTAAGTATT ACTTATCGCT	360
TGTACAACT CCGTGAAATT AATGGGCACA AAATTAGAAT CAAGCAAAT TGCTCTCTCT	420
TCTGATTAA CAACAATATT GCCTCTGACA GAGTCAACAG AAGAAGAATT GCTACTCCCA	480
GTTTTCTTA ATTTAATATT CACTTTTGCT AAAGAAACAA GTTGTCTAG TATCTCTCCA	540

1057

TCGATATGAC TTATATCTGA CGCTTTAGCA ATAGCTTTAA TTTGCTCAAT TGGAACAAAC	600
TTACGAACAA GCTCTCTACG TTGTGCCCTGC ATAATGTCCTT TTAGGGTGTA TCCTTTTGCA	660
AGTAACACTT CCTTGTTAAA ATGGTTGCTA AGATGCGCTT TTACAAGTGT ATCAATTTCA	720
TTAATTCGCT CAGCCTCTAG TAACAATTGC TTTTCAACAC GCTCTCGATC TTCAACTTCT	780
GCAAGTTCTT TTGTTATTCG CTCATTTATA CTCATCACGC CTTACCTCTT TAGGGGGTTT	840
ACATTGTCTG TTTGCTCTTT AAAGCGCATG TACTCTTCAA ATTCTGCGC ACTTATAACT	900
TTAGTATCAG CCTTATTTTG CTGCTCTTCT TTATCTTG TG CTTGCAGGTC TTCTTTTCT	960
TTTTTCTCAG TCATCTTTTA ACTCCTTTTC TCAAAATGAG AATAATTTCT CTTTTAAAAT	1020
CGCTAGCTCC TCATTATCAA AGGmGCTACT TTGTATAAGC TGGTTATATT TACTGTAAAG	1080
CTCAATTAGC TTTATATCTC TTTCCACTTT TTGCTCTTCA CTTAACATAA TCAGAGAATT	1140
AAACTcATAT CAAGCCCGAA ATACTTgTAA GTTTCAAGTT ACAAGCGTTC TCAACTTGTT	1200
CTTGcACACC CTTTAAAAAA TCGTAATAAT TACTCCTATC CCCTTTACCA TCATTTCCTA	1260
GCCCTTTAGC CTGTTGTTA AAACCTCTGG TTAAGGGCTC TTtAGTATCT GCACCAATTT	1320
TtGCCTtAAT TAATGCTAAA GCCTCCTTTA AGTAACTAAG GTCGTATTTA ATAACCTCTA	1380
AACTAGCACT AGGGGTGG	1398

(2) INFORMATION FOR SEQ ID NO: 74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

ATAATAGGCC CAATAAGAA TATTTTGAAC ATGAATAATT ATTTAATTAC CAATATAAAG	60
CTAAATACAA AATAAATTCA ATATATCTTT AAATTCTAGA AAATTTTAA TCTAAAAAA	120
TCATTATTAT AGTGCCCAA ACAAATAAA ACTTAACTG GGAAAATTAG TGTTACATAA	180
AATGAATAGG GCTTAAGACA AATTCTTTAT AAAAACTTG CTTTAAGCCC TATTTACGA	240
TCATATTGTG ATTCGAATCC GCGTCGAAT ATTTATAGTA TAACAAAAAT TAAATCATAG	300
TCAAGTTGTA TTTTAAATAA ATTTTAATCT TAATTACTAA AACTTTACAA TATAACTAA	360
ATTGCTATAA GAGTATTTAC TTTTATAGCA ATTTTAGTTA TATTGTAAAG TGATCAATTG	420
TGAGGAGAAA CTTTATGAA TTCAAAAACA ACAAATAAAA CCACTAGAAA TTGCTATAAT	480
AAAGTTCAAC ACAAATTAAT AGTTCTTATT TCAACAATAT GCTATCTAAA CAAAACACAT	540

1058

AAGAAATATA CACAAAAAAC CATACTCTAT TATTTTAATA AAAATCTAAG AAAAAACGGT	600
CAACCTATTT CTACACTAAG AACTATGCAA AAGTATATTT ATAGACTACA AAAAGAAATA	660
AAAGTCACAA AAAACTACTA ACTATTTCTG ATAACAATAT CGATATCCAA ACCATGTAAT	720
AGAAATCCCA AACACATAGA GCCAGCCCCC CAAAATACAA GGAATTAAAA TCAAGCAACA	780
CATAAACCAT TTCAATAACT TCTAAGTATA AAATGCCAAA GCATAAATTT TGCTATTGCT	840
TAAACTATTT TCGAGTATAC ATCTGTATTA AATTAAAGCT TGTTTTTTCT ATCAATGAAA	900
TCATCTTTTG CATCCTTGTC AAATACAATT TCACTTTAAT TTTAATAAAA AATAAAATAT	960
TTGGACTCAC CAATAGGCTT CAGTGCCCGC ATTAAACCTA AATGTTTAAT TAAAAATTTT	1020
TGGATTGTTA TTCCAATGC TTTTCTATC TTGAAAGAAC TTTAAAAGTG CTTTCAAGAT	1080
AGTTTCTTTT TGCACGTTAC TTGAATTTAC ATTCAAATAA TAGGGCAAGT TGCTTTATAT	1140
ATACTCTTTA TTTTTTTTGA TTTTGTATT TAAGTGTTGA TATTATTAGT AATATTTTAA	1200
ACTTTACTCT TAACTAAAAG CTGTGTTTAT TGTTAAAAAT AAAACACAAA CAATACCCTA	1260
TAAATAGTTT AATATTGCAA TATTATTTAA ACTATAAAAA TATGTAAATA ATAATTTATA	1320
AATTAATAAA AAACATATAA GGGAGCTTTC TTAATGAAAA TCAAAAATAT AGCAACATAT	1380

(2) INFORMATION FOR SEQ ID NO: 75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1326 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

TnAGAGCAnG GATCCAGGAG AAGTTAAAGA TCCTATAATG TATAAATGGT TTTCGCCTGA	60
TCAAATTGAA GATGTTGATC TTCAGATGGG CTACCAAAGA ACTGTAAAGT GGGATGCGTT	120
TTTAAATGCT AATCCTACAA CGATTGCTAA TGAGGTTAAT ACTATTTCAA CTATTGGATT	180
TAGTTCTGAA GTGGTAAGAC TTAATTACTT AAAATTACAG TACAAATTTA GGCACTTAAA	240
GCAGGCGTCT GAAAAATTTT ACACTTCAGA CTCATATCTT GGTGACATTA ATAACAATTT	300
ACTTCCTTTC TCTCAAGCCT ATAAGCTTGC AAGTAGCGAG ATTATTAAAC TTATTAAATCA	360
CTTTGTACTA ACAGGCACTG TTTCAATTCA AAAAGATGGA AAAAAACAAA AACGTCTACT	420
TCCAATATG TATGGACTTC TTAATATGCC ACATCAAGTA AAAGAAGAAG TTGCTAGTGG	480
TGATAAAGAT AAAATGGATA AAATATTTGA AAAAATTGAG GCGGGACTTT CAAAGTTAGA	540

1059

GCTAGGAGAC GAATTTTCTA CACCTATGAT GGTAATAGTT GACCCTACAA CTTGCTCAA	600
ACTCGTAAAG CCATACGCAG CAGCACAGG TGCAGCAAGT AGCTGCGAAA AATGGGAGGA	660
TGTTTTGATT CAAACTATCA AGGCTATTAA TAATAGAGAA GATGTCTACA TTGAAACTTC	720
AAACTTGCTA AAACATCAAA TACTTATTTA CCCATTAAAC CCAGAGCTTA TTAAGTTTAA	780
ACCTAGCAaG TATATGTTAC CTACACCAAA TGaACAAGTG GATAAAGATT CAACTGATAT	840
TGcTCATTCA TACATTGATT TTGTTTTAGG AGGGTTACTT GCTACTAGAA AACTATTTTT	900
GCAAGTACAT ATCAAACAAA GTTAAAAGTA TAAGGTAAGT GAAAATGAGT GAACAAGAAA	960
ACTTACAAAC ACAAGTTGAG GCTGAAGAAG AACTTTTGGT AACAAAACCT TATTCTGAAG .	1020
TGTTATTGTT ACTAGGAATA GACAAACTTG CATTAAAGCAG AAAAAATTTT CTACTTCATT	1080
TATCTTTACT TCAAGCTATT CTAGTAACAC GTGGTATTGA TGCTAGTTCA CTTACATATG	1140
AACAAATATT TTTACTTACC TTTTACCATA TGGGTTGTCA ATTAAGAAAA CAGGGAGTTG	1200
TTGAGAATT TGAATTTGAT AGGATCAAAA AAGAGAAATT CAATGAACTT GAACTTGATT	1260
ATtATCCTAG TAGCAGTGGA GGCGAAGAAG GTGGCGAGGG GGGTTGTGGC TCAAACAAGA	1320
ATTTTTT	1326

(2) INFORMATION FOR SEQ ID NO: 76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1309 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

GGGCTGCTAG ATTAATTGCA GGTAGCAGTT GCTTGATCTG CAAAATTATC TATATTGCCG	60
CCGCTAAAAA ACCCTTGAAC GGTAGTTTTG AAGGTGTTTT TTCCCTTCATC ATTTCCATTA	120
CATTTATCAA GTTCAGTCTT TATATGTTCA AGTGCTGATT TAATTTTGCC TTCATCATTT	180
TCTAAGAATT TATCAAATTT TCCAACACCA GTTAAAGCGG TTTTAAACCA GTCAAGTTGT	240
GTTTTTTGAT CATCAGATAG CTTTCTCTA AGCAGGTCTT CTTTAGATTT AGATTTAGGT	300
TTTCTTGTG TTGCTTCTTT TTGGGTAAA TCACGCTTTT GTCTGCTTTT TGTCTGCTTG	360
GTATTTGTAT CATTAGAATT ACAGCCGTTT AGCATTAGTA AAAACAAACA AAATAATATG	420
TTGATAATTT TCATTGTTAC TCCTTTTTTT ATTATTAATA TTCACTTAAC TAAGTATTAA	480
TACTAAATAT GGGATAAACA ATTATTATTT GAATTGATAT GTTTTAAGTG AGGTAGTAGC	540
TATTTAGAAA TGAAAGCAAA TATTAGCCCG GCTATCATTG TGATAGACAT TGCTCCCATG	600

1060

ATTCCTAATA CCCATTAAAG CATTTCTGAA AGAGACATTA AATTCTTTTC AACATTGTCT	660
ATTTTAGTGT TTAAATTCCT TTCTACAGTA TCTATTTTGG CATTTAAATT CTTTTCACA	720
TTGTCAATCT TAGTATTAAG TTCGCTTTTA ATAGCATCAA TCTTAACATG TAAATTCTTC	780
TCTACGGCAT CAATCTTGAT GTCTAAATTA GATATAYCCT TTTGTAAATt CTTTTCTACA	840
GATCTATCT TAGTATCTAA ACTATCTATT TTTAGATTTA AATTCTTTTC CACATTGTCA	900
ATCTTAGTAT TAAGTTCGCT TTTGACACTA TCTATTTTAG AAATAAGATT ATCAAATTTT	960
ATATCaAATT GTTTTCTAA ATTTTCTAAA TCTCTATATG TTAGCTCATT GTGATAATAT	1020
CTTTTAGATA AATCTTGTGC TATTAGTTGT TCCATGCCCA GCCTAATAAA TTCTTTATAT	1080
ATTTGTCTT GAGTTACACT TGCAATATTT GTTGACACTG TTTCCATAAA ATTTTCCCTT	1140
ATGGTCATAT TATACACTAT TTTAGATTGA TTGGCTTTAG AGATTTTTAT ATGTAAAGGA	1200
GAAATTCTTG CAAGAAAAAC CTTTTTGTA TTTACATTTT TAACTGGGAA TATTTATTAT	1260
AGACTTTTTC CGCTATTGGT TTTGTTTTTT TAATGTACTC TAAATACTG	1309

(2) INFORMATION FOR SEQ ID NO: 77:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1300 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

TATCTATATC ACCATTTTTA AAGAATTC TG TAACCACAGT TTTGAAAGTG GTTTTTGT	60
GTTCTGCTTG ATCACCATTA CAACTATCAA GTTGAGTTTT TATATGATCA AGTGCTGATT	120
TTATTTTATC ATCATCATTT TCTAAGAATT TGTCAAATTC TCCAGCACCA GTTAAAGCGG	180
GTTTTAACCA GTCAAGATGT GTTTTTTGAT CGTCAGATAG CTTTCTCTA AGTAGTCTT	240
CTTTAGATTT TGGTTTTTCT TGTGTTGTTT CTTTTTGGGT TAAATCACGC TTTCCCGTC	300
TTTTTGTTTG TTGGGCATTG TTTTTTAAAG TGTCATTATC ATTAGAATTA CAGCCGTTTA	360
GCATTAGTAA AAATAAACAA AATAATATGT TGATGATTTT CATTTGTTACT CCTTTTTTTA	420
TTATTAATAT TCACTTAACT AAGTATTAAT ACTAAATATT GGATAACAA TTATtATTtG	480
AATTGATATT CTTTAAGTGA GGTAGTAGCT ATTTAGAAAw rAAAGCAAAT ATTAGCCCGG	540
CTATCATTGT GATAGACATT GCCCCATAA TTCCCAATAC CCATTTAAGC ATTTCTGAAA	600
GAGACATTAA ATTCTTTTCA ACATTGTCTA TTTTGGCATT TAAATCTTT TCTACAGTAT	660

1061

CTATTTTGGC ATTTAAATTC TTCTCTACAT TATCAATCTT AGTATCTAAA TTAGATATAT	720
CTTTTTGTAA ATTCTTCTCT ACATTATCAA TCTTAGTATC TAAATTAGAT ATATCTTTTT	780
GTAAATTCCT CTCTACATTA TCAATCTTAG TATCTAAATT AGATATATCT TTTTGTAAAT	840
TCTTTTCTAC ATTATCTATC TTGGTATTAA GTTCACTTTT AACAGCATCA ATCTTAACAT	900
TTAAATTCCT TTCTACAGTA TCTATTTTAG AAACAAGATT ATCAAATTTT ATATCAAATT	960
GTTTTTCTAA ATTTTCTAAA TCTCTATATG TTAGTTCATT GTGATAATAT CTTTTAGATA	1020
AATCTTGTGC TATTAATTGT TCCATGCCCA GTCTAATAAA TTCTTTATAT ATTTGTTCTT	1080
GAGTTACACT TGCAATATTT GTTGACACTG TTTCCATAAA ATTTCCCTT ATGGTCATAT	1140
TATATACTAT TTTAGATTAA TTGGCTTtAG AGATTTTAT ATGTAAAGTA rAATTTCCTG	1200
CAAGAAAAAc CTTTTGTAA TTTACATTTT TAACTTCAGA TATCAGTTT AAATTTTTTA	1260
CTGTagATTT TTTACAAAA CAGTATTGCA AAAACTCTnA	1300

(2) INFORMATION FOR SEQ ID NO: 78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1295 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

GAATTAATAA GCAGAGATGA TAATTTTTTA GCGTTATTC ATGAACGTGA AGACTTGAAC	60
AAAAGGATAG CAGAAAACGA TACTTtCGAT TTAAATAAAG ATTaTATAAA AGAATATGaA	120
ATTACACTTG aAAAAATTTTT TCAGTTGTCA AAAAAATTTT TAATTCATA ATATATAGGG	180
AAATGAAATG AGTGTAAT TAAACATAT GAATATAAAA ATAAAAGATc GTATTAATAC	240
TGGcAAAAAT CAAAAGCAAA TTGaAATTAA TTGTGATGAA GaTAAAATGG AACGATTCT	300
ATTTTTAAAA GAAAGGCTAA TAATCAACTT CAAAAAGAA ATTCACAATA AAATAGAAAC	360
AATGAAGATC TTAAAAGAGA TTAAAGATAA AGAATATTAT AAATTAGATG GCTATCAAAA	420
CTTTGAAATG TTTACTAGGA ATTACAAAAT AGCAAAAAGC CAGGCTTATG AATATTTAAG	480
AATrGCAAAAT GCAATAGAAG AAGGrYTAGy TyrGGArAAA krCATAATCG AAAACGGTAT	540
AyAGAATTCT TTATTTTTTT TAAAGGATAA AGAAGGGGrG AAgTTAAAA ATCCAATCGA	600
AATTTTATCA GGCCATTAAG ATTTCAAGCTT AAAACAGAAG ATGCATACAT ATATTACAA	660
TCAAAAkCAA GATTTACTAG TTTTTTGCTA GAAAAATTAC TTAAAGATAA AGAAGAATTG	720
CTTAATGAAA TTATGAAAGA ATATAAGGAG TGTAaaaaAT ATAATTAAAA ATTTAGTATA	780

1062

GATAATTTTG TGTTAAGAAT ATTAACCTAT GTGATTTATC AAATATATTA TTTAGATAAG	840
GTATTTGATA AAAAACAGGG AATTTCTTTG TTTATAAAGT AGTTATTTAA ATCATAAAAT	900
GTCAAAAAAA TCGGGGTAGT AAAGTAAAAA GTAAAAGATG ATTTACAAAT AAATATGCAT	960
ATTATTTGAG AATAATGTAT TGATTTTAAC ACCAACAAAA TTCATTTTCC AAATGATATA	1020
AAAGTTTTTA TAAATGAGCT TATAGGGTCG TTTTCAAAAT TAGGCTATTA TAAAGAGGCA	1080
AAAGAACTT TGCAAAATAT TTTTGTATA TTAGATAGTA ATTAAAAATG ATTTAGTCTA	1140
CTCAATAATT TATATGAGAT AATAAAGTAT ATTAAGGATA TGTGCTTTAT TAATAAAAAAT	1200
AAAAATAAAA ATAAAAATAA AAATAATTAT ATCTTAATAA AAAAATTGGA AATACCGCAA	1260
TTATTGATAA TTTATCGAAT TTAGATACTA ATATA	1295

(2) INFORMATION FOR SEQ ID NO: 79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1284 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

TATCnTTTTT CCTCAAAAGT TTAATTGGAA AATAAAAAGT TATnCTCTGG TGATATTAAT	60
AATTTTATTA TTGGGAATTC ACAACGCTCA GTTGAAGTTA ATGTTTTGGG ACAATTTGAA	120
AAGCTATGTA AACTTCTTAA AATTCCTTAT ATCCCAAGAC ATACAAATAA yTCATATATA	180
TTAATTGATT CACTtCGTAT TAATCTATAT GGAGGAGATA AGGCAAGTGA TTTTGAAAGA	240
TTTAGAGGCA GTAATTCGGC ACTTATTTTT GTTAATGAGG CTACTACTTT ACACAAGCAA	300
ACTTTAGAGG AGGTCTTAAA AAGACTTAGG TGCGGACAAG AAACATTTAT TTTTGATACT	360
AATCCTGATC ATCCAGAACA CTATTTTAAA ACCGATTATA TTGATAATAT AGCGACATTT	420
AAGACATATA ATTTTACAAC TTATGATAAT GTGCTACTTA GTAAAGGATT TATCGAAACA	480
CAAGAAAAAC TCTATAAAGA TATACCATCA TATAAaGCAA GAGTTTTGCT AGGTGAGTGG	540
ATAGCAAGCA CCGATTCAAT TTTTACACAA ATAAATATTA CTAATGATTA TGTATTTACT	600
AGCCCCATAG CATATTTAGA CCCAGCATTT AGTGTTGGmG GGGATAACAC TGCATTATGT	660
GTTATGGAGC GrGTTGATGA TAAGTATTAT GCTTTTGTAT TTCAAGACCA ACGACCAGCC	720
AATGACCCGT ATATTATGAA TATGGTTAAG ACCGTTTTAG AAAATTTTAA TGTACATACA	780
yTTTATTTAG AAGATAGAGA CAATACAAAA GGTGCTGGTG GATTGACyCG yGAATACATs	840

1063

TTGCTAAGAA ATAATATGGG TCAATATTTT AGAATTGTTC CAGTTAAGCC AAAGTCTAAT	900
AAATTTAGCA GAATAACArC GTTAATTACG CCGTTTAYTT ATAAGAACT KTACATTACr	960
AAGTACAGCA GTTCTTCTGT ATTTAATGAT ATTTATTCGT ATAAAGGAGA TAACAAAACC	1020
CATGATGATG CTCTTGATGC AATATCTGCA GCATATTTGA TGTGTCTTT AGGGTATAGA	1080
GAGAGAAGTG TTCACTTTGG CAATCAAAGA TTTTGTAA TTTTATTGAC AAAAATAATA	1140
GTTTTTGCTA TCATACATCT AATTTAATAA AGAGAAATAA AAGGTGTGTG ATTTAAGAAA	1200
AACAAAATTA ATAGATAAGA TAAGTTCCT AGAACTATAT AAATACTCAA TATTTTTTAG	1260
GAATTATATA GAAAATGTAG CAGA	1284

(2) INFORMATION FOR SEQ ID NO: 80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1271 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

GCTTGAAAAA TTTCTTTCGG GCGCTTAAT GGAAGAATCA TTTCTTATTA GAATGTGGTT	60
AACTATTTTA AATTTTTTTC AGAAAGAATA AAAGCAAAGA AGAATATATA TAAAGCTTAT	120
GTTATAAAAA ACCTGGAAAA TCAAATTAAT GAAATGTTGT AAAAATCCAG TAATAGATTT	180
TAAGAAGAGA ATGTTTGCAT GTTGGTTTTG TGGAAATGTT TTTTAGTGTT TGCCGATATT	240
CAATGGAATT GAAAGAATTT TTTAGGAAAT TAGAAAAAGG TGGTATTGTT GTTGAGCAAA	300
CTATTTTAGA AATTATTCAA AGCAAAGTTC TTAACCTCTAA GAACAATTTG GAAGAATTTT	360
TTAGATGAAG GTGAATATGA GCTTTTTTTA AAAAAAGAAA AAACCCAAAA CGAATTTAGA	420
AGAATCTCTT AAGGGTCAAG ATAAATGAAT ATATTAATTC TATTCATCT AGTACTTACA	480
AAATCGTCTC GGATATGTTT GAGTTTATT ATGTTTAA TAGTTTGGCG TTTTCCCTT	540
ACAAATCTTT TTTTTCATTT TTTAATGTAG ACCTTTTAGA TAGTGCTGAG AATATTAGCA	600
TTGTTGACTT TGAAGGTTGG ATTTGGGGGG AATCCTCTAG AAGTCGACCT GCAGGCATGC	660
AAGCTTGGCA CTGGCCGTCG TTTTACAACG TCGTGACTGG GAAAACCCTG GCGTTACCC	720
AACTTAATCG CCTTGCAGCA CATCCCCCTT TCGCCAGCTG GCGTAATAGC GAAGAGGCC	780
GCACCGATCG CCTTCCCAA CAGTTGCGCA GCCTGAATGG CGAATGGCGC CTGATGCGGT	840
ATTTTCTCCT TACGCATCTG TGCGGTATTT CACACCGCAT ATGGTGCACT CTCAGTACAA	900
TCTGCTCTGA TGCCGCATAG TTAAGCCAGC CCCGACACCC GCCAACACCC GCTGACGCGC	960

1064

CCTGACGGGC TTGTCTGCTC CCGGCATCCG CTTACAGACA AGCTGTGACC GTCTCCGGGA	1020
GCTGCATGTG TCAGAGGTTT TCACCGTCAT CACCGAAACG CGCGAGACGA AAGGGCCTCG	1080
TGATACGCCT ATTTTATAG GTTAATGTCA TGATAATAAT GGTTTCTTAG ACGTCAGGTG	1140
GCACTTTTCG GGGAAATGTG CGCGGAACCC CTATTTGTTT ATTTTCTAA ATACATTCAA	1200
ATATGTATCC GCTCATGAGA CAATAACCTT GATAAATGCT TCAATAATAT TGAAAAAGGA	1260
AGAATATGAA T	1271

(2) INFORMATION FOR SEQ ID NO: 81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1269 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

GAATTTTCA AAATTACAAA ACTTTAACCC AAAATGGTAA AACTTTAATT TTTTGTAATT	60
TTTACATAAA AGTGTTAACT TTAAAATyCC AAACCTTATA ATTTTGGAAA ATTATCAATA	120
CTTTTTTAAT TTATTCTTTA TTTTCAAAAT AATCTTTATA TACTTATATA TTATGTATAA	180
GTCTGTAAAA GAACAACAAG AAAAAGGAAT AGATCATACA TGCAGAATAC TTATTCTTAC	240
CGAAACAATA TTTGAAATAA ATTTAATATT AGAAAATTAT TCTCAAAAAA CTCTACTCAA	300
AAAGTATAAC GAAAATCTCA AAAACAAAAA TCTACCTCCT AGTAATATAT CAACAATGAA	360
AAAATACTTA AATCAATTAG AAAAAGAAAT AAAAATCATA GCAAAATTCT ATTTTAAAAA	420
CGATCAATCT CTAATTTATT ATAACTTAA TTATACCCTA GAAAAAATTT GGTAAAACT	480
AATAGAATTA TTCTACAAAG AATTAAAACA ATTTATACAA AAGAACACTA CTACTTAATT	540
GTAAATACAT TATAAAATAA TCTTATTCAA AACTTTAGAA ATATATTGTT TTACGCTAAA	600
AAAATTTAAA AAATACTGTG CCATATTTGT AATATAAATT TAATATAATA GGGGGCTAAT	660
TCATTATGGA TGGAGTAaTT AACGATACAT TGGTCGCAAG AATGAAAAAG CAAATTAAAT	720
TTAATAAGAA TAAGTTAATC ATTCTTGTC A AACACTAGA TCATATGAAT AAAGAATTAC	780
TTTATAGTGC AAATAAACT TACAATTATG TCTTAATACA AAACAATTTT AATGAGGCTC	840
TAGCTAAAAC TTATCAACTT AGGGTTAATT ATAAACCCTT ATTAGAATAT CTTGAAATAT	900
TAGAAAAAAA TCCAAAAGTA ATCTTAAAC GTCCACAAA TAAAGAAAAT GAAAGCTTTA	960
TAGGCCTTTA TACTCTCTT TACCCTTTAG AAGATTGTTG CACTAAAATT TATAATTCTC	1020

1065

ATCCTAATAT TTAAGCTAAT ATAATCCAGA AAATTATTTT TCGGAAATAG CATAATGCTT	1080
TAGAGTATTA AAGGCCTAAT AAAGAACAAT TAAACTAAA AAATATATAA ATAAACCGTA	1140
AATTAGGAAA ATTAATGTGA CACCAAATGA ATAGGGCTTA AAACAATTTC CTTTAAAGAA	1200
ATTTCTCTAA GCCCTACTTC ATTGCTTATT ATTACGTCAA TTCGAGCATA AAGCCGAAC	1260
AATTTATAG	1269

(2) INFORMATION FOR SEQ ID NO: 82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1225 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

CGGCCTTTTT TGTTGCAGCA TGATCAAGAA TCCCTTTTAAA TTTAATGGTG AATTTGTCGC	60
TCACTAAGCC CTCACTTGCT TAAAATTAAT TCATACAATT CTTTTTCTAA TTTAATCTCA	120
GCAAGTCTAT TGACCTCTAA AgCTCGTCAT AAGGCAATTT CTTTACATTG TCGTACGAGC	180
AAaTATTCAT AATTACTGGA AAATAATATT TGTCGTTCTT AATCTCGTCA AGCagTTAAA	240
ATATTTTTTT CTAGTCTCAT TAaGACTTGC AATAGCTTTA TCAATATCTC TATCTCTTTT	300
GCTCATTTAG CAACCAGCTC ATTGGAATTT GATGTACTTG ATGAAAGTGA AGTGGCTACT	360
TTTTTCATAAT CAAAATTTTC ATTAATATAG TCAAAAGCAA CAAAATCACC AACATTATTT	420
TCATACTCAC TCAAATATAC TAAAGCGGGC TTTTTTAGAT CATTGTCTAA ATGAAAAGTA	480
TTAAATTGTG CAGTGTAAT TATTGCAACA AGATAGTCCT TATAATAAGA AATAAATTCT	540
CTATTTTGAT CAAAATCAC ATAGAATTCG TCTAAAAATT TTGGACTTAT CATTAAGCTT	600
GTGATTTCTC TTAAGTATTT AACCTCATTA AGCTTTAAAA CAGCGTCACT TTGATTAAAT	660
CCTAGCACCT TTATCCCATT CATAGACTGG TAATACTTTT AGTGGATATT CATAAGTTTT	720
ATTTTTAGTT AAAATTTTCA TTTTATATCT CATTATCATA ATAAGACTCT CCTTTTAAGT	780
GTGTTTGGT TTAGTTTTTT GGCAATTAAT AGCCCTAATT TCAAAAGATA CTTTTTCGGC	840
CTCAGCAGAA TAACCTCTTG AAGGCTCTTC AGTAAAAATT GCATAGTTAG AAATAATTTT	900
GGTAGCAATT CTATCATTGA AACTAAATC AAGCATTTTA TCCTCTTTTC TCACATCCAT	960
GTGTGAAAAC TGTTTCATCAG AAAGTTCAGT TAACAAAATG TAGTCATGAC TACCTAGTGT	1020
CACTTCAATG TTGAAAACAT AAGTTATTGT TTTGGGATCT CTTAAGCTTA TTACAGGCAT	1080
ACCTTTATCT TCACTACTAA TCACTGCTCT TGTGTAGGT TCGCTGTAA GCTCTAGCTT	1140

GCCACTATGT AACTGCGGTA CCACCAATTG AAAAATAAAC TTCTCTTAAA TCATAAAATT 1200
GCATTTTTAG ACCCCCTTTT TAGCA 1225

(2) INFORMATION FOR SEQ ID NO: 83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

CGGCTGGTGC TGTTAGTGCT GTTAGTGGGG AGCAGATATT AAGTGCATT GTTAAGGCTG 60
CTGGTGCGGC TGCTGGTGAT CAGGAGGGma AGAAGCCTGG GGATGCTAAA AATCCGATTG 120
CTGCTGCTAT TGGGAAGGGT GATGCGGAGA ATGGTGCGGA GTTTAATCAT GATGGGATGA 180
AGAAGGATGA TCAGATTGCT GCTGCTATTG CTTTGAGGGG GATGGCTAAG GATGGAAAGT 240
TTGCTGTGAA GAGTGGTGGT GGTGAGAAAG GGAAGGCTGA GGGGGCTATT AAGGGAGCTG 300
CTGAGTTGTT GGATAAGCTG GTAAAAGCTG TAAAGACAGC TGAGGGGGCT TCAAGTGGA 360
CTGATGCAAT TGGAGAAGTT GTGGCTAATG CTGGTGCTGC AAAGGTTGCT GATAAGGCGA 420
GTGTGACGGG GATTGCTAAG GGGATAAAGG AGATTGTTGA AGCTGCTGGG GGGAGTGAAA 480
AGCTGAAAGT TGCTGCTGCT ACAGGGGAGA GTAATAAAGG GGCAGGGAAG TTGTTTGGGA 540
AGGCTGGTGC TGGTGCTAAT GCTGGGGACA GTGAGGCTGC TAGCAAGGCG GCTGGTGCTG 600
TTAGTGCTGT TAGTGGGGAG CAGATATTAA GTGCGATTGT TAAGGCTGCT GATGCGGCTG 660
ATCAGGAGGG AAAGAAGCCT GGGGATGCTA CAAATCCGAT TGCTGCTGCT ATTGGGAAGG 720
GTAATGAGGA GAATGGTGCG GAGTTTAAGG ATGAGATGAA GAAGGATGAT CAGATTGCTG 780
CTGCTATTGC TTTGAGGGGG ATGGCTAAGG ATGGAAAGTT TGCTGTGAAG GATGGTGGTG 840
AGAAAGGGAA GGCTGAGGGG GCTATTAAAG GAGCTGCTGA GTTGTGGAT AAGCTGGTAA 900
AAGCTGTAAA GACAGCTGAG GGGGCTTCAA GTGGTACTGA TGCAATTGGA GAAGTTGTGG 960
ATAATGCTGC GAAGGCTGCT GATAAGGCGA GTGTGACGGG GATTGCTAAG GGGATAAAGG 1020
AGATTGTTGA AGCTGCTGGG GGGAGTGAAA AGCTGAAAGT TGCTGCTGCT ACAGGGGAGA 1080
ATAATAAAGA GGCAGGGAAG TTGTTTGGGA AGGCTGGTGC TGATGCTAAT GGGGACAGTG 1140
AGGCTGCTAG CAAGGCGGCT GGTGCTGTGA GTGCTGTTAG TGGGGAGCAG ATATTAAGTG 1200

(2) INFORMATION FOR SEQ ID NO: 84:

1067

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1182 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

GCTACAGAAA TAAAAATTTT AACACAATT ATTTTATTA TTTCGGCCTT TTTTCTCAA	60
TTTTTATTGT CCCAAAAAGG TAACAATAAA ACGAATAACC TAGAAGAGGT GGCCAATTTG	120
TTATTTAAAA ACTTTAAAT TTTTGTCAAT GCATTTTAAA TTCCAAATTA CTTTTCATA	180
AATAAATAAA CTTCTCTTTG CGCAAATGGA AATCCAAACC GATCACTAAA ATATTTCTTA	240
AAAAATTATA TTCAGCTAGC CCAGATATCA TTTGCTTTTC ACACTGAAAA GCATCCTCTT	300
GAACACTAGA ATTAAAAACA CACTGTTTTT AAAATTTTCA ATTTAAATTA AAGATTGTAT	360
TTTGGCAAAA AATTTTCTAT ATCTATTTTA TATTCTCTGT CTTCATTAGA AATTAACATA	420
ATCTTTAATC GTTTTAATTT TTTGATTTTC TTAAAAAACC CTTTAGAAAT AGTAACACAC	480
AAGGTATTTT TTA CTACAAA AGGAAATTCT AAATGAAAAA ACTTTTCATT TATATTCGGA	540
TCACCAATGT TAAATCTTT TAATTGCTGC CATTTCTCAC TTGGTAAATT ATTTTCATGC	600
TTTGAACTT TAGCATCTTC AAATCCTTCA AAAATTACAC TTTTAAAACC TAAATTTTA	660
TTGTCATGCA CTTTAAAATC AAACCTATAA ACGGTAGATA ACGCTTTATA AGCATCTGCA	720
CGATAACCTG TCGCTTTTAT CATCTTTTTA TGCTTAAGCT CAGGAATTAT AAGCTGTGAT	780
TTTATAAAAA CCAATTCTTT CAAATTACTA TCTTTAAAAA GATATGTATA GGTTCATCA	840
ACAAAAACAT TATCATCAA CTTTCAACA ATTTTATTAT AAATAACATT GTTTTCTTTT	900
TGTTTGTA AAAGAAACC TAAAAAATA CAAATTAATA GTAACCCAAA AAATAATATT	960
TTACCCATTA ATAATCTATC CTACTTATGA AAAATCATAT CAAATGCACT ATAAAAATGT	1020
GAGCTATTTT CCCTGCTTAC CCTGAAAGAA TATTTTTTTT CTCATTATTT ATCTCATCAA	1080
AACATTCAAC ATATACATCA ATTCCATTTT CTTCTGGCGA ACTTCTTAT TTTATTCCAT	1140
TTTTTCACTG GAAATCCAAG GAAACTCATA TCCAAAATTT AA	1182

(2) INFORMATION FOR SEQ ID NO: 85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1178 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

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GnACnAGGAA CCGGCACTGA CGAGTCATTT AGACTGATTT TCAAGACCTT TTTAAATGTA      60
GACATTGAAG TTACTACTCC TGAAGCTGGG GTTATTGATA TCTCTTTAAA AGGGGTAATA      120
AAAACAAAC TTTACTACATT TATTTTCGCT AGCACTAAGA AAGGAAAACG ACTAAAAAAG      180
ATAATTCTTA GAGAAAAGAA GCCGGGATAC GCTGCATCTA AAAAAGCTTT AGTATTTAAC      240
TCACTTCCTA AaGGCTatGA TCATTCAATT TATGCTTTTA TTAAGAGAAT TATTCCTATT      300
GGTAGAGTTC TCAAAATTA TAATACAGAT GGTAACAATA TTATTACTTT CAATAACTAA      360
GGAGGTTTTA TGGCTGATGA TCAAGAAAAA TTACTGATTG ATGAAGAAGA AACGGTTCAA      420
ATTAAAGATT TAAATAAGGT TACGACCGTT AACAATACTG ATCTTTTACT GCTTGATGAT      480
GGAGCTGCAA GCAGCAATGC TATCACCTTT AAAAAGCTTCT TAAAAACCGT TAATCACCAA      540
ACATTTAAAG GCGAAGAGCT AGGCTATTTT AAAGAGATAA TTAAATCTAC AATCGCTACT      600
GAACTTGACG CTGATAAAGA TTTTATAAAA AGCATTTACG ATTTAATCGT TGACAAGCTA      660
ATTGAGAATG AATCTAGTAA ACTTTCAAAT CTTTTTAGTA AAATCAAATC GCGCCTTACA      720
GATAGCATAT CATCAGCCAC TTTATCTAGA AGTGATGATC TTTTGATAAT GCCTTCATCA      780
GATACTATTC AAAAAACACC CGTTCCTAAA CATATACTTG GAGTACCATC AAATTTTACT      840
TATGGCAGCA TAACTAGAAG TACTACACTT TATCCTTCTG ACTATGAGAA TAAAGCGATA      900
TCTATTAATA TGGAAGACAA TGATGATGTA ACTCTTATTT TTTACAAAAA TTACGATAAT      960
GATCCCATTT ATCTGGATAT TGAGATTCAA GTAAAAATCA ATGGATAATA GGATGCAGAA     1020
AAAATCATTA AAAC TTATGT nTTCTGATGA AATTACATAC AATTGGGTTT ATGAAATACG     1080
GGCCCTCGCG GACTATTCAC CAGAACTCCC ATTATAACGG AnGGTATATC CAAAAAAGAG     1140
CCTCCTGTAT GGAGATCGTC CCGATCTTTA AAAC TGTA                               1178

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(2) INFORMATION FOR SEQ ID NO: 86:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1177 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

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CATATGTATA AAAAAATTA TTTTGTGACG GCTTTTTTACA GAAATTATTA TAATAAATAA      60
AAGCTTTATT AAATCTCAT GTTAAAGAGC TTAAGAAAGC CGCTGGCTTA GCTCAATTTA     120

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1069

TTTTAGATAA ACTCACTAAA CAATTAAATT CAGTTCAATT TAGAATTAAA ATTATTTTGT	180
ATTTGTTAAA ATAAAAGAAC CTATTTAAAT TCTCTTGTTA AAAAATTCAA ATAAGTTCTA	240
CTTTAAAGCT ATATACTAAC TTATTACTTT ATAAAATTTT AATCATTCTT AATTTAAAAA	300
ATGCTTATTG AATATAGAAT AAATAATTGG AGCAAGCGTT ATTCCCATT TTAATAATTAC	360
TTGTATTGTT CTATTACTTG CAGTAAGTTC GTTTTTTAAA ACATTTATTT TATTATCTAG	420
GCTAAATATA TCCyTTtGTA AGGTTTTTTC TACACTATCT ATTTTAGtAT TCAAGCTaGA	480
TATATCTTTT TGCAAAGTTT TTTCTACATT ATCTATCTTA GTATCTAAAC TATCTATTTT	540
AGAATTTAAA TTCTTCTCTA CACCATCTAT TTTGGCATTT AAATCTTCT CTACAGTATC	600
AATCTTAACG TCTAAATTGG ATATATCTTT TTGTAAATTC TTTCTACGC TATCAATCTT	660
AAAAATAAGA TTATCAAATT TTATATCAAA TTGTTTTTCT AAATTTTCTA AATCTCTATA	720
TGTTAGCTCA TTGTGATAAT ATCTTTTAGA TAAATCTTGT GCTATTAGTT GTTCCATACC	780
CAGTCTAATA AATTCTTTAT ATATTTGTTT TGAGTTACA CTGCAATAT TTGTTGACAC	840
TGTTTCCATA AAATTTTCCC TTATGGTCAT ATTATATACT ATTTTAGATT AATTGGCTTT	900
AGAGATTTTT ATATGTAAAA TAGAATTTCT TGCAAGAAAA ACCTTTTTGT AATTACATT	960
TTTAACTGGG AATATTTATT ATAGACTTTT TCCGCTATtG GTTTTGTTTT TTTAATGTAC	1020
TCTAAATATA TGTTAATATT ATGTCTTACC GCAGTTATGG AGTGnTCGTC TTTTAGnGTT	1080
GATAAGTCTG GATAAGGATA TCnGGATAAT TGGATCATTA ACTTTAACTT TTGGTTTAGC	1140
CAAAAAnGnT ACCAGGnACA TAACATACTC TGAAAGT	1177

(2) INFORMATION FOR SEQ ID NO: 87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1137 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

TCACGnCCAT GTtGtAAAAC TGTTCATCAG AAAGTTCAGT TAACAAAATG TAGTCATGAC	60
TACCTAATGT CACTTCAATG TTAAAAACat AAgTTATCGT TTTGGGATCT CTTAAGCTTA	120
TTACAGGCAT ACCTTTATCT TCACTACTAA TTACTGCTCT TGTTGTAGGT TCGCTTGTA	180
GCTCTAGTTT GCCACTATGT AGCTGTGTAC CACCAATTGA AAAATAAACT TCTCTTAAAT	240
CATAAAATTG CATTTTAGCC CCCCTTTTAA GCACTTAAGC TGTTTGTATA ATCAACTATA	300
TCTTGAGTAG TGATTACTAA AGCAACAGCA TTAATGCTAA AGTTATAAGT AATATTCACA	360

1070

CTAAGTTCTA ATTTAAGTTG TGGTGTAGGA GAAAGGGTAA GGTTTAAGTT TTTATACTCT	420
ATAATCAATC CCCTGTCGAC AAACCTTTTA AGAAGACATT CAATTGCTGA AGTATATGCA	480
TTGTCTCTAG CACCACTAAG TTGTAGTGCA GATAATTTGC TATTTTGCCT ATTGTTTTTG	540
TTCCAAATTC TAATAAGCTC AATAATCGCT TCATTTTTTA TATAATGATA AGTGAAAAGC	600
TCGTCTATTG AACTTCCAGC AAGATCAACG CTCTCTTTAA AGGCAGGCAT ACCATCAAGA	660
CCAGTTTCAT TAAGAAGTGA ATAAAAGTTG ATTTTTCAG TTCGCAACTT TCCAATTACA	720
GTATCATCAA CAAGTGGTGT AGCAGCCAGC GGCATGCCAT AAGGATTTAC AGCATGAAAA	780
ATACTAGCCT GATGTAAATA TTGACTTATA AATTTGAGGT GTAAATTGTC TTTATTATTA	840
CTGTAAACAG CAATATTTCT TTCTTTTCA GTATTGCCCT TATCTTTAAA TAGTTCTTTT	900
ATTTCTTGTT CTTTAGTCGA GAATACAAA AAAATTGAAG GTGTTTTAA CTTATCATAA	960
TCATCTTTAT AAATCTTAAG TCCATCATCG GAATTATCAC CCTCAGTATT AATAAGTACA	1020
ACAAAAGTGT GTCTATGTAC TTTAAGATAT TTTTAACT CTTCGGGTT ATCCTTATAA	1080
ATAAAAAGAA CAGCGGATTT TAATGATTCT TCACTTGAAT TGAAAAAATT TGACATT	1137

(2) INFORMATION FOR SEQ ID NO: 88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1091 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

GTGATTTTTG AAAGATATGG ATGATTGTAG GTATTTATGA TGTCGCACTC AAAATTATTT	60
TCAGGTGCAT ACGCCTTAAA CCCTTTAAAT ATTTGAGTTA AATGATTTAA TACCATATCT	120
AAAGTGAAAA TCATTCAAGT GTTACCTTAT AAGTAATCTC TGATAACATT TTGGCTGTAT	180
CAACAAGTGG AATTGCTGCA GTGTTACTAC CCCTTTTAAA CTTACTTTTG ATTGTATTAG	240
CCTTTAAGGC TGGAGTGACT TGTGCTGATA GTAGATAATT TTCATAGTAC CTTATAAAAG	300
CTTGTCCAAT AGCCTCCATT CCCTATTTAG GGTCAAGATT AACTTAGAA TTTATATAGC	360
TATTATTGAT ATATTCTCTA AACTCArAAC TACTAGcAAT TTTGGTTAAA TGTTTTCTTG	420
CTGGTAAATT GCTATTCCTT TTTTCATGCA TTTTAGCAAT ACCTGCACGA CCACCAAACC	480
ACCCAATTTT CAATTCCATT TTAAATTCTA GTTTGTCCAT ATAAATTCCT TTAAACCAA	540
AGTAAATAT CCGATTGAAG AGTCAATACT AAATATTTCA AAGTAAACTA AATCTGCAAT	600

1071

TGATATTCGG	TCTTTTAGTT	CATAGTTAAG	GTCTTGATAT	GTGTAAAGTT	TGGAATATCC	660
TTGAATATCA	GACATATCAG	AATCATAAAG	AATTGCAAGT	TCTTGTGGCT	TTATGTCAAT	720
AATAACTCCT	GCGAATTCAG	TGTACTTATT	TTTATCAAAT	ACTCTCTGAT	AAGAAGAATC	780
ATTTTCAAGC	TTTACAACAG	TACCTTTATA	AAACTTTAAG	GGTTTAGGAT	CCTTAAATAC	840
GTTGATCAT	CGAAATGACA	TATCAGAAAG	TCTTTTCTA	ACACCATTCA	TTAGACAAC	900
CCCACACAAG	ATGGCGTTGA	AGTTTCTCTT	TTTATTTT	CTAAAAATGC	ATCAAGTTGT	960
GAACAAAAA	TCTTGTTTGA	GCCACAACCC	CCCTCGCCAC	CTTCTTCGCC	TCCACTGCTA	1020
CTAGGATAAT	AATCAAGTTC	AAGTTCATTG	AATTTCTCTT	TTTTGATCCT	ATCAAATTC	1080
AATTCTCGAA	C					1091

(2) INFORMATION FOR SEQ ID NO: 89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1081 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

GGGAAATAAA	TTCAAGAAGC	AGGTATAATA	ATTTTTATAA	AAAAGAAGCA	GATTTTTTAG	60
GTGCTGCTGT	AGAACTTGAG	GGGGCTTATA	AAGCTATTAA	GCAAACCTTA	TTATAGATCA	120
CAAGGTATAA	ATTTAAGGCT	TAAGCCAATT	TATCAAAAGA	GAGGCATGTT	TCTTGTTTTA	180
AAAGCATACT	TTGCATACTT	CTCTTTTGAG	TACTACTATT	TGAAAAGCTA	TAAACTTTAA	240
CCTAATAGAA	AAGCCAAATC	TTTTTAAAAA	TTTCTAAAAA	ATAATTCTAC	ATACTCTCCT	300
TATTACATTA	AAAAATATTA	TTGCTTATAT	AAGGCACATA	GTATAAAGAC	ATTAATCAAA	360
ATTACCTTTT	ACTAAGGTTT	CAATCTCTCT	AAACATGGAT	AAGAACTACT	TGATCAAGTT	420
ATAACAATCA	AAACCCACTT	TCTTTAAATA	AAAAATCTTT	TAATAATAAA	ACCAAAATTC	480
CAGCCTTACT	AAAGACCCTT	ACTCTCTCGT	GGATTTAATC	TTCTTTATAT	ATAAGGGTTA	540
GGCGTATCTA	AAGATTTAAT	CATTTTGAAT	GATAGGGAAG	AAGAATTCAT	AAAGAATAGG	600
CAAAAGTGGT	TTAGTTTACT	GGAGCATATA	CATTTAATTA	TAAATAAGAA	ACAATATTTT	660
CCATAAGAAC	TGGAGTATAT	AAATCATAAG	AATAACTATT	TTATAAAGAA	TAAGTAAAAG	720
TAGTTTAGTT	TACTGGAGTA	TTTATCTATG	TTAAAAGTAA	ACGCACGGCG	TATAAAGCCC	780
CTACTATAGT	ATCCAATATT	TTTGAATTT	AGGTCAATGT	TGTTTAGTGT	GTAAATAAGA	840
ATTATTAAGT	GTGAAGATAG	CCTATTTTTG	CTATTCATAC	TTAATATTTT	TTTTAAAAAT	900

1072

TTTTCCAAAT AGTGCCCCAG TAATTTTTAT TATTATCAA ATAAAAATAT ATGTCTTTAC 960
 ATTTATATTT CTAAATTGCT TAATTTGCAA AGAAATATTT TTTACGATTA AATAGTAGTA 1020
 GGATAGTTTA GTTCTAACCG GAGTTTTAGT TTATCTGGTA TTGGTTGATA GTAGnChTGT 1080
 A 1081

(2) INFORMATION FOR SEQ ID NO: 90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1078 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

GATCCATATG TGTCCCCTTT ATTTTAAAT AAAAGATATA TATTAAAGA CAGTTAGGCC 60
 TCTTTTAGGC ATATTTTGT TTAATAAAAA ATATTAAATT AGGGTTTATA ATTTTATAG 120
 ATGAAAATAA AATAGAAGAA TCTAATTTAA CTAAACAATT TTTGTTTAGT TAAATGATA 180
 TAGGGCTTTG CAAAGTAGAT ATAATTAAAG AAAATCTAAA ATCGCTAAAT AAAACTATTT 240
 AAAC TAAGCC CCATAATGAA AAAGTTT TAG TAAAAATATT AAAGAATATT TTTACTAAAA 300
 TAAAAATTAA ACCAGCATTA ATAATACTTA CATTAGATGA TTAGCTACTT TTTTAAATTA 360
 ATAAATTTTG CATTTAAAGT TCTATCCAC TTATAAATAT TGACTATATC AATAATTTTT 420
 CaAGCATTGG TACATTTTAT ATTCTAAATA TTTCGTTTGG TCGCTAATT GTTGACATAG 480
 GAATTATAAA AAGGCCATCA TCTTTTAAAT TAAAAAGTAA AATAACTA ATAAATAAAG 540
 ACCATCAAGC CCCGTCCTTT TTTTACTAAT AATACAATTG CATTGATTAT GGTGTTATT 600
 GATATTATTT TTTACTTTGA CAATGAATAT GAAAAAATTC TTTATTCTAA ATAAAGAAAT 660
 TGGTATTGGT AATTGCAATT TATTATTTTA TTTATATTTT TTAAAAAATA TAAATAAAAT 720
 ATAATAAAGA TTTATGGTAG AAAGCAAACA TCAAAAATAT TATTTTTATT CATTATTTTT 780
 GTCAGAACTT GCAAGGACTT TGCCACATGC TGTATTAAT ATTATTTTAA TAAATAAAGG 840
 GTTATCACTA AAAGATATTG CTATGGTACA AATTTGTTAT ATGGTAGCAA TTATTATTTT 900
 TGAATTTCCA TCAGGTGTAA TATCAGATAT TTTTGATAGA AAAATTGTTT ACTTGGTGTC 960
 AATTTTCTA TTAaTGmCTT CTATTTTAT TGTGCTAAA ACCTCTTCAT TCGnGTTTAT 1020
 TTGTGTTTCA GGTTTATAnA nGGGATGTCA GcNGcNATAG CACTGGCACG ATGACATA 1078

(2) INFORMATION FOR SEQ ID NO: 91:

1073

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1030 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

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CCATTTTAAA AAATCAAATT TTACAATACA TTATTATTTG CCACCTTGTA AATATTTTCAT      60
AAATAGGGCA TTCAAAATTG GCCCTAGAAT TGCTGCTGTT ATTATCATAA AATGTACTAG      120
TCTGTTACCC ATGCTAAGTT TTTGATTTAA ACTCTTTTCT ACATTGTCTA TTTTGATATT      180
CAAGCCATCC ATTTTtaggt TTAAATTCTT TTCAACATTG TCTATTTTAG TGTTTAAATT      240
CTTTTCTACA GTATCTATTT TAGAGTCTAA ATTATCCATT TTTAGGTTTA AATTCTTTTC      300
AACATTGTCT ATTTTAGTGT TTAAATTCTT TTCTACAGTA TCTATTTTAG AGTCTAAATT      360
ATCTATTTTT AGATTTAAAT TCTTTTCAAC ATTGTCTATT TTAGTGTTTA AATTCTTTC      420
TACAGTATCA ATCTTATrT CTAAATTAGA TATATCCTTT TGTAATTTCT TTTCTACAGT      480
ATCTATCTTA GTATCTAAAC TATCTATTTT TAGATTTAAA TTCTTTTCCA CACTATCTAT      540
TTTGGCATTT AAATTCCTCT CTACACCATC TATTTTGGCA TTAAATTCT TCTCTACACC      600
ATCTATTTTG GCATTTAAAT TCTTCTCTAC AGTATCAATC TTAACGTCTA AATTGGATAT      660
ATCTTTTTGT AAATtCTTTt CTACGCTATC AATCTTAAAA ATAAGATTAT CAAATTTTAT      720
ATCAAATTGT TTTTCTAAAT TTTCTAAATC TCTATATGTT AGCTCATTGT GATAATATCT      780
TTTAGATAAA TCTTGTGCTA TTAGTTGTTT CATACCCAGT CTAATAAATT CTTTATATAT      840
TTGTTCTTGA GTTACACTTG CAATATTTGT TGACACTGTT TCCATAAAAT TTCCCTTAT      900
GGTCATATTA TATACTATTT TAGATTAATT GGCTTtAGAG ATTTTATAT GTAAAATAGA      960
aTTTCTTGCA AGAAAAACCT TTTTGTAATT TACATTTTtA ACTGGAATA TTTATTATAG      1020
ACTTTTTTCG                                     1030

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(2) INFORMATION FOR SEQ ID NO: 92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1028 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

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TTTTGTTGAA TTTCTGTTA AATTTCTGA ATTGGTGTGA TTGCTTGTGT TTTTtagATT      60

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1074

TCTAGAATTG TTGCTTCGTT TTGTTTTTTT TAGACTTTTA GAAGTGGTAG GATTTTTTGG	120
TTCGTTTGGG TTAACATTGC CAAAAGGTGC ACATGATATG CAAATTGAAG TTAATATTGC	180
TGTAATAACG TTAAGTTTAA TAATATTTAA TTTAAAGTTT TTCAAAATAT TCTCCTTATA	240
AATTTGAATT AATATTATT AATTTTAGTT CAAATATATA ATATTACAAT TTAATATCAA	300
TATCAAATAA GTTTAATATT ATTTGATATT GAAAATTTAA TTTCTATTGA TGTTTTTAGC	360
GTGGATTAG ATTGCATGAA TTTTAAAAAT AAAAGTTAAT TCTTCTCTTT TTAATAATG	420
AAGTGTAACA ATTTGTTTGG ATTTAATGGG TTTAATCTAA GGATCAAGAT GAGGAATTTA	480
GAAATTATAA CGAACTAAAA GAACAATTAA AATTAAATTT GAAATCTGAT ATTAATAATA	540
AAATTCAAGA AATGAAAATT CTACACGAAA TTAAGCAAAA ATAACTTTAT AAATATGACT	600
GTTTTTAAAAG TTTTAAGCAG TTTATAAAGT CTTATGTAAT TGCCAGAAGT CAAGTGATA	660
TGTATTTGAA AATTTATGAG AAAGTTTATG AAGGGTTTAT TTCTATTGAA AAAGTTAAGG	720
AAATGGGGTT TGTAGCTGCA TATAAAAATA TACTAAAGAA CAACTCGTCA TATGTATATA	780
AAGAAAACAT GATTGAAGAA AATATAGCAG AAGATGGTGA TAGTCAAAAT ATGTCTATTA	840
AAATTTTAAT TAAAGATAAA GAAGTTTATG ATTTTTCGAA AAAAGATACT AAAAGAATAT	900
CTTTTATTTT AGGGGGGTTT ATTAAAGCAT TATTGAATTA AGTTGGAGAA TTTTCTTTT	960
TGTATTTTTA TTAGCAATAT ATTTTCCCAT AGAGGCTTTT TGTGTCTACT AGAATAGGTA	1020
ATAAGATT	1028

(2) INFORMATION FOR SEQ ID NO: 93:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1002 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

AATTTTnAA AAAAAAAAAAT TTTTTTTTTT AACCCCCAGG GnAAAAATTG GGGAAAACCC	60
CCCCAAGGCC GTCCTTTATG GGTCTGCCT TTAGCCCCAG AGGACGTAA AATTGGATTT	120
ATTCAACTT TTTATAATTA AAATTGGCAC TGTAAGGAGT TTAAACAACA AACTCAGAGG	180
CTATTGTTAC AATACCCGAA TTTGAAGATT TAGAAATTCA CACAAAAAAT ATCTCTAATA	240
TCAGTTTAGA ATTATCAAAA GGTGATAACG TATTGCTACT TCAATCAAGC GTTAATATTT	300
TTGATAAAAA TAACGATAYC CACTTTGACA AACATCATTT TTATATACTT AGTGCAATTA	360

1075

GCCCAAAGAC TTTAAATCTA ATTTCTGATA CTGTTAAAAT TAAAGCAAAC AATAAAATTG 420
 AAATAGCCAA TGAAATAACT TCCTTAAAAT CAATTCTAGA GAGTATTGTA AGTGCTATTA 480
 ATGGAATTAC TGTAAGGA CAAGCGGTCG TTGACTATGC AAGCTTACAA ATAGCAACAT 540
 CTAGAATTAG CAATAATATT AATAGTTTGT TTAAGTAATT TTTGCTAATT ATGGTATAAT 600
 TACTAGTATG GATTTAAGAT TAGGCAATAA TTTTGAATTG GTATTTAATA AAGATATATC 660
 ACTTGTGAT GGAATTGATG AACAAAAACA AAGaTTTTTG ATATTTTTTAA AAACCTTAAG 720
 GGGTAGTTTA AGCTATGCTC CTCATTGGGG ATTGGACTAT TTCTTACTTT TAAAACTGTT 780
 AAAAATTAAC AATCTTCACG CTGTAAAAA TTATTTTCAT GAAATATCTA AAGAGCTTAA 840
 CTTAGrTTTA ATAAATATTT CAACTACTAT ACAAGACAAC AAAGCACATA TATCCyTTTT 900
 TTTCTCGGGC GATGTTTTTAA ATATGGAGtT TAATTTaTGA GctAGTTTTT GATTCTGrTT 960
 TgGcwTTTTAA AACGTACatT AAGGgTATTG TAAGAGCTAA AA 1002

(2) INFORMATION FOR SEQ ID NO: 94:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 998 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

GGGCATTATG TACTGATAAT GATGATGCTT TAGAAGATCT TTTTAAAAAG AATGCTGAGC 60
 TTAAGAGTAT AGAATATTGG GTAAATATTT TAAAAAATA TTTCAATAAA ACTAATAGAT 120
 TTGATGATCT AAATAAGCTT AAAGTATTTA TGTCTGATAA TCGAGACGTT TATAAAACAA 180
 AAGTATTAAA ATTCTTTTGC ATGTTGAAAA AAGAAAGACA ATTTAATTAT ATATTTGCAG 240
 CATAGCAATA TTAAAGCCCC CAAATAGGGG GCTGTTAGCT ATTAGGAACC ACCATTGTTG 300
 CAGTTACTAA CCGCATGTGT TGCAAAATTA TCTATATTGC CGCCGCTAAA GAAACCCTGA 360
 ACTGTTTGTT TGAAGGTGCT TTTTGTGTGT TCAGAATTAT CCCCAGTACA CTTATCAAGT 420
 TCACTCTTTA TATGATTAAG TGCAGATTTT ATTTTGCTTT CATCATATCC TAAAAATTTA 480
 TCAAATTCTC CATCATTACC CAGAGCTTCT TTAAACCAGT CAAGGTGTGT TTTCTGGTCT 540
 TCAGATAGCT TTTCTCTAAG TAGTTCTTCT TTAGATTTAG GTTTTTCTGG TGTGCTTCT 600
 TTTTGGGTTA AATCACGCTT TCCCCTGCTT TTGTTTGTGT GTGCATTGTT TTTTAAAGTG 660
 TCATTATCAT TAGAATTGCA GCTATTTAGT AGTAGTAAAA ATAAACAAA TAATATGTTG 720
 ATGATTTTCA TTGTTATTTT CTTTCCTTAT CTCCAGTACA ATATGTTGAG TAAAAATAAA 780

1076

ATTTATTCTT GTAATTATAG AGCTTATTTT TAAAAATCTT TAAAAATATT AATTGAGAGA 840
TTTATATTTT TCGAATGTTG TGCTAGCnTT TATTTTATTA TTATTGAATA TAGGAGTAAC 900
TAATGAGAAA TAAAAACATA TTAAATTAT TTTTGCATCA AGGGATTTGT AATGGCTGTA 960
AAGCATATGT AGAAGAAAAG AAAGAAATGA TCATAATG 998

(2) INFORMATION FOR SEQ ID NO: 95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 996 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

AAAAATATTT TTATTTATAT TTTATTGTAA TTATTCTTAA ATGATATATA ATATCAATTA 60
AGAATAATTA TTATTTATAA TATATATTCC TACTTAGATA AAAGGAGATA TTTTATGAG 120
AAAAAGTTTG TTTTATATA CATTATTAAT GGGAGGATTG ATGTCTTGCA ATTTAGATTG 180
CAAATTATCT AGTAACAAAG AACAAAAAAA TAACAATAAT GTAAAAGAAG TTTCGAATAG 240
TGTCAAGAA GATGGTCTTA ATGATTTATA TAGTAATCAA GAAAAGCAAA AAAGCTTTAC 300
TAAAAATTTT GGAGAATGGA AATATGAGGA TTAAATTAAT CCTATAGAGC CTATAATACC 360
TTCAGAATCA CCAAGAATA AGGCTAATAT ACCAAATATT TCAATTGTGC ATACTCAAAA 420
AAAAGAGATA AAAGAGGAGG ATTTAATCCC TTCTACTAAT GAAGAAAAGG AAGCTGATGA 480
AGCAATTAAA TATTTAGAAG AAAATATTCT TCAAACTCT AAATTTTCTG AATTAATTAG 540
AGAAGTACGT GTACTTAAAG ATGAATATGC TTAAATAAAC TCTGATTTTT ATGATGTAAT 600
TGAAAAGATT CACAATAAAA AAACATCATT AATGGAAAAT TATAAGAACA ATAGAGATAA 660
GATAAATAAA TTAACACTGT TGCAAAATAA TTAAAGATA AATATTGAAC TTGAGCAGCT 720
TATAAATATG ATTGATATTG CAGAAAATGA AATAAGATCT GCGGCTTTCT TTTTGTACAC 780
CGCTCAGAAA AGGTAAAAG AAAGTATTAT TAAAAGATTA GAGAGTAAAA ATAATAGATC 840
TTATTATGCA TTAGAATTGT CTAGACAGGC TTTAAGTGAC GCAAGAAGTG CTTTAAGCAG 900
TTTAGAATCT TTTGCTTTTA AAAGAGCTGA ACCAATGGTA AGAAAGAAAA AAATAAAAGA 960
GCTTATTAAA CATGCAAAAA CTGTTTGTAGA AAGTCG 996

(2) INFORMATION FOR SEQ ID NO: 96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 986 base pairs

1077

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

CGGACTATAT ATACTAAAAG GGACTTGTGC TTGTATTCTA TTGGCTAGTT GTTCTTTTAC	60
AAGATGAGCG TCAAAGCGTA CATaGTATTG CCAAAAACAG TCATTTTGAG TAAAGAAATC	120
ATATCCTTAT ATAAGGATGT TAGTATTCCC CCGTTTAATG AkATATGTTT ACCAGTCATT	180
ACCGGATTGT AGCTTACATA TTCCGCTTTT CTATCATAAT AATTGATAAC TGGTCTTTTA	240
GAACAAC TAG TATTATAAGT GCGTGTTATG AGTTCATTTT TTGGTTTAT AAAAAACAAT	300
TGAGGAATAT ATCCAAAACC TTTTAGATCC ATTCTAGGAA ATAACACTAA AAAATTATCT	360
GcTCCGAAAA GGGCAAATAT TTGGGTTATt ACATCTCTTA TTATTCGAGT AATCTCCCTG	420
ATTTCTTcTT TtCAATATCA TTAATTTTTT CCTTGATTTT TTTCTTTtCA ATATCATGAT	480
TGTTAGTAAT TTTATTATTA ATATCTATTT TGTTAGCTGC ATTGTTAGCA ATTTTTTTGT	540
TACTTGTCAT AAGTAATTAC CTTTGTGAAA AATTATGGTG TGCTGTTAGC ATTGTCTgAT	600
TTTGAATTC TTCTTGAGT TTTTGTAGAG CCGCACCTC ATCTCCGCC ATCCATCCAG	660
GTAGCATCGA TTTtAATTTk GCAAAGAAAT AATtAAGATt AAAAATACTT TtAATGCCAT	720
tAATtAtGGG ATAATAAtGT GTGTTTCAAA CGCAAaGTCT TtAAaGTAAT aGTTATCTTA	780
TAAGAGGTCA AGTAAGGGTC CAAGACAGTA GTGGTTAAGT TTTGAAGAGT TTGCTCAGCT	840
GAGGCCAAAT TACTTGAATA CTCTCAGCAT ATTGACTTTT TTGTAAGGCC GAAAGATTAA	900
AATCCTCGAA CATTTCCATC ATCTGGTAAn TCTAGACTCT AGAnCTACTT GTGCCCCGCT	960
TTGCCAGGCC ATTTGGCATC TTCTAT	986

(2) INFORMATION FOR SEQ ID NO: 97:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 976 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

ATTGAGCACT CCTTTACATA TTCATCAAGC TCGCTTTTTA AAGAATTAAT TTCTCCATTA	60
ACAACTTGCT TGTTTTTTTT ACTACTTGCT TTATTAAAG CGTCAATTTC GGCTCTTAAA	120
TTTTCTATTT TAGTATGCAT ACTAACAAGC TCAACACTAG AATATTGCTT AAATGCATTT	180

1078

ATAAATCCTA ATTCTAAATT AGCCCGCTCT AAATCCAATT CGCTTCTAAC TTTCCTAGCG	240
TTAACTTCTG ATCTAAAGGT TTGCGACAAA AGGTGTTCAA AAGTATCTTC ACTAATTGTT	300
ACTCTAGAAT CCTCGCTAAC AGAAGTTTCT CCACTTTCCC ATTTTGTCT CATCTCCAC	360
ACATTTACCC TAGAACTCC CAATTTAACC GATATTTCTC TATCATCTAA CGATCCTTCT	420
CTAAAGTATG CAACATAATC ATtAAAAGAC CTTTtagctc TTTTCAAAAC AATTTCTCCT	480
AAAATAACTA AATTAACAAA TTGTTACTCT AAATAGTAAA TCAATTGTT AATGTTAAC	540
ATTAACtATT ATCTTATTGA TATCTATTGA CAGGTGTTTG GTATTTTTTT GACTTTTATT	600
GATTTAGAAA TAGCAATTAA CTAATTTATT GAATTTTGCA ACAACTTGAC TATATAAATT	660
AGGGAAAATC TTTTATTGTT TTAATTAGAT CATCGCTTGT AAAAATTCTC TTATCATAGT	720
TGTGkATCCT TATAAATAGT ATATCTTTAA ATTCGTTGAT CATAATTAAT TGATATTGTT	780
TTGAAACTTT TTGATAAATA TGGTTAAGAA TACCATAAAC AGCCCCAAA AATATCATGG	840
AATCATACTC TCCTAATTTT TTCAAACATT TCTTTAGCAT CCCTTCTTG TCGCTATAAT	900
CAACTTGCAT ATTTTTGGAA TTTTATATT TTnTATTAA ATATTTATTT TTCAGAACGT	960
CTTTAATAAT TTnTT	976

(2) INFORMATION FOR SEQ ID NO: 98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 968 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

GTCAGGCTTT TTACAGAAAT TATTATAATA AATAAAAGCT TTATTCaATT CTCATGTTAA	60
AGAGCTTAAT AAAGCCGCGG GCTTAGCTCA ATTTATTTTA GATAAACTCA CTAAACGATT	120
AAATTCAGTT CAATTTAGAA TTAAAATTAT TTTGTATTTG TTAAAATAAA AGAACCTATT	180
TAAATTCTCT TGTTAAAAAA TTCAAATAAT TTCTACTTTA AAGCTATATA CTAACtTATT	240
ACTTTATAAA ATTTTAATCA TTCTTAATTT AAAAAATACT TATTGAATAT AGAATAAATA	300
ATTGGAGCAA GTGTTATTCC CATtATTAAA ATTACTTGTA TTGTTCTATT ACTTGcAGTA	360
AGTTCGTTTT TTAAACATT TATTTTATTA TCTAGGTTAA ATATATCCTT TTGTaAGGTT	420
TTTTCTACAC TATCTATTTT AGTATTCAAG CTAGATATAT CTTTTTGCAA AGTTTTTTCT	480
ACATTATCTA TCTTAGTATC TAAACTATCT ATTTTGGCAT TTAAGCTCTT TTCTACATTG	540

1079

TCTATTTTGG CGTCTAAACT ATCTATTTTA GAATTAAAGTT CATTTTAAAC ACTATCTATT	600
TTAATATTTA AATTCTTCTC TACATTATCT ATCTTAGTAT CTAAACTATC TATTTTGGCA	660
TTTAAGCTCT TTTCTACATT GTCTATTTTG ATATTCAAAC CATCTATTTT TAAATTTAAA	720
TTCTTTTCCA CATTGTCTAT TTTGGCATCT AAATTAGATA TGTCTTTTGT CAAATTCCTC	780
TCTATATCAA TTATTTTCTC TTTTAAAAAT TCAAAGTTGT AATaTCATTA TGCAGAAAAA	840
CAAAATCTAT gCTtCCTgCT AAACCTATA TTAAAAATTC GTTTTAAATA CCTTTCTAAT	900
GGTTAATAAT GGTTTGGTAA TGGCCTAAAA TTGGTTCCAT AAGGATTAAAC CCTTTTAAAT	960
GGTTTATA	968

(2) INFORMATION FOR SEQ ID NO: 99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 954 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

GCAGGTCGAC TCTAGAGGAT CCCCTTTAAAC TAGAATTTTT CAAAATGATA AAACCTTAAAC	60
CCGAAATGAT AAAACTTTAA TTTTGGCAAT TTTATTCTCT TGTTTTTTTT AAAACGATTA	120
GAATAATCGT TGAKCAGGTT TATTGATTAT CAATAAACCT GATCTATAAT ATTATAAGCG	180
GTPTTTGCAA GTPTAATAGG AGCTATAATA TCCATGAACA AATTATTGAT ATTCATTATT	240
TTATTAGTCT TTTCATGTAA TTTAAGTAAT TCTGATCAAA ATAATCCACT AAACATGTCA	300
AATAAGAAAA AAATAAGCGA ATATCAAATA AATGAGTCGT CAAACAAATA TTCAATTTTC	360
AAACGAAATT CAAGCGTTAA AAGATACACG TTCAACCATT ATTACTAACC AAAATGATAA	420
TATTAATTCT ACTATTAACCT ACCCACCTTA TATTCAAACCT ATCTTAAAAA TAGAAAAACA	480
AGTTGACGGA AATATTAATG GGATGACTAA AGAAAGTGGC ACAGAACTA AAAAGCTTTT	540
AGAAATCTA AATGGGAATA TTTCTCGATT TAAAGATGCA ATTCAATATG GAGGAAGTTT	600
TAGGGCTAAA GATGTTAGAG AAAATCAAAC CCAAAAAGAA AACAACAAAG ACTCGCATAT	660
TCATGTCGAC GATTTTAAAG AATACATACA TTTAATCATG CCTAGCATTA cAATAATGCT	720
GATAGTAGTA GTAGTTATTA CTATACCAAC TACATAATAA ATGGAGACAA TTTGTkaAGA	780
ATTATTAGCA ACTTATAAaA AATCTTTATA AATTACCAAT ATTCTTGACA ATTTTAATAC	840
TATTTTTTTT ATATACTATA ATATTATGAA AAAAAATCAA AAAAAACAAGT GCTCAGAAAT	900
AGAAAAACA CAATTAGAAA TAATAAATAA CCAATCAGAA ATAGAAAAAC AACG	954

1080

(2) INFORMATION FOR SEQ ID NO: 100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 946 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

AGAAGAAAAT AAATTATACA GATCTTCTGT ATCTTTTAGA TATTTTTTTT ATGATGAAAA	60
TACAAAAAAG AAATTAGGGT ATAAAAAAT AATAACAATT TTCAATTTCG TTGATAAAGG	120
AAGTGATGCA ATAAAGTTTC CCATA'TTTAA TGGAGGATTA TTTGCACAAG ATAAGGTTAA	180
ATATTTAAAT AATGAAAGTT TACTCAGTAT TAGTGAGATT GAAGAAATAT TAGTCAAAAT	240
ACTTTTCTTT GAAGAAAAAA ATATTAAAGA TAAAAAATTT GTAAATATT CAAGGCTAGA	300
TCCTAAAAGC TTTGGAGAAT TATACGAAAC TCTACTTGAA TATGACCTAA GAATTGCAGA	360
TACTACTGTT CATCGTATTG TTGAAGACGG GATTTATCTC ATTCGTACTG AAGAAGAGCT	420
TGAAAACAAT AAAGTAAACA AAATTGCTAC ATATCTTAAA GGGAATATTT ATCTTACATC	480
TAGATCACTT GATAGAAAGA AAAGTGGGGC ATATTATACT CCAGATGATT TAACTGATTT	540
TATGGTTATA TCATCAATTG AAGAGCAGCT TAAACCAAG TCCCCTTTAG ATATAAAAAT	600
CATTGATAAT TCTTGTGGAT CAGGGCATT TTTAATTTCT TGTCTAGATT ACTTAACAGA	660
AAAGGTATGG TACGAGCTAG ATAAATTTGA AGATGTAAAA AAAGAGCTTG ATAAAGAATA	720
TGGGATTATT CTAAAGAAA GTGAGGAGTA TGATATTCAA GATAGTATAA GTAAAGAATT	780
GGTGCTTAAA AGGATGCTGC TAAAGAGGTG TATTTATGGT GTTGATATTA ATCCTATTTT	840
GTTTGAAATT ACTATGCTAA GTTTGTGGAT TAATACCTTT ATTTTGGAA CGCCACTAAG	900
CTTTATTGAG CATCATATAA AACAGGAAA TGCTCTCTTG GGATAT	946

(2) INFORMATION FOR SEQ ID NO: 101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 913 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

CTTTGACTCA AAAC'TTACC CTTTAAATTG CTAAC'TTAA CTTGAAAATA CTAAACTTTA	60
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1081

ACCCGAAATA ATAAACTTT AACTAGAATT TTTCAAAATG ATAAACTTT AATTTTTGCA	120
ATTTTATTCT CTGTGTTTTT TTAAACGAT TAGAATAATC GTTGAKCAGG TTTATTGATT	180
ATCAATAAAC CTGATCTATA ATATTATAAG CGGTTTTTGC AAGTTTAATA GGAGCTATAA	240
TATCCATGAA CAAATTATTG ATATTCATTA TTTTATTAGT CTTTTCATGT AATTTAAGTA	300
ATTCTGATCA AAATAATCCA CTAAACATGT CAAATAAGA AAAAATAAGC GAATATCAAA	360
TAAATGAGTC GTCAAACAAA TATTCAATTT TCAAACGAAA TTCAAGCGTT AAAAGATACA	420
CGTTCAACCA TTATTACTAA CCAAATGAT AATATTAATT CTACTATTAA CTACCCACCT	480
TATATTCAAA CTATCTTAAA AATAGAAAA CAAGTTGACG GAAATATTAT TATTAATGGG	540
ATGACTAAAG AAAGTGGCAC AGAACTAAA AAGCTTTTAG AAATTCCAA TGGGAATATT	600
TCTCGACTTA AAGATGCAAT TCAATATGGA GGAAGTTTGA GGGCTAAAGA TGTTAGAGAA	660
AATCAAACCC AAAAAGAAAA CAACAAAGAC TCGCATATTC ATGTCGACrA TTTTAAAGAA	720
TACATACATT TAATCATGCC TAGCATTAAC AATAATGCTG ATAGTAGTAG TAGTTATTAC	780
TATACCAACT ACATAATAAA TGGAGACAAT TTGTTAAGAA TTATTAGCAA CTTATAAAAT	840
ATCTTTATAA ATTACCAATA TTCTTGArAA TTTTAATACT ATTTkgTTaT ATACTATAAT	900
ATTAAGAGAA AGA	913

(2) INFORMATION FOR SEQ ID NO: 102:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 910 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

TCGCTATnnG AGCTCGGTAC CCTGATAAGG CGAGTGTGAC GGGGATTGCT AAGGGAATAA	60
AGGAGATTGT TGAAGCTGCT GGGGGGAGTG AAAAGCTGAA AGTTGCTGCT GCTGAAGGGG	120
AGAATAATGA AAAGGCAGGG AAGTTGTTTG GGAAGGCTGG TGCTGGTAAT GCTGGGGACA	180
GTGAGGCTGC TAGCAAGGCG GCTGGTGCTG TTAGTGCTGT TAGTGGGGAG CAGATATTAA	240
GTGCGATTGT TAAGGCTGCT GGTGAGGCTG CGCAGGATGG AGAGAAGCCT GGGGAGGCTA	300
AAAATCCGAT TGCTGCTGCT ATTGGGAAGG GTAATGAGGA TGGTGCGGAG TTTAAGGATG	360
AGATGAAGAA GGATGATCAG ATTGCTGCTG CTATTGCTTT GAGGGGGATG GCTAAGGATG	420
GAAAGTTTGC TGTGAAGAAT GATGAGAAAG GGAAGGCTGA GGGGGCTATT AAGGGAGCTG	480
GCGAGTTGTT GGATAAGCTG GTAAAAGCTG TAAAGACAGC TGAGGGGGCT TCAAGTGGTA	540

1082

CTGCTGCAAT TGGAGAAGTT GTGGCTGATG ATAATGCTGC GAAGGTTGCT GATAAGGCGA	600
GTGTGAAGGG GATTGCTAAG GGGATAAAGG AGATTGTTGA AGCTGCTGGG GGGAGTAAAA	660
AGCTGAAAGT TGCTGCTGCT AAAGAGGGCA ATGAAAAGGC AGGGAAGTTG TTTGGGAAAG	720
TTGATGCTGC TCATGCTGGG GACAGTGAGG CTGCTAGCAA GGCGGCTGGT GCTGTTAGTG	780
CTGTTAGTGG GGA _g CAGATA TTAAGTGCGA TTGTTAAGGC TGCTGGTGCG GCTGCTGGTG	840
ATCAGGAGGG AAAGAAGCCT GGGGATGCTA AAAATCCGAT TGCTGCTGCT ATTGGGAAGG	900
GTGATGCGGA	910

(2) INFORMATION FOR SEQ ID NO: 103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 888 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

AACATGTAAA AGAATAAGCA TTA _{ACT} CGCG CATTCTTTGA TTTAAAACAA CCACCCGAAC	60
TACTAAAAAC CTTATTTTCA ATCGAACTCA TTGATTTTGA ATATTTT _{TTA} AATTTTAAAA	120
GAACATCGTC AAGTTCTTTA ACTGAATCTA AATAAGGATC TTTTGCCTGT ACTTCTTCAG	180
CCTGTCTTGT TTGACGTTTA GATCTAGGAG CAACTGGAAT TTCTGATTCT AGCCCTAATT	240
GTGGATTATC ATCAACATTA GGAGCTTTAG CTTGCCCTTT GCCTTTT _{TAA} GCCATAATTT	300
AATTACCTTT TAAAGCTCTA TTCCCAAAAA CACTAGCAAG CACTATAGAT AACTCTTCGG	360
TTAATTTATG TACTTTTGAA AGTGCTATAG CATTACAGA TTTATCATTT CCCCATTCT	420
TTTCAAGCTC TCCTTGTCGA TTAAAATGCA GCTTATCACC TGGGTTTACA CCATTTCCAT	480
TTTTCTTAAA TGTTAAATAC CCCGTGAAGT TATTTGTAAT TGGA _{ACT} TACA GTTGCCATGC	540
CAGTAACTC ATCTATATCA GTGCATATTC CGTACAAGTC ATCCCCACCA CCAGCCTCAA	600
CTTCTAGTTC TGTTGTACCA TCTGCACTAA AACTAAGCTT GACTCCACGC TTGTATGGAT	660
ACCCTTTAGC AGGATAATTT TCTATTTTGT CTTTACTACT AGTAAAACT CCATCCGAAT	720
TGGAGTAAAT TAGATTTT _{TTA} TCTCTAAAAT CTACAGAATT ACTAAGCAAA CCAGTATCTT	780
GCTGAGGATT TTTCATTAAT GCTTTAATTT CTGCAACTTT TTTATCAAAC TCTTCTTTTA	840
TTTTTGTAAT ACCATCGCTC ATTAAAACT CCTTTAAGCA ATACTGGT	888

(2) INFORMATION FOR SEQ ID NO: 104:

1083

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 883 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

GATAGTAATT AAGTCCTACA ACCAATAGTG TTAAGTTGCA TTAATTTGTT CTTTCCTTAT	60
CGATAGGTCT CTTCTTCCT GATTGAATTT CAGATCATTA GATATTTTGA GACTTTCTTC	120
ATCAGAATTA ACTCAAGTCA ATGCATTGAT TGATTTTCTC ATTTAATGGA GCTAGTGCTT	180
TATTTATTGC TGGGGTTAAT GCACTCTCAA GTCTTTCCAT ATTTGCTGTA TAGATTAATT	240
TAAATGAGA ATACAGCTCA TAAACCAAAA AGAATCCTTT ATGTGCAATT TCATCAAATT	300
CATCTTCAAA TTTAGAAAAT ATATCAATAA GGGTTGATAA AGACGTAAGT CCAAGCTCAA	360
CATTATCTTT GGATAATTTT ATAAGTTAAT CTCTTTTTTT AATGTGATTT TGCCATTAC	420
CATTGCCATT CTAAAAATC TTGCCTATTA CAATAGTCAA TATGTCTTTT AATAAAGGCT	480
TGAGAAGAAT TAACACTCCT AAAACCAATA CTGTTACAAA AATCATTACG GCTATAAGTT	540
TAATTTTCAAT TAAATTGATA AGAAGTTCTG TTAATTTAAT AGTATCCATT TTTAATCCT	600
TTATTTTAAT TTTTATTG TATATACATT ATATCAAAAT CGTAATTTTT GCTAAAAAAG	660
TTTGACGCTT TTAAAGCTGC GGGATGGGGC CCCCTGATAG GTAGGCTCTT TTTGAATAT	720
ACCATCCTTT ATACATGGGA AATCTACTAG ATAGTCCTTG GGGAGCGTC TGTTGCTCA	780
TAAGCCATAC TTGTTTCACT TTCATCGGAA TATCTTAGAT AAAGTACTTT ACTCTCGCTA	840
TTACTGTAGT GTTCTGCGTC AAGCTCAATA TCAAGGTAAA TGG	883

(2) INFORMATION FOR SEQ ID NO: 105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 857 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

CTATTAATTG CCAAAAAACT AAACCAACA AACTTAAAA GGAGAGTCTT ATTGTGATAA	60
TGAGATATAA AATGAAAATT TTAATAAAA ATAAACTTA TGAATATCCG CTGAGAGTAC	120
TTCCCGTCTA TGAATGGGAT AAAGTGCTAG GATTTAATCA AAGTGACGCT GTTTTAAAGC	180
TTAATGAGGT TAAATCTTA AGAGAAATCA CAAGCTTAAT GATAAGTCCA AAATTTTATG	240

1084

ACGAATTCTA TGTGATTTTG GATCAAAATA GAGAATTTAT TTCTTATTAT AAGGACTATC	300
TTGTTGCAAT AATTTACACT GCACAATTTA ATACTTTTCA TTTAGACAAT AATCTAAAAA	360
AGCCCGCTTT AGTATATTTG AGTGAGTATG AAAATAATGT TGGTGATTTT GTTGCTTTtG	420
ACTATATTAA TGAAAATTTT GATTATGAAA AAGTAGCCAC TTCGCTTTCA TCAATTACAT	480
CAAATTCCAA TGAGCTGGTT GCTAAATGAG CAAAAGAAAT AGAGATATTG ATAAAGCTAT	540
TGCAAGTCTT GATGAGACTA GAAAAAATA TTTTAACTTG CTTGACGAGA TTAAGAACGA	600
TAAATACTTT TTCCAGTAA TTATGAATAT TTGCTCATAC TACTCGGTTA AAAAATTGCC	660
TTATGACGAG CTTTtagaAG TCAATAGACT TGCTGAGATT AAATTAGAAA AAGAATTGTA	720
TGAATTAATT TTAAGCAAGT GAGGACTTAG TGAGCGACAA ATTCACCATT AAAtTTAAAG	780
GtATTCyTGA TCaTGCTGCA ACAAAAAAGG GCCATTGAAC CAGGATATTT CTAAAATGGn	840
AAAATTATCn TAAACCT	857

(2) INFORMATION FOR SEQ ID NO: 106:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 846 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

AGTTGTCTT TTGCGAGATG CGCGTCAAAA CGTAGCATAG TATTGCCAAA AACAGTCATT	60
TTAAGTAAAG AAAGCATATC CTTATATAAG GATGTTAGTA TTCCACCGTT TAATGATATG	120
TTTTCAACCAG TCATTACCGG ATTGTAGCTT ACATATCCG CTTTTCTATC ATAATAGTTG	180
ATAACTGGTC TTTTAGAACA ATTAGTATTG TAAGTGCGTG TTATGAGTTC ATTTTTTGGT	240
TTTATAAAAA ACAATTGAGG AACATATCCA AAACCTTTTA GATCCATTCT AGGAAATAAC	300
ACTAAAAAAT TATCTGCTCC GAAAAGGGCA AATATTTGGG TTATTACATC TCTTATTATT	360
CGAGTAATTT CCCCgATTTC TTCTTTTCA ATATCATTA TTTTTTCCTC GATTTTTTCT	420
TTTCAATATC ATTAATTTTT TCCTCGATTT TTTCTTTTC AATATCATTA ATTTTTTCCT	480
CGATTTTTTT CTTTTCAATA TCATGATTGT TAGTAATTTT ATTATTAATA TCTATTTTGT	540
TAGCTGCATT GTTAGCAATT TTTTGTAC TTGTCATAAG TAATTACCTT TTGTAAAAAT	600
TATGGTGTGC TGTTAGCATT GTCTGATTT TGAATTTCTT CTTGTAGTTT TTTTAGAGCC	660
GCACCCTCAT CTCCGCCCAT CCATCCAGGT AGCATCGATT TTAATTTTGC AAAGAAATAA	720

1085

TTAAGATTAA AAATACTTTT AATGCCATaA TTATGGGATT AATAAGTGTG TTTCAAACGC 780
AAAGTCTTAA AGTAATAGTT ATCTTATTAA TGAGGTCAGT AAGGGTCCAA GACGTAGTGG 840
TTAAGT 846

(2) INFORMATION FOR SEQ ID NO: 107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 840 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

CAATGAAATA GTTAGAGAAA TTAAAAATGT TATTA AAAAG CACAATTTGG AGCTTGATAT 60
TGAGCAATAT CCAATTTCTA TAGAGGGTCA ATATGGCATA GTTGATTATA TTAGGACTAC 120
ATTCTACAGT ACAAGTACTG GATATGAATT TTCTTTTGAT ACGCGAATTC CTACAGAAra 180
TTtACAATGG aACAATGAAA ATGGGTCTAA AGTTACAAAT ACAGTGTATC AGATGTTTGG 240
TTCAGGCATT ACTTATGTCA AAAGGTATGC TTTAGTTGCA GCTCTTGGTA TAGAAAGTGA 300
AATAGATACT GATGCAGCTC CTATTTACAA TAACCACGAA AACGAAAATT CTATGCCTAG 360
CAAGCAAGTT AGTGTTAATC AAAAGCAAGA ACAAAAAAGA GAACAAAAAC AAGAAAAAAA 420
TCAACTAAAC AACTTTAATA AAAACTTAAA ATCTGGCAAG GCTTATTGCT ATGAAATTTT 480
TAGAGACGCA CTGTTTAATA TAAAAAATTG GGTAATGAA GGTGAAGAAA AAAATAATAT 540
AAATGCTCTT ATTCGGGCAT TATGTACTGA TAATGATGAT GCTTTAGAGG ATCTTTTGA 600
AAAGAATGCT GAGCTTAAGA ATATAGAATA TTGGGTAAAT ATTCTAAAAA AATATTTCAA 660
TAAAACChAT AGATTTGATG ATCTAAATAA GCTnAAAGTT TTTATGTCTG ATAATCGGGA 720
TGTTTATAAA ACAAAAAAnTA TTAAATTCT TTTGCATGTT AAAAAAAAAA AAGACAATTT 780
AATTATATnT TTGCCAGTGT TGCCATATTA AAGCCCCCCA ATAAGGGGGC TGTTTAnATT 840

(2) INFORMATION FOR SEQ ID NO: 108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

GGCCGACTTT GTTTTATCTA CAATAACTTA TTTTAGTTTG AAAATTACAA GCAAGCCTGA 60

1086

AACCATTCAT TATCCCTATG GACACAACT AATGGAAAGC TTAATAGCTT TTATCATGGG	120
AATAATTATA CTTATGACAG GATTTACACT ATTTCTAAAT ACAACCGGAT TAAATAAATT	180
TATCACTCTT GGGGGAGAGT CTGGATTTAA TCTACACATA CACCAGAACA AAAATAAAAA	240
TGATACTATA TATGAACATG ACCATTGCCA TTCACACGAT CACGATCACG ATCATAACCA	300
CGACCACAAC GAAGAAGACA AAAAAACAT ACTAGAAATA TTTTCAAATA AATGTCTAGA	360
AGCAAAAGCA AGCTTTCGAT AAAACCCGAA GTTGTTCGC TAAAGTGACA AGGATTAAAC	420
AGGATTGTAT TTTTCAGCAG CCTATTTTAT AAACGATCTG CATTTAGTAA ATAGTTTTTA	480
GTTAGGAAAT AATGTAGGAT TACTAAGTGT GATGTCTGAG AGAAGGGACA AGTATTGTAG	540
CGAGCTTAAA TCCTTATTAT CGTTGGCCAG TAATTTAGAG GTAGGGGATC GGGATAAAGG	600
ATTGGCCAGT TTATAAGTTG GAGGGAAGGG CAAAGGATGC CTTAAAATCG GTAATCGCTC	660
CTTAAGGTTT AGGGTTAACA AGTTTGGCCA CCAATTAACC TCCAAAAAAA GGCCAGGCAA	720
AAATACCCAT TAAAGGCAGG ATTTCCGGTT TGGGAATTGG CCCCAGACCA CCTCCAAAAG	780
GGCCATGGAA GGTTCGGGAA ATTGTTAGG TAAA	814

(2) INFORMATION FOR SEQ ID NO: 109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 808 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

GGCAAAACCA GTTCTATTTT GTTCAAAATC AATATTCGAC TCTTCAGAAT TTAGTTTTAA	60
ACTTTTGATT TCATATTTGT TTTCAAACCTC TTCAGTTGAT TCAAATGCTA TTATCTTAGC	120
TATAGGTACT TCTTGACCGA ATATTTTATA GTTATTGTCA TTAATGCTAT AATTAAGTAT	180
AGCTAAAGGT AAGCAATGAA TAAGTTTTGA ATCGGATGGG TGAAAAAATA TAAGAATACT	240
TAAGCTCTCT AAGATTTTCA ATTAAATTGT TATTTTATC TTTTATATCT TTTAAATCAC	300
CAGATTTTGC CCATGTAACA TAACCACTTG CAAGTATTTT AAATGCCTCT CCTTCTTTTA	360
TTTCGTTTAA TTCGGGTTC TTAAGGTAA GACAAATATT GCTATTACTC TCTTCAATGG	420
GCTTTTATC ATATTTTATA ATATTTCCCT CTTC AATTAT CTAAAAATCC AAAACCTCGG	480
TTTGTACT GTTGATTTTT GAAGATTTTG GTGTAGTCAA AAAGCATGAA TAAAATAATG	540
GTATATATAA AAATATATTC AAAATACATA TGTCTTTTT CATAAAATTT TTCCATTAAT	600

1087

TGTATTCTT TCTATTCTC TCTTCACTTT TAAATATTGT TGATAAGCAG TGGGTCTAGG	660
CATAAAACGA TCATACTCAG GGCTCCCCCTC TTCGCCAGAA TACTTAATAT CTGGAGAATA	720
TAACTCGCTT ATACATGAAT ACAGCCAATA AACTTCACTT TTAAATTAT TATTCTGCTC	780
ATTTTTTACC CTACCAAACA ACTTAATC	808

(2) INFORMATION FOR SEQ ID NO: 110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 804 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

TGGGAAACAT TATATCTAAC AACCCCTAGT GGTACTTTAC TTGAGGGGGA CATAGAAATT	60
GATGGCCTCA ATTCAACTGG ACAACGAAAA TCCTACAAAA TATCGCTAGG AAAAAGAAAA	120
TATGTTTATA TGAAAGTAAA GTATAAACTT GACCTTAAAA ACTATCTCTA CTTAAACATA	180
GACTCTCAAA TTAGAGACAT TTATTCTAGG ATTATTTCAA ATAACATTC TGATATGGGA	240
ATTAGCTTTG AATATCAAGA CTTTTTTGCT CCAGTTAATG AAGTTAAAGG AATTAAATTT	300
ATGGAATAA GTGCCTGTAT TAAAGACACA GACACTGAGA GTATTGCAAA AATTACTGAT	360
AGCGATTTTA AAAAAATCA AGATATTACT ATTACTGATG ATACAATGCT CCTTTTCAAT	420
ACTACAGATA GATTGCTTAT TGATATTGAT AGTTAACAAA TATGAAAATA CCTAATTTAT	480
TCAATGGCAC TGAAGTTCAT AAATTTATAC TTACAGAAAC AGAATATGCA CAAGCATTGC	540
TTAATGAACT CAAGTCTCTT AATTCTAACT TCCTATCCAT TAATGTAATA GAAAATATAA	600
AATCAAGATA TATTGCAATA TGGATATCTC AAGTTTTATC TATCTTTTAT GCAAAAACTC	660
AAACTTTACA AAGTATTACA AGCAATATTA ATAGCGTTAT TTTTGCTTTA CGCCATATTG	720
GTACTGATGA GTCGTTTAGA CTAATTTTCA aGGCCTTTTa AATGTGGACA TGAAGTTACT	780
ACTCCTGAAG CGGGGGTATG GAAA	804

(2) INFORMATION FOR SEQ ID NO: 111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 800 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

1088

GCGTGAGATG TTAATTTTAA CCGCTTTAA AGCAGAATAG TCCATCCCCA TGAGGAGCAT	60
AGCTTAAACT nCCCCCTAAG GTTTTAAAA ATATCAAAAA CCTTnGTTTT TGTTCATCAA	120
TTCCATCAAC AGTGATAAAC GTTATTAAAT ACCAATTCAA AATTATTGCC TAATCTTAAA	180
yCCATACTAG TAATTATACC ATATTTAGCA AAAATTACTT AAACAAACTA TTAATATCAG	240
AATTAAATTTG AGCGGTTGCT ATTTTAAAGC TTGATTCGTC AATTACTGAG TCCCCTATAA	300
TTTTTATACC ATTGATAGCA CTAACAATAT TATCTAGAAT TTTTTTTAAG CTAGTTGTTT	360
GGTTTGCTAT TTCAATTTTA TTATTCGCTC TAATTTTAAC AGTATCAGAG ATTAGATTTA	420
AAGTCTTTGG GCTAATTGCA CTAAGTATAT AAAAATGATG TTTGTCAAAG TGAATATCGT	480
TATTTTATC AAAAATATTA ATGCTTGATT GAAGTAGTAA AACGCAATCA CCTTTTGATA	540
GTTCTAAACT GATATTAGAG ATATTTTTTG TGTGAATTC TAAATCTCA AATTCGGGTA	600
TTGTAACAAT AGCTTCTTGA GTTTGATGTT TAAACTCCTT TACAGTGCCA ATTTTAATTA	660
TAAAAATGTT TGAATAAATC CAATTTTTAA GGTCTTCTTG AGCCAATGCC TGGCCATAAA	720
GGCGTTGATT CATTCTGTAA ATTTCATAGT CTTCaTTCaT TCTaATTCTa GTCCCCTTTA	780
tTTTTTACgt TTTGTATTAG	800

(2) INFORMATION FOR SEQ ID NO: 112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 798 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

GAAATAGCTT TTTAAGTTTT CTAAATCATC TTTAATATCA ATAACCTCTA TAAAGTATTA	60
ATGATGAATT TTTGGGAATG TTTTATGGAT TTAAAAGATT AACAAGACCA CTTTTTTTAA	120
ATACGAAGAT ATTATTACAA AACTATCAA AACTGTACCC ATGTATAAAA TTCATTACAT	180
AGAATTTAGA TTTAAGAAAG GAAGTGTTTT TTGTTATATA AAAGCAATTC ATGTTTTAAT	240
AAAAAAAGAA AAATTTAAAA AAAATATGCT CAAAGTCTAT TAGAGAGAAT AATTAATCTA	300
GAACATAAAG TATTAAAGAT AAAGCAATTT TTTTAAAAAA TATATAAAAA TCGAAACAAA	360
AAATTAAAGA TATAGTAAAA TTGTATTTGT AGCAATATAC TTGTGCTAGA GGCTATGAAT	420
CTCTAAAGAT TTTAGCAGGG GAGAAAATAT GAAAAAAGT TTTTATCAA TATACATGTT	480
AATTTCAATA AGTTTATTAT CATGTGATGT TAGTAGATTA AATCAGAGAA ATATTAATGA	540

1089

GCTTAAAATT TTTGTTGAAA AGGCCAAGTA TTATTCTATA AAATTAGACG CTATTTATAA 600
 CGAATGTACA GGAGCATATA ATGATATTAT GACTTATTCG GAAGGTACAT TTTCTGATCA 660
 AAGTAAGGTT AATCAAGCTA TATCTATATT TAAAAAAGAC AATAAAATTG TTAATAAGTT 720
 TAAGGAGCTT GAAAAGATTA TAGAAGAATA CAAACCTATG TTTTAAAGTA AATTAATTGA 780
 TGATTTTGCG GGATCCGT 798

(2) INFORMATION FOR SEQ ID NO: 113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 798 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

AGCTTTTGCA TAATAATTTT CATCAAATAA TTCCCATATT AAATCCTCCC AAATATCATT 60
 AATTTTACT TACAGCTTTA TTTCCAAATA CTGCTACTTT TATTAAATAA ACATCGTTAC 120
 TAATTTGTTT TGCATCAGAC AACGCTATTG CATTAATAGT TGCCTTATTT GGTGGTGCTC 180
 CAGTCACCTT TTCAAGAGCA CCGTCTTTAT TAAAAACAAG TTTGTCTTTT ACTTTAAGCG 240
 TAGAATCTTT TGCTACTAAA TAACCCTCAA AATTATTTGT AATCGGAACA ATAGTGGCTG 300
 TTTTGCTAAA CTCATCTATA TCAATGCATA TTCCGTATAA ATCATCTTCA CCACCAGCCT 360
 CAACGTGGGG TTCATAGTGA ATTTGATCAG CTTTTTCCTC TTGAATAACT CTTTTTACCC 420
 CACGCTTATA TGGATACCCA GAAAATGGAT GATTTTCTAA TTTGTCAAAT TTGCTGGTTC 480
 TAGTGCCTCC AGAGGCAAAA AATTGTATGT TTTTATCTCT AACTCTACA GAATTGCTAA 540
 GCAAACCAGC GTCATGCTGG GGATTTTTC TAAACTTTTC AAGTTTACTT CTCTTCTCTT 600
 GaTAATCTTT TACTAATTGC GTTGTGCTG cCATTTGTTT AACTCCTTTT ATTGcCCAAG 660
 GgCkAwCCrC CAGCTtCAGG TGTTACTGTT TTCTCAAGGG CCTCTATTGG CCAAAAATTG 720
 GCAAACCTTT TTTTAAAT CCCTAAAAA AATTTTAAA AATTTAAAGG GAAAAATTTA 780
 AACCCTTTCC CCTTTTGT 798

(2) INFORMATION FOR SEQ ID NO: 114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 783 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

1090

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

GGACTCAAAA CTTTACCCTT TAAATTACTA AATTTAACCTT GAAAATACTA AACTTTAACC	60
CAAAATAATA AAACCTTAAC TTGAATTTTT CAAAATTACA AAACCTTAAC CCAAAATGAT	120
AAAACCTTAA TTTTTTGTA TTTTACATA AAAGTGTTAA CTTTAAAATC CCAAACTTTA	180
TAATTTTGGG AAATTATCAA TACTTTTTTA ATTTATTCCTT TATTTTCAA ATAATCTTTA	240
TATACTTATA TATTATGTAT AAGGCTATAA AAGAACAACA AGAAATAGAA ATAGATCATG	300
CATGCAGAAT ACTTATTCCT ACCGCAACAA TATTTGAAAT AAATTCAATA TTCGAAAATT	360
ATTATCAAAA AACTCTACTC AAAAAGTATA ACGAAAATCT CAAAAACAA AATCTACCTC	420
CTAGTAATAT ATCAACAATG AAAAAATACT TAAATCAATT AGAAAAAGAA ATAAAAATCA	480
TAGCAAAATT CTATTTTAAA AACGATCAAT CTCTAATTTA TTGCAAACTT AATTATACCC	540
TAGAAAAAAT TTGTTTAAAA CTAATAAAAT TCTACAAAA ATTCTACAAA GAATTAAAC	600
AATTTACACA AAAGAACATT ACTACTTAAT TGTAATACA TTATAAAATA ATCTTATGCA	660
AATATTTAGA AATACAAATT GTAAAGATAT ATATTTTAT TTAAATAAAT AATAAAAATT	720
GCTGGCACAC TAATTTGGAA AAATCTTTAA AAGAnATACT AGGTATGAAT AGCnAAAATA	780
AGC	783

(2) INFORMATION FOR SEQ ID NO: 115:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 768 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

TTCTATATAA ATATTTTGTA ACTTTTTTGC TTATTACAGA CTAAGCCTAA ACGTCCTACA	60
ACCCCATAAA TGCAACGCTC TGCAGCTTGA CACATTTAAA GTTTGGGCTA CTCCCTTTTC	120
GCTCGCCACT ACTAAGGGAA TCTCTTTGAT TTCTTTTCCT CAGGGTACTT AGATGGTTCA	180
CTTCCCCTGG TATCGCCTCT ATTATTTAAA TAATAGATAG CTAGCATCTT GCTAGCTGGA	240
TTACTCCATT CGGTAATCTT GGGATCAATA AATGTTTGCT TCTCCCCAA GCTTTTCGCA	300
GCTTACCACG ACCTTCTTCG CCTTAAAGCT CCTAGGCATT CACCATAGAC TCTTATTACT	360
TTGACCATAT TTTTATCTTC CATCTCTATT TTGCCAATTT ATTTATACAA CATAAAATAA	420
TATATATCTT TGTTTAATAC ATGTCAATAT ATATTTTATT TTTTATGTTA TTAAACAAC	480

1091

ACATTCAAAA ACACCAATAT TTAAAAACA TAAAAATAAA ATCAAAGTTT AAAGTATAAA	540
AATAAAAACC CTGGCAATAA CCTACTCTCC CGCGAACTCG CAGTACCATC AGCGAATAAG	600
AGCTTAACTT CTGTGTTCCG AATGATAACA GGTGTTTCCT CTTTCTTTA ACCACCAGGG	660
TTTTTACAAG GAAGACAAAA ATATgGcCAA AGATACGGGT AATTAGTATT AGTCAGCTTA	720
ATATATTGCT ATACTTACAC TTCTAACCTA TCGACCTGGT ATTCTTTC	768

(2) INFORMATION FOR SEQ ID NO: 116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 765 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

CTTTACGCCT AACTTACCCT CCACGTGTAC AACCCCTTAA CAACCCCTTA ACTTACCAGT	60
GACCCCTTA ATATGGTAGT TATGGGGGAA CGCTTAGAAT AAAAAAGTCA TCTACGACAC	120
CCCCGATCAT AGACCTGACT CTTGTTATCC CAAATCACTT CAGCGCCCTC GCAACTTATG	180
GGAAAAAGTT CCTAGAAAGA TGTATAGAGA AGTGGAATCA AAGTAATAGG CAATTCCGAA	240
GTGAATAAGG GAGAAAGGAT TTCCTATGTT ATAGGGAGAC GCTAGACATA GTGCTTGCGA	300
GACTGGATTG TGCTTGATGG ATAGAACCTA GTTTAGTGTG TACATCCAAA AAATGGACTA	360
AATCAATAGT ATAAGGCGAA TTGCCAGCGA TGAGGTCTGA ACCAAATTGC CTCACATCAG	420
GCGATAACAG TTACTIONTAA CAGTTGCCAC TTCGGCTACT CTATCTTGCG TGCTTATTGT	480
AGCACTCTGG AGGTCCTGTT GTTAAGCCAG CATTAGCACA GCTCCTCCAC TCGGGGTTCG	540
GAGTATAGAG TAGTCCTAAC TGGCAAGGAT TCCCCCTCTG GTTGCTAGAG GTCGAATTAC	600
CCACCCAACA ATAGTTGCAT TGTGGGGGGG GTGGGTACCT ACTACTCGGC ATATACTCCC	660
CCCCTTTCGA GACCTCCCTC GAGGGTCGAG GGAGCATTTG ATCATAGACG TTCATCCCAG	720
ACATGGCCTT TCGGGTTTGA CGTCTCGCGA CCCCCCTTCG GGGAC	765

(2) INFORMATION FOR SEQ ID NO: 117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 755 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

1092

GAGCCATTAT TGGCTCCTAT TTTACTAGCT GCAC TTGAAA TTCTTTTCTT TTTTAGGAAC	60
AAATAACGCT CTTTAAATTA AAAGGCATAA TGCTATATTG TATTCTAAAT CATATACAAA	120
GGACAGTTCT TTATATCATA AGTGCAAAAA TAAAGTCATA AATTCAATAA AAAGGAGGAA	180
AACTCTTCTA GAGTAGTAGA AGAGCAACCA AAAATTAATG AAAATTTTTC TACACAAGAA	240
TCTATACAAA AACTGCCCCCT TTAGTGCAAC ATACAAAACG TGAATCTTGT ATATTACAAT	300
AATAGATAAT ATTATTGCAA CAATCCTAAA TTACAAATAC AGAATATGTT ATTAGCCCCA	360
AAAAGGGGCT AATACATTTA CTTTAAATTA CAAGTTATTC GAACCATAAT TGTTCAATAT	420
TAATTTCAAA TCTTTTCTTA TAGCAAGAAA TTTTTCATAA ATCAATATTA GATAATCATC	480
AAAATTGCTT TTATCAAGCA CATACAAAAG TTTAAAAAAA TCTACATCAT CAAGACATAA	540
ATAGAATATG AAAACCTTAT TTTCAAACAC ATTATCACCC AGCTTTACTT TAATTTTACG	600
AAAAAGGTTG ATTAATTCCT TAGACTTTTT TGGCCCCAAA TTAAAAAAA ATTCATTTAA	660
AATGTTTGA CTTT TAGGCG GAGACAATAT ATTTATTGTC TCCGCATCAT TTTCTATATC	720
TAAGAATCGA CTCATAGGAA CTTATAAATG ACTTT	755

(2) INFORMATION FOR SEQ ID NO: 118:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 753 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

CTCAGCCAAG ATACTGGTTT GCTTAGTAAT TCTGTAGATT TTAGAGATnA AAATCTAATT	60
TACTCCAATT CGGATGGAGT TTTTACTAGT AGTAAAGACA AAATAGAAAA TTATCCTGCT	120
AAAGGGTATC CATAAAGCG TGGAGTCAAG CTTAGTTTTA GTGCAGATGG TACAACAGAA	180
CTAGAAGTTG AGGCTGGTGG TGGGGATGAC TTGTACGGAA TATGCACTGA TATAGaTGAG	240
TTTACTGGCA TGGCAACTGT AGTTCCAATT ACAAATAACT TCACGGGGTA TTTAACATTT	300
AAGAAAAATG GAAATGGTGT AAACCCAGGT GATAAGCTGC ATTTTAATGC ACAAGGAGAG	360
CTTGAAAAGA ATGGGGGAAA TGATAAATCT GTTAATGCTA TAGCACTTTC AAAAGTACAT	420
AAATTAACCG AAGAGTTATC TATAGTGCTT GCTAGTGTTT TTGGGAATAG AGCTTTAAAA	480
GGTAATTAAA TTATGGCTTT AAAAGGCAAA GGGCAAGCTA AAGCTCCTAA TGTTGATGAT	540
AATCCACAAT TAGGGCTAGA ATCAGAAATT CCAGTTGCTC CTAGATCTAA ACGTCAAACA	600

1093

AGACAGGCTG AAGAAGTACA GGCAAAAGAT CCTTATTTAG ATTCAGTTAA AGAACTTGAC 660
 GATGTTCTTT TAAAATTTAA AAAATATTCA AAATCAATGA GTTCGATTGA AAATAAGGTT 720
 TTTAGTAGTT CGGGTGGTTG TTTTAAATCA AAG 753

(2) INFORMATION FOR SEQ ID NO: 119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 747 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

TGATTTTAGC TGTTTTGTAA mCCTAAAGTG GATTATAATA ATTGGGCCTA CTAGTCTGAA 60
 TCCTAGAGTC AATAAACTT ACATAATTG TATCTTGCGG CAATTTTCGT TTCCTCCTTT 120
 AAAATTTTCGA TTGCTTTTAC ACTAGCATG AATGCTATAG ATGCACTGTA TGCATGGTTG 180
 CTATATTTTG TGCCTAAATT AATCAGTCCA ACTGTTTGCA TATTAGATGT TGGGTAAATG 240
 TAGAAGTTAA TTTTATTAAT ATATTCGGGT TGTAGACTGG GCAAAGTATA CTTATGAGCT 300
 TTATTGTGTA GAAAGTCACT AAGCATACTA TAAAGCATT ACATGCGTGA ATTAGCTTCA 360
 AAGTCTTTGG CGTTTAACAC TATTGCAATA ATATATATTT GAAAATTTAT ACTAAATTCC 420
 AAAGCATTTT CATAAAATAC ACCkGCTyTA kAATTATGAT CAAATAGATT TTCTGTACCA 480
 GCAAATTTCA ATGCTATTAT ATTTGAGCTA GCAGCTGTGA TTTTGTAAAG ATATGGATGA 540
 TTGTAGGTAT TTATGATATC GCACTCAAAA TTATTTTCAG TTGCATACGC CTTAAACCCT 600
 TTAAATATTT TAGTTAAATG ATTTAATACC ATATCTAAAG TGAAAATCAT TCAAGTGTTA 660
 CCTTATAAGT AATCTCTGAT AACATTTTGG CTGTATCAAC AAGTGGaATT GCTGCAGTGT 720
 TACTACCCCT TTTAAACTTA CTTTGA 747

(2) INFORMATION FOR SEQ ID NO: 120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 744 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

ACACTTAATT CAAAAGTACT AAGCTTTAAC CCGGAAATCT TAAGAAGATT TGAGAATTGT 60
 AAATTTTAAC CTAAAAGCA GAACCTCATA AAAGTTTGAC TTTTACCCAT AACAGTATAT 120

1094

AATATTAATA TGTTTTTTTT CAAATTTTTT TCAAAACATA AACCTGCTAG GAAAAAAAT	180
TATCATAAAA TCAATCCGGA TGAATTCATT CTAATTAGCG AACATCTTAT CAATTCCTAC	240
AGCATTACTC ACCAATTACT TGGGATTATC ATGGCCTCTG GAATTCCATT AACTCATATA	300
AAAAAATCAA AACATCAAAA CTCCTTACAA TTTCAAATCT GATATATTTT CTTATACGTT	360
GAACAACGGT TTGCAAATTC AAACACATTC TCTAATTTGC TCTAACAAAA TTTCTAGGTG	420
TATTGAAAGT TTAAACAAAA ACAGATTACT ATCTATTGGT GCAGACAAAA TTAATTATGT	480
AGCAAAAAAT ATTTTGTGATT TTAGAATTAC TACTAAACAA CTAAAAATTA TTCATTCTTT	540
GATTGCTAGG TCAAAAGAAA CACTACATGA AATCAGATAT AACTCTCATT CACAAAACCT	600
CTTTTGTAGT AAAACACCCT GTATTTTAAA TCTGTACCAA AAGCTCAAAT ATATCAAGTC	660
ATTCCGCACC TCTAAAGCTC AATCAAAATA ATCTAAATTA TTATCGAAAC AGCTCCAATG	720
AGCTTACATC TACTATTACA AATT	744

(2) INFORMATION FOR SEQ ID NO: 121:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 721 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

AGTTTGThTA TTCCTAGTAA CAATAACATT TCAGAATAAA GTTTTGThAC CAAAAGTTtT	60
CTTCAGCcTC AACTTGTGTT TGTAAGTTTT TTTGTTTCGCT CACCTCGATT TACCTTATGT	120
TTTTAACTTT GTTTAATATG TACTTGCAAA ATAGTTTTTC TAGTAGCAAG TAACCCTCCT	180
AAAACAAAAT CAATGTATGA ATGAGCAATA TCAGTTGAAT CTTTATCCAC TTGTTCAATT	240
GGTGTAGGTA ACATATACTT GCTAGGTTTA AACTTAATAA GCTCTGGGTT TAATGGGTAA	300
ATAAGTATTT GATGTTTTAG CAAGTTTGAA GTTTCAATGT AGACATCTTC TCTATTATTA	360
ATAGCCyTGA TAGTTTGAAT CAAAACATCC TCCCATTTTT CGCAGCTACT TGCTGCACCC	420
TGTGCTGCTG CGTATGGCTT TACGAGTTTG AGCGAaGTTG TAGGgTCAAC TATTACCATC	480
ATAGGTGTAG AAAATtCGTC TCCTAGCTCT AACTTtGAAA GTCCCGCCTC AATTTTTtCA	540
AATATTTTAT CCATTTTATC TTTATCACCA CTAGCAACTT CTTCTTTTAC TTGATGTGGC	600
ATATTAAGAA GTCCATACAT ATTGGGAAGT AGACGTTTTT GATTTTTTCC ATCTTTTTGA	660
ATTGAAACAG TGCCTGTTAG TACAAAGTGA TTAATAAGTT TAATAATCTC GCTACTTGCA	720

(2) INFORMATION FOR SEQ ID NO: 122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 720 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

CAATTCAGC TCTTAAATTT TCTATTTTAG TTCGCATACC AGTAAGTTCA AACTAGAAAT	60
ATTGCTTAAA TGCACGTATA AATCCTAATT TTAAATTAGC AACTCTATA TCTAATTCAC	120
TTATACTTT CCTAGCGTTA ACTTCTGATC TAAAGGTTTG CGATAAAAGG TGTCTAAAG	180
TATCTTCACT AATTGTTACT CTAGCGTCCT GGTTAACAAT ACTTCTCCA CTTTCCCACT	240
TTTGTCTCAT TCTCCACACA TTTACTTTAG AAACCTCTAA TTTTTCGCT ATTTCTCTAT	300
CATTTAACGA TCCTTCTCTA AAATACACAA CATAATCATC AAAAGGCCTT TTAACTTTTT	360
TCAAAACAAT TTCTCCTAAA ATAACAAAT TAACAAATTG TTAAGCTAAG TAGTAAAGCA	420
ATTTATTAAT TGTTAACATT AACTGATAAC TTCTTGATAT TTAGCGGGGA ATATTTGTTG	480
GCCTTTATTG ATTTAGTTTG CTGCTATTTT TATAATTTTT GATTTAGAAA TAGTAGTTCA	540
TTAATTTATT GCATATTACT ATAAATAAT TCTACTTTTT CGGAAAAATC TTTCATTTCA	600
TTTCATAAGAT TTTTACTTGT GAAAAGTCTT TTATCATAAT AGTGTATACT CAAAAATAAA	660
ATATCTCTAA ATTCTTCAAT CGCATCTATT TGAAAGTCTA ATCTAATAC TTTTCTCCTA	720

(2) INFORMATION FOR SEQ ID NO: 123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 715 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

TAATAAAAAA CTAAAGCTGT TCAACTGCAA TTGTTGCACT TGAAATTTTT TATACTAAAA	60
TAAAATACAA ATAATTATAT TAACAAATAT CGATTTTAT AAAAAATAAG TAAAGTAGT	120
CTAGTTTACC TGAGTATTTA AATACTTTTA ATTGAGGATG TTTTATTTTA AAAAGGAGTG	180
TAAAGCTATG TCAAAAGCTG TTGACGAAGT ATATTGCTAT TCTTGTGGCA AGATTAAAAA	240
AAGATGCTGA GATTTGTATT TCTTGCGGAG TCAGAAATAA ACAAACCGAA AACTACAATA	300

1096

AACTTATAGT ATTTTACTA TGCTTACTTT TTGGTTATTT AGGAGTTCAC AGATTTTATG 360
TAGGTAAAAT AGGAACTGGT CTATTATACC TATTTACATT TGGATTTTTA TATGTTGGAG 420
TTTAAATCGA TCTTATTAGA ATAACAACAA ACAAGTTTAA ATGTAATTAA AAGGATTCTT 480
TAGTAAATTT TTTATTAGTC TTGTTAAAAT TATTTTTTAA TTTTTTAAGC ACATTTTGTG 540
TGAAGTCTA TTTCTATAAT CTTTGATTTA GAAATAGCAG TTCACTAGAT AATAATAAAG 600
CTAAAATTAA TATyTLAGTA TTTAATAATT CTTGAgAAAA nGTAAATTG GTATATGTTT 660
ACTTGTATA AAAAACTCTA TCTGGGTAGG ACTTTTAATG TTTAATAAAA TAGTG 715

(2) INFORMATION FOR SEQ ID NO: 124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 715 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

GGAGGATTTA ATATGGAATT ATTTGATGAA AATTATTATG CAAAAGCTGT GGCAAATATC 60
ATAGGAGAAG TTAAAGATCC TATTATGTAT AAATGGTTTT CGCCCGATCA AATTGAAGAT 120
GTTGATCTAC AAATGGGATA TCAAAAAACC GTAAATGGG ACGCGTTTTT AAATGCTAAT 180
CCTACAACAA TTGCCAATGA GGTTAATACT ATCTCAACTA TTGGATTTAG TTCTGAAGTG 240
GTAAGACTTA ATTATTTGAA ATTACAGTAT AAATTCAGAC ATTTAAAGCA GACTTCTGAG 300
AAATTTTATA CTTCAGATTC ATATATTGGG GACATTAATA ATAATTTACT TCCTTTTGCT 360
CAAGCGTATA AGCTTGCAAG TAGTGAAATT ATTAACTTA TTAATCACTT TGTATTAACC 420
GGGACTGTTT CGATTCAAAA AGATGGGAAA AATCAAAAAC GCCTGCTTCC AAATATGTAT 480
GGGCTGCTTA ATATGCCCGA GCAGATAAAA GAAGAGGTTG CTAGTGGTGA TAAAGATAAA 540
ATGATAAAA TCTTTGAAAA GATTGAGGCT GGACTTTCAA AGTTAGAACT GGGCGACGAA 600
TTTTCCACCC CGATGGATGG TAATAGTTGA CCCAGCAACG TCACTTAAAC TAGTAAAACC 660
ATACGChGCA GCACAGGGTG CAGCAAGTAG TTGTGAAAAA GGGAAGATGT TTTAA 715

(2) INFORMATION FOR SEQ ID NO: 125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 714 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

GTATAAAAAG CAAAAGAAAA ACATCTTCCT TCACAGAATA GTTGCCCAAA TCCAATAATA	60
ATTCATACTG GTTGAAAAAT TTCCAAGAAA ACGCAAATTA TTATTGGTGT TCATATTGTT	120
CAACATCTAG ACCAAACCGA AGTGGAGTGG CCTTTTCTTT ACTTCATTTA GTAAGTTTTT	180
AATAATTAAA CCAACAGGTA GTATTAAAC AAAGTTTTAA TACTACCAA GTTTTAATGG	240
CTCCTTCAA ACAGCAGTTT TAACCGTTTC ATTCTCTCTT CTGCTAATAG TAACTGGTCA	300
TATTTAGTCA TTCCTCTCAA AACACCAATT GATGTAGCAA CAATTATCAA ATTACTAACA	360
TTAAAAAACT AAAAATATTA TAAAATATCC AAAAATAAAA ATATTCTTAT TAATTAAATA	420
ATTAATACTA ATTATTTAAT TATAGTATTA TTGCATTATA TTATAGTTAA GGAGAATATC	480
TATGAAATAC CATATAATCG TAAGTATATT TGTTTTCTA TTTTAAATG CTTGCAATCC	540
AGATTCTAAT ACCAATCAA ATAATTCTAA AAAGGAATTA AAAACAGGAA GAATCCCTAA	600
TAAACAAATA AAAAATGCCC TACTTGgATG ATTTAAAAAA TTTAATAGAA ACAGCTAGTG	660
CAGGATAAAA AAATATGAAA AAAATTAGGA AGAAGAACCT TCAAACCAAT ATGG	714

(2) INFORMATION FOR SEQ ID NO: 126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 708 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

GnATTAAGTGG GAAAAATTT CTCAAGTGTA ATTTTATATT CTTTATATA ATTTTCATTT	60
AAATCGAAAG TATCGTCTA TGCTATCCCC TTGTTCAAGT CTTACGTTT ATGAATGGGG	120
CCTAAAAAAT TATCATCACC GCCTATTAAT TCCAATAAGT GTTTTCATTA CCAAATTAC	180
ATTTTTTGCA TATTTTTTAG TTTAAGTTA TTAATCTTT TTTACTTTT GTTTTCTCTT	240
TTTTATTTTT TATTTTTATA AATCACTTTT ATTTAAATA TATGTATACA TATATTTTTT	300
TTACTATCTC TTTTAATAAG CCCAGACAAA TAATTACAAA TATCACACAT TAAGCAACAC	360
ACGTGCTCTT GCAATTTTGA TTTTAAAGC CAATCTCAA AAAATTTTAA AAAAATTAT	420
TATATTTATT GATTGCCCT TAAGAACTT TTTTATTAT GCyTTTATTA TAACTTTGTA	480
AAyCTTtCAA TAGTTTAACT TAGATAGATC GGAAATACC TTGnCTATTA GGGCTTTATT	540
ATAACTGTTA AATTTTGnGn TTTTTGTGA AAATTTATAT TGCCAATGAT AAAAATACGC	600

1098

CAATTTAAAT TAAACATTTT AATAATGTCC AAATCCTCCT TATATAAGGC ACATCATAAA 660
 TCAATTTTAC TGAAAAACA AAAAGCATAT CTAAGATTTC ACCCTATT 708

(2) INFORMATION FOR SEQ ID NO: 127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 703 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

GGCCAACATG AACTATAGCC TAAAAATCTA AAAGACTAAC TTGAATTTTC TAAAAATCGT 60
 AAATTTTAAC TCAAAAATCT AAACCTGCAA AATTTTAGAT TTATTACAAA GAAGTCTATC 120
 ATAACTTCG TATAATCTTG TTTCAACTCT ATCTAATCTG GCTTTAAATT CATTACCAAA 180
 GCAACTAAAT CTTTAGTTTC AAATTCAAAT ACCACTCTTT TATCTAAATT ATCTATTTTA 240
 AAAACCTTTA GCAATATCTC AGTTCTTTT TTCTACCTCA TTTTTTAGTT TAAAAATTTA 300
 TTTTATTTT TTTTATTTA CTTATTTATG ATAAAAAATT TTATTATTTA GTAAATAATT 360
 ATCATATCCT TTTATTAAAG AAGAAATATA ATCTTCTCCT TTTTTTTTAT TCTTTAATGC 420
 CTTAAATCA CCAAGCAAGG TGATAAATC TTCCTTAGCT AATGAGTAAA GACTAGCTAT 480
 AATAAATTA TTTTCATTTT CTTTCTTTT AAAAAATCA TCTTCTTTAT CTAGTTTCAG 540
 TATTTTATTA ACTTTTCTT TATCAAACTT AAAATATTCT AAGTAAAGTA AATATTTAAA 600
 GTTTTCGGGA TCATTTTGG CTATCAGTAA AGAAGTATTT TTTGCAAGAT TTAAATATAA 660
 AGGATTACTT AAAATTCCT TTTCTCGGG TTGAGGCATT GGG 703

(2) INFORMATION FOR SEQ ID NO: 128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 699 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

CCGACTCAAA ACTTTACCCT TTAAATTGCT AACTTTAACT TGAAATACT AAACTTTAACT 60
 CCGAAATGAT AAAACTTTAA TTTTGTCAAT TTTATCTCT TGTTTTTTTT AAAACGATTA 120
 GAATAATCGT TGAKCAGGTT TATTGATTAT CAATAAACCT GATCTATAAT ATTATAAGCG 180

1099

GTTTTTGCAA GTTTAATAGG AGCTATAATA TCCATGAACA AATTATTGAT ATTCATTATT	240
TTATTAGTCT TTTCATGTAA TTTAAGTAAT TCTGATCAAA ATAATCCACT AAACATGTCA	300
AATAAAGAAA AAATAAGCGA ATATCAAATA AATGAGTCGT CAAACAAAATA TTCAATTTTC	360
AAACGAAATT CAAGCGTTAA AAGATACACG TTCAACCATT ATTACTAACC AAAATGATAA	420
TATTAATTCT ACTATTAACT ACCCACCTTA TATTCAAACCT ATCTTAAAAA TAGAAAAACA	480
AGTTGACGGA AATATTATTA TTAATGGGAT GACTAAAGAA AGTGGCACAG AAATAAAAAA	540
GCTTTTAGAA ATTCCAAATG GGAATATTTT TCGACTTAAA GATGCAATTC AATATGGAGG	600
AAGTTTTAGG GCTAAAGATG TTAGAGAAAA TCAAACCCAA AAAGAAAACA ACAAAGACTC	660
GCATATTCAT GTCGaCAtTT TAAAGATACA TACTTTAAT	699

(2) INFORMATION FOR SEQ ID NO: 129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 695 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

GTGGCAAATA ATAATGTATT GTAAAATTTG ATTTTTTAAA ATGGTACATT ATAATATTGA	60
TAAAGAGTAT TATCAATTAA CACTTAATTT TTGCTTTTTC ATAAATTAGA ACTTATTTGA	120
ATTTTTTAAC AAGAGAATTT AAATAGGTTT TTTTATTTTA ACAAATACAA ATTGATTTTA	180
ATTCTAAATT AGAATATATT CAATTATTGA AAAGCTTATT TAAATTATTT TAATAAGCAA	240
ATTTGATTAA ACCCTAACTT TATTAAAATA ATTTATGTAA AAAGTTGTCA AAAATAGTTT	300
TTGTTATACA TATATATATG TATGTAAATA GCTAAAAAAG TTTATTGCTA TCAAAACAAT	360
CCAATCAAGT TGGGTTTAGC TAAGTTCTTA GATAAGAGAA TTTAAATAAA CCCAACTATT	420
TTTTTGTAAT ATTTTTTGTA AAAAAGCCTG AAAAAAATAG TTTTGCTAT ATACTTATAT	480
TTTTTACTAT AAAAGGAGTA AAAAGATGGA AAATCTTTCA AACAATAATA ATCCACAAGA	540
AAATATTCAG GGAGAGCTCA AAATGATAAG TATTAATCAA CAAAGTTTTA CTGGTTGTGA	600
AATATTTGAG GAAAAATCTT CTCCCATTAA AGAAAAAAGT AAATTAAGTA AGATAGGTAA	660
GAAATTACCA GGAATAAGTA GTCAAGAATG TTTTA	695

(2) INFORMATION FOR SEQ ID NO: 130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 684 base pairs
- (B) TYPE: nucleic acid

1100

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

CAAGCAAGGG TTAACAAC TA CTTAAAGAC AAATTTAATA AAAAAGGGAA TCTAAATTTA	60
GAGGAGTGTA ATAATAATAA TAATAATAAA GAAGAAGAAG AAGAAGACAT AAGAAATAAT	120
AAAATAGAAA AATGTCAAAT AAAAAAATAT TTCAACAAAT GTAAC TTTT ATCCGAAGAA	180
GCTAAGTCCA TTTTAGAATT AACATTAGT AAGAATAAAA CAATTGAAAT AATAAAAAATA	240
ATAAAAAAAA TTGAAACCGA CTTAACAAAA AATAAAAAACA AAGTTTGTTT TAAGAAAAAG	300
CAAAAAATGT TGAAAGAAAT ACTAAGCAAA ACTAAAAAGC AATTAGAAAA AAAAGGATAT	360
GACACCAAAC AACTGAAACT CAAAATCGAA AACATATATA AAAGTTATAA AACCAAGCCC	420
CATTTTATTA TTGAAAATAA AAAATACAAA GACCTAGACA AAATAAGGCT TAAACTAGAA	480
AAATCAATTG AAATTAAAAA AGAAAGTATT ACAAAAAAAT ATATACATAT AAAAGTAAAT	540
ATTTTCAACA TACTAATAGA ACAATTGAAA AAAGTTTGG TAATAAAAAAC TTTAAAGCCA	600
ATTATAAAAA ATTATCTAAA TAGCAAAAA ACCCTAGAAT ATGATAAAGT GTTCAATACC	660
TATTATTATG nACTATTAGA AACT	684

(2) INFORMATION FOR SEQ ID NO: 131:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 673 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

GTATAAATTA TCTTTTAAAT TTATTACTAA ATCTCAAATT AGATATATAC TTTGTGTTTG	60
TGCATAAACC AACTCCAGCT TTAAACAGAT CACAAGCGCT AAAGAACTTA CTAATCTACT	120
TGCAACAAAC ACCAAACTT TGAAATAAGA AATTCAGTCA ACCTTAATAG CAAATCAAGA	180
AAAACCAAAT CTAGATATTG ATAATTGACG TACAAAAAGA AATAGACAAC ATAATTTCAA	240
ATCTAAAAGA GTTTATTAAA ACTCTACAAA CCCTACATTA AAATCTGCTT AGCATAGCTA	300
AGTATGCTCA ACAACATCTT AAAAAATTCA ATTCCAAAAA TAAATCTAA AAATTGCACT	360
ATTATTTAAA TATCAAACT TAATTATTAG GAGGTAATAT TAATATGAAA AAAATTTTCA	420
CATTAATATT AATTTTGTAG TTAACGATGC AAATCTTTC TTTAAATTC ACTTCAAAAT	480

1101

ATAAAATTCA GAAATATGCT GAAAGAGAAA AGGAGTTCAT TCAAAACCAG AAATTAGAAA	540
AAATTTTGAA AGACCCCGAA AAGACTAAAA AGGCTCTTTT GCAATACGAA AAAGAACAAT	600
TGATAGATCT ATGGATTCCA GTAATGTAA ATTTATTTT ACCTTTTGA GTGGGGCTTT	660
TGTCCAGGAG ATT	673

(2) INFORMATION FOR SEQ ID NO: 132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 660 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

CGAGTATTTT GACTCAAAAC TTTACCCTTT AAATTGCTAA CTTTAACTTG AAAATACTAA	60
ACTTTAACCC GAAATAATAA AACTTTAACT AGAATTTTTC AAAATGATAA AACTTTAACC	120
CGAAATGATA AAACTTTAAT TTTTGCAATT TTATTCTCTT GTTTTTTTTA AAACGATTAG	180
AATAATCGTT GAKCAGGTTT ATTGATTATC AATAAACCTG ATCTATAATA TTATAAGCGG	240
TTTTTGCAAG TTTAATAGGA GCTATAATAT CCATGAACAA ATTATTGATA TTCATTATTT	300
TATTAGTCTT TTCATGTAAT TTAAGTAATT CTGATCAAAA TAATCCACTA AACATGTCAA	360
ATAAAGAAAA AATAAGCGAA TATCAAATAA ATGAGTCGTC AAACAAATAT TCAATTTTCA	420
AACGAAATTC AAGCGTTAAA AGATACACGT TCAACCATTA TTACTAACCA AAATGATAAT	480
ATTAATTCTA CTATTAACTA CCCACCTTAT ATTCAAATA TCTTAAAAAT AGAAAAACAA	540
GTTGACGGAA ATATTAAATGG GATGACTAAA GAAAGTGGCA CAGAACTAA AAAGCTTTTA	600
GAAATTCTAA ATGGGATAT TTCTCGATT AAAGATGAAT TCAATATGGA GGTAGTTTTA	660

(2) INFORMATION FOR SEQ ID NO: 133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 656 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

AGCACTTTAA AGAAAAAAAA GAAGAAAGAT ACCAAAATAG AGTTGCCAAC TATTTCAACA	60
AAAATTCTGA TTCAAAAATG GGTAGTGTGC AATTGGGGGA GTGTAATAAT AATAATAATA	120
ATATAAAGA AGAAAGAAAA ATTAACGAAA TAGAAAAGTA TCAAGTAATA AAATACTTCA	180

1102

ACAAGTGTGA CTTTTCATGT AAAGAAATTC TTCCAGTTTT ATTAACATTA AATATTGATA	240
AAGAAAACAT AATTAAAATA ATAAAAATCC TAAAAATAAC CGAAATTAAC TCAAAAAATA	300
AAAATATACG CCCTACTAAA TCTTGTATTA AAAAAAACA AGAAAAATTA AAGGGAATTC	360
TATGTAACAC TCAAAAAGAA TTAGAAGAAA ACGGGTACAA TCCCAAACAA TTAGAAATAA	420
ATTTTCAAAA AATATACGAA AATTACAAAT ATAAACCCCA TTTTATTATT GAAAATCATA	480
AATATAGCGA TTAAACAAC ATAAACGTA AATTGGAAAA GTCAcTGAAA GAAAAAAGA	540
AATTCTCAAC AAGATTATGA aATTTAAAGA TAAACGTTTT CAATATCCTA TTGAACAAC	600
AAAAAAGAA ACAATATTGA nTCTAAAGC CCTTATAAAA GAATTTTGAA TACCA	656

(2) INFORMATION FOR SEQ ID NO: 134:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 652 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

TGnAATTAAT GTATCAAGCG ACTCTTTGTA TCCAGTACTT TTAAGTAAAT ATGTAGTCCT	60
AACAACAGGA ACTTCACCAT TTTTACCATA CACAAAAGTT GGAAATTGCC AAAAACCAAG	120
CTTTAAATTG TGATTTTTTA TAACATTTTG AATTACTTCT ACTATGACAT TGAAATCTTG	180
ATACTTATAT CCGTATCCTT TAAGACTTTT GTCAATACGT GGCAAGTTCA TTCTTAAAGT	240
ATCCATATCA TTTAAAAAGT CTATTTCTGC TTGAATATTA TTTTGTATTT CTGATTATT	300
ATTGTTTGAA ACATTGTTCA TGTTTTCTCT CTTTATTTAG TAATAAATAA GTATATAGCA	360
AAACTATTTT TTGTCAGGCT TTTTACAAAA ATTTTACAA AAAAGAAGTG GGACTtAACC	420
AAACTCTTTT CTAAAGAAT CTCGTTAAGT CCCCATAA TTATTATTTT TTGCAAATTA	480
CTAAATAAAG GTAGTCAAAC TGAAATATGT TCAAATAACT ACGCTGTTTG TAGTGTAGCC	540
CAATTTTTAA TTAAATCAA TCAATCTTTT ACTAAGTTAT AAAAAGTATA TTAATTTAAC	600
AAAATTAATA ATTAATTTT AATATTTTTT TAGAAAAGTA TTTAnCTTTA AA	652

(2) INFORMATION FOR SEQ ID NO: 135:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 649 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

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nAATTTCGAGC TCGCGTACCC AGAAAGTTCA GTTAACAAAA TGTAAGTCATG ACTACCTAGT      60
GTCACCTTCAA TGTTGAAAAC ATAAGTTATT GTTTTGGGAT CTCTTAAGCT TATTACAGGC      120
ATACCTTTTAT CTTCACTACT AATCACTGCT CTTGTTGTAG GTTCGCTTGT AAGCTCTAGC      180
TTGCCACTAT GTAAGTTCGT ACCACCAATT GAAAAATAAA CTTCTCTTAA ATCATAAAAT      240
TGCATTTTTTA GACCCCTTTT TAAGCACTTA AGCTGTTTTG ATAATCAAcT ATATCTTGAG      300
TAGTAATTAC TAAAGCAACA GCATTAAATGC TAAAGTTATA AGTAATAkTC ACGCyAAGTT      360
CTAATTTAAG TTGyGGkGTA GGAGAAAGAG TAAGAYTTAA ATTTTTTrTAC TCwATwATCA      420
GTCTCTATC CACAAACCTT TTCAGTAAAC ATTCAATTGC TGAAGTATAT GCATTGTCTC      480
TAGCTCCACT AAGCTGCGT GCAGATAATT TGCTATTTTG CCTATTGTTT TTGTTCCAAA      540
TTYTAATAAG CTCAATAATC GCTTCGTTTT TTATATAGTG GTATGTAAAT TGTTTCGTCTA      600
TTGyACyTCC AGCTAGGTCA ACACCTTCTT TAAAGGCAGG TAAACCATC      649

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(2) INFORMATION FOR SEQ ID NO: 136:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 644 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

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TAAGCAAAAG GnCCTAATGT TCAnGATAAT CCACAATTAG GGTTAGAATC AGAAATTCCA      60
GTTGCTCCTA GATCTAAACG TCAAGCAAGA CAGGCTGAAG AAGCACAAGC AAAAGATCCT      120
TATTTAGATT CAGTTAAAGA ACTTGACGAT GTTCTTTTAA AATTTAAAAA ATATTCAAAA      180
TCAATGAGTT CGATTGAAAA TAAGGTTTTT AGTAGTTCGG GtGGTTGTTT TAAATCAAAG      240
AATGmGCGAG TTAATGCTTA TTCTTTTACA TrTTCAAGCT TTGCAGACAA AATAGAAGAA      300
TACCTTTATG ATCCAGCAAA TAGTTTTCCA TATAAGCGTG GGGTTAAACT TGTTCAAAAA      360
GAGAAYTCTA TATATGTTGA AGTTGGTGCT GATACTGATA TGTATGGGAT ATGTGTAGAT      420
GTATGTGAGT TTAGTAGTAC TGCGTATGTA TTACCAATTA CGAATAACTT TGAAGGGTwT      480
CTTGTTACAA GAAATCCGAG TATAAAAATG GGaGAAATAT kGGaTATAAA TAACAATGGG      540
GTTATaTCAA GGCTGGTGGT GGGCCmCCAA cCGyAATTAA TGCATATGCC CTCTCTGaTT      600
CATTACAATC AATTTTGGCA CCCGAAGATG AAGATCAAGA TCAG      644

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1104

(2) INFORMATION FOR SEQ ID NO: 137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 636 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

AAAAAGTAAT GAATCATGCA TGCAGATTAC TTATTCTTAC CATAACAATA TTTGAAATCA	60
ATTTAATATT AGAAAATTAT TCTCAAAAAA CTCTACTCAA ATTTTATAAC GAAAATCTCA	120
AAAACCGAAA TCTAACTCCT AGTGTATAT CAACAATAGA AAAATACTTA AACCAATTAG	180
AAAAAGAAAT AAACGTCATA GTCGAATTCT ATTTTAAAGA CAATCAATCC ATAATTTATT	240
ATAAACTTAA TTACACCCTA GAAAAAGTTT GCTTAAACT ACAAGAATAC TACAAATTAT	300
TCTACAAAAA ATTAAAACAA TTTTACAAA AAAACACTAC TACTACTTAA TTGTAAAAAA	360
TTATATCTTT GCAAATTAAG CAAATTTAGA AATATAAATT GCAAAGATAT ATATTTTAT	420
ATGATAAATA ATAAAAATTA CTAGGAATAC TAACTTGGA AACTTTTGA AAAAAATAAT	480
AAAAATGAAT TACAAAAATA AGCTATCTTC TCACTTAATA ATTCTTATTT ACACACTAGG	540
CGACACTGAA CTAAATTTAA ATATTGAGTA CTATAGTAGG GGCTTTATAC ACCACGTGTT	600
TAATTCTAAC ATACATAAAT ATTGCAATAC TACTGA	636

(2) INFORMATION FOR SEQ ID NO: 138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 632 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

CCAATAACAT GACTTTAAAG GTTGCTTATT GACAATATGT TATTTTCAA CTTTGTGCT	60
TGAGAACTTT TTTTTCAT TTGCTGTAA AGTCCGTTA AATGAGATTC AAGCTTAGCA	120
ATATCTGTTT TTATAGAATC CTTATCATCT TGATAATCTA ATAAAAGTTG GTTTAACATG	180
TCTGATACGA TTGATTTTAT GGATAATAAT TTTTCAAACG AATTTTAAAG CTTCTCTAAA	240
TTTGAAATTT CTAGTTTATC TAAAGCATCC TTTTATAGGAT ATAAGTGATT AATCGCTGTA	300
TCAAAAGTTC TTCCAAGGTT GCAAAAAGTG CCAAATAGGA GGGTTTTTTG TTTTGATTGA	360

1105

ATTAAAATCT TTGAAAGATT CGCTAACTTA TTGGTATTAA TAGGATTTAA AGTAGCATAA	420
GTGAATTTTC TATAGTTTTT AGATCTATCG GTATTATCTG CTACCGTTTC ATATGATGCT	480
ACCCAATAAA TTTCTTTGAA AATTGATATT CCATATTGGT TTGAAGGTTT TTCTTCTAAT	540
TTTTTTTCAT ATTTTTTCT ATCCTCGTTA GCTGTTTCTA TTAAATTTTT TAAATCATCA	600
AGTAGCTTAT TTTTATTG TTTATTAGG AT	632

(2) INFORMATION FOR SEQ ID NO: 139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 628 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

GACTTCTTTA ATAGATCAAA AAGCTCACTT CCATCACCCC CAAGAACACT ATTAACAGCG	60
GGGATCCTCT AGAGTCGACC TGCAGGCATG CAAGCTTGGC ACTGGCCGTC GTTTTACAAC	120
GTCGTGACTG GGAAAACCTT GGCCTTACCC AACTTAtCGC CTTGCAGCAC ATCCCCCTTT	180
CGCCAGCTGG CGTAATAGCG AAGAGGCCCG CACCGATCGC CCTTCCCAAC AGTTGCGCAn	240
CTGAATGGCG AATGGCGCCT GATGCGGTAT TTTCTCCTTA CGCATCTGTG CGGTATTTCA	300
CACCGCATAT GGTGCACTCT CAGTACAATC TGCTCTGATG CCGCATAGTT AAGCCAGCCC	360
CGACACCCGC CAACACCCGC TGACGCGCCC TGACGGGCTT GTCTGCTCCC GGCATCCGCT	420
TACAGACAAG CTGTGACCGT CTCCGGGAGC TGCATGTGTC AGAGGTTTTT ACCGTCATCA	480
CCGAAACGCG CGAGAcGAAA GGGGCCCTCGT GgATACGCCT AwTTTTATAG GkTAATGTCA	540
TGaTAAtAAT GGtTTCTTAg AACGTcAGGg GCcAyTTTTT GGGGGAAAAG TGCGGGGGAA	600
CCCTAATTGG TTAATTTTTT CAAAATAC	628

(2) INFORMATION FOR SEQ ID NO: 140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 621 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

ATACCGCTAA ACTCATCTAT ATCGGAACAC ACTCCATATA AATCGTCTCC ACCACCAGCC	60
TCAACTTCTA GTTCGGTTGT TCCATCTCCA AACTAAGCT TAACACCCCG TTTATACGGA	120

1106

TACCCTTTAG CnGGtAATTC TCTATTTTGT CTTTACTGCT AGTGCAAACC CCACCAGAAT	180
TGGAAAAAAT TAGATTTtGG TCTCTAAAAT CAATAGAATT GCTAAGCAAT CCTGAGTCTT	240
GTTGGGGATT TTTCATTAAT GCTTGAATTT CTGCAACTTT CTTATCAAAT TCTTGTTTAA	300
TTTTTGTTAT ATCACTCATT TAAAACTCC TTTAGGCAAT ACTTGTTCTT TTATGTCTTT	360
TTAGATTTTC ATAAAATTGA ATTTCGTCTTT GCTTGTATGT ATTACTTATC GCTTGTACAA	420
ATTCTGTGAA ATTAATAGGT ACAAATTAG AATCAAGCAA ACTTGCTCTT TCTTCTGATT	480
TAATAGCAAT ATTCCCCTTA ATAGAGTCAA CAGAAGAAGA ACTGCTACTC GCATTTTTTC	540
TTAATTTAAT ATTCACTTTT GCTAAAGAAA CAAGTTGCTC TAATATCTCT CCATCGATAT	600
GACTTATGTC TGATACTTTG G	621

(2) INFORMATION FOR SEQ ID NO: 141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 608 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

TCCAACATAAT AGTTATTGAT TTGTTCTTGT AGTCAGACGA TAAGCGTTGG TCCGTATGCA	60
AAATTtCTTC CATGTGAAAA ATCTGATGGT GCTCCAAGCA GTTGTtTTGG AACGGGTGTT	120
TTTTGAATAC TTGAAGAAGA CATTATCAAA AGATCATCAT TTCTAGATAG AGTGGCTGAT	180
GATATGCTAT TTGTAAGGCG TGATTTAATT TTAATAAAAA GGTTAGAAAT ATTAGTAGAA	240
TCGTTGTAA TTAATTTGTC CGTTATTTTA GCATAAATTG TTTCTACAAA ATCTGTATTG	300
GCTGCAAGTT CTTCGGCAAT TGTAAGCTTA ATTATCTGCT TAAAATAGTC TAATCCTTCT	360
CCTTTAAATA TTTTGTCTTT AGAAGCATCT AAAAAGTTTT TAAAGGTGAT AGCATTACTG	420
CTTGCAGCTC CATCATCAAG CAGTAAAAGA TCAGTATTGT TAACGGTCGT AACCTTATTT	480
AAATCTTTTA TTTGAACCGT TTCTTCTTCA TCAATTAGTA ATTTTCTTG ATCATCAGCC	540
ATAAACCTC CTTAGTTGTT AAAAGTTATA ATATTGTTAC CATCTGTATT ATTAATTTTG	600
AGAACTCT	608

(2) INFORMATION FOR SEQ ID NO: 142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 591 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

1107

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

CTCCAATAGC GCTAAAAGAA TTAAATATAC TTGCTACTGA TGCTAGTTTA TTTATATCTT	60
GAATAATATT TGCGAATTCC TTTAATTCAT GAGGATCCAG GGGGCTTAAA ACAGTATAAG	120
TGTGTCTTCT ATATCTTATA GATCTTTCGG TATTGTCAGA TATATCTTCA GTCCCTGGCC	180
CCCAATTCAA TCCCCTAAAA GACGTCATCC CGTAATGGTC TTCAGGTTCT TTTTCCATAC	240
TTTTTACATA TTTTCTTTA AAATTGTAGG CCGATTCTAT TTGCTTTTTT AAATCATTAG	300
ATAGCGTATT TTTTAGTTGT TGTTTTCTTA GTTCTTCCTT CTCTTCTTCT TGTGTTTTT	360
TCTTAAGCTC TTCTTCTTGT TGTTTTTCTT TAAGCTCTTC TTCTTGTTGT TTTTCTTAA	420
GCTCTTCTTC TTGTTGTTTT TTCTTAAGCT CTCTTCTTG TTGTTTTTTC TTAAGCTCTT	480
CTTCTTGTTG TTTTCTTCTA AGCTCTTCTT CTGTTGTTT TTCTTAAGC TCTTCTTCTT	540
GTGTTTTTTT CTTAAGCTCT TCTTCTTGT GTTTTTTCTT AAGCTCTTCT T	591

(2) INFORMATION FOR SEQ ID NO: 143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 586 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

GTGTTAGTGT CCCCATGTGA ATGGGTGCAC TAAAAAATTA AAAAAATAAA TTAAATATAG	60
GAGGATTAAT TAATGCTTAT TAATAAAATA AAACAAGATA ATAGAACTTT AAGACCGGAG	120
ATACAAAAAT GGGGTTGTTa CTTTTTGTGT CTGCATTATT ATACAAGTCT ATTTAAGCAA	180
CGTGAATTTA ATGCATATGA AATAAATACA GCGTATTATA GATTTATAGG ACTTGTTTAT	240
ATCAAGAGCA ATTGTTTTAT TATAAATCCA TGTATGATAC TTAATTATTA CGGAATTAGA	300
AGTAGCGTGA GATATGAAAC TGCAAATTAT TTGGGTGCAG CAAATGAATT TGAAATAAGT	360
GAAGTTAAAA TCGATAAGGk TAATGGATAT CACTTTATAT CAACAAAAAA TAAAGAAATA	420
TTATATGATT CACTTGaTTT AAAGCCACGT GGAAAAATAT TTAAAGTAAC TTCmAAACGT	480
wTwTTTAAAC tGrAATAGTT TaCTAAgTTT AAGGCACTTT TaGCACATTC ATAgCTgAAT	540
TTaTTAGCAG rAGrTAGGcC GTAGGATATA ACCAATTTCA TTGGTT	586

(2) INFORMATION FOR SEQ ID NO: 144:

1108

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 585 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

GTGTTTTTTA GCAATTTATT TTCAACTCTT TTTATGTTTT TGATTATTTT AATCATAGTA	60
TCTTTATCAA CATTTAATGT TAATAAAAAT GGAAGAATTT CTTTACATAA GAAGTTACTT	120
TTGTTGAAGT ACTTTATTAC TTGATATTTT TCTATTTTCGT TAATCTTTCT TTCTTCTTTT	180
ATATTATTTT TATTACTTAA ACACCTCCACT GAATTTACAC TACTATTTTT GGAAACATTG	240
TCTTTAAAAT GKTATTAAAC TCTAGATTTA AATCTAGAGT TTTTTyGyTC TTTAAAGTAC	300
TTGTTGATTT TCTGGTAACA yTCTTTTTTA GGATACTTTA GCTTATAGTA AATTCAGTT	360
CCACAATTTA CACCCATrTG TTGGTAGTAA TTAGTTGTra CTTTAAATAC TTTTCTAAT	420
TtGTAAAGAT AATTTtGCAT tGTTCTtAGw GTAGTGGGAG CTAGACCAkT CcTTTTtAGA	480
TTTTtCryTaw AGyArTAGAG TATGTTTTGT TCGTGtATt TCTTATCTTT TTGGTTAGG	540
TAATCTAGCG TTGAAGTAAG AGAGATTAAT TTGTGTTGGT GTTTG	585

(2) INFORMATION FOR SEQ ID NO: 145:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 575 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

GGGAGATTTA ATATGGAATT ATTTGATGAA AATTATTATG CAAAAGCTGT GGCAAATATC	60
ATAGGAGAAG TTAAAGATCC TATTATGTAT AAATGGTTTT CGCCCGATCA AATTGAAGAT	120
GTTGATCTAC AAATGGGATA TCAAAAACC GTAAATGGG ACGCGTTTTT AAATGCTAAT	180
CCTACAACAA TTGCCAATGA GGTAAATACT ATCTCAACTA TTGGATTTAG TTCTGAAGTG	240
GTAAGACTTA ATTATTTGAA ATTACAGTAT AAATTCAGAC ATTTAAAGCA GACTTCTGAG	300
AAATTTTATA CTTCAGATTC ATATATTGGG GACATTAATA ATAATTTACT tCCTTTkGCT	360
CAAGCGTATA AGCTTGCAAG TAGTGAAATT ATTAACTTA TTAATCACTT TGTATTAACC	420
GGGACTGTTT CGATTCAAAA AGATGGGAAA AATCAAAAAC GCCTGCTTCC AAATATGTAG	480

1109

GGCTGCTTAA TAGCCCGAGC AGATAAAAGA AGAGGTTGCT AGTGGTGATA AAGATAAAnG 540
 GGTAAATCT TGAAAAGATG AGGCGGACTT CAACT 575

(2) INFORMATION FOR SEQ ID NO: 146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 571 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

TTGGTTCCCA nCnTATTTTCG TTGAAATTGT GATACTTATA GCCATAACCT TTAAGATTTT 60
 TATCAATCCC CGGCAAGTTC ATCCTTAGGG TTTTCATATC TCTTAAAAAG TCAATTTCTG 120
 CTTGATTAAT TTCTTGTTGA TTATGTTTTT TGCGGTTTTT CATTTTTTTA CTCCGTAAGT 180
 TATAATTTTC TTATATATAA ATATATAGCA AAAACTATTT TTGTCAACTT TTTTAAATAA 240
 AAATTTTGT TAAAAGACTT AGGGCTTTCG TAAATCTCT TTTAAAAGAA CTTAGTAAAG 300
 CCCTAATATT TTTACGATCC AATATTCAAG TAGGAAATAA TGAAAAATTA TTTCTACAA 360
 AACTATATTT AGTTTAGTTC AACCTTAAAT TAAATCAAT TAATATTATT AACTGCGGT 420
 CTATAAAAT ACAAAATAT AAAGCTTTTA TAAATCTTA TTTTAAAAGA ACTTATAAAA 480
 ACCTATCTC TAAATTATTT ACAAAATCT AAAATTAGAT TTTTAGTTCT TCATATTTCC 540
 TTAAAAGTTT TTTAAGAAAA TCTTTTGTAT T 571

(2) INFORMATION FOR SEQ ID NO: 147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 555 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

AAGCGTATAA GCTTGCAAGT AGTGAAATTA TTAACTTAT TAATCACTTT GTATTAACCG 60
 GGACTGTTTC GATTCAAAAA GATGGGAAAA ATCAAAAACG CCTGCTTCCA AATATGTATG 120
 GGCTGCTTAA TATGCCCGAG CAGATAAAAG AAGAGGTTGC TAGTGGTGAT AAAGATAAAA 180
 TGGATAAAAT CTTTGAAAAG ATTGAGGCTG GACTTTCAAA GTTAGAACTG GGCGACGAAT 240
 TTTCCACCCC GATGATGGTA ATAGTTGACC CAGCAACGTC ACTTAAACTA GTAAAACCAT 300
 ACGCAGCAGC ACAGGGTGCA GCAAGTAGTT GTGAAAAATG GGAAGATGTT TTAATTCAAA 360

1110

CTATTAAGGC TATTAATAAT AGAGAAGATG TTTACATTGA AACTTCAAAC TTGCTGAAAC 420
ATAAAATACT CATTTATCCA CTAAATTCTG AACTTATTAA ATTTAAACCT AGCAAGTATA 480
TGCTACCTAC ACCGAATGAA CAAGTTGATA AAGACTCAAC CGATGTAGCT CTTCTACATT 540
GATTTTGT TTG 555

(2) INFORMATION FOR SEQ ID NO: 148:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 549 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

GTTTCTTCTT GGAGAATTTT GATTTGAAGA TTTTGAATTT TGAGATTCAT TTTCAAGATT 60
TTGGTTATTT TCTGATGGAT TTTTGTGGA ATTTCTGTT AAATTTTCTG AATTGGTGTG 120
ATTGCTTGTG TTTTGTAGAT TTCTAGAATT GTTGCTTCGT TTTGTTTTTT TTAGACTTTT 180
AGAAGTGGTA GGATTTTTTTG GTTCGTTTGG GTTAACATTG CCAAAGGTG CACATGATAT 240
GCAAATTGAA GTTAATATTG CTGTAATAAC GTTAAGTTTA ATAATATTTA ATTTAAAGTT 300
TTTCAAAATA TTCTCCTTAT AAATTTGAAT TAATATTTAT TAATTTTAGT TCAAATATAT 360
AATATTACAA TTTAATATCA ATATCAAATA AGTTTAATAT TATTGATATT GAAAATTAAT 420
TTCATGAGTT TTAGCGGGAT TAGATGCATG AATTTAAAAA TAAAGTAAT CTCCCTTTTA 480
AAATATGAAG TGnAACAAATT GTTGATTAA GGGGTTAATC CAGGAnCAGA GGGAATTAGA 540
AATATAACG 549

(2) INFORMATION FOR SEQ ID NO: 149:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 544 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

TTTTGTAATT TTCATATTCA TTAATTAAAT GATAAGACTT CTTTTTTTAA TGaAAAAATA 60
TATTTCAAAA ATAAATAAG CTCTTTTAGT ATCTTCTTTA CAAAATTCGT AAAACCCCTT 120
GTTTTTTATT AAAATCCTAA TAGACATTTT TCTATTATTT ACTTCAGGCA AATTTTCTTT 180

1111

TTTTTACGTT TGATAAATTC TCTTTTAACT GTCTTTGTAT TCCTCTAAAG CCCTATTTTTT	240
TAATTTTATC TATATAACA GGCCTCCTCT AAAACCCTTT TTCCGTAAAC TTTTTTGTCT	300
ATACTTTGTA TTAATAAATT TCCTAAAAGG AATTTTAAAA TTTTCTTTTA TTAAATCTTT	360
AAATACACTT TGATCTTCTT TTATACAAAG GGGAAATACA TGGCTTGATT CACTGCATCT	420
ATTTGAAACA AAACATCTCT ATAAAATTCT AGAGGTAAAA GAATGAAAAA AATTATTTGT	480
CGATAAAAAT CCTGTTGTAA TAAGGGTTAT ATTATTCTCn ATTTCCnAAA TATATTTTTT	540
TATA	544

(2) INFORMATION FOR SEQ ID NO: 150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 533 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

GAGACTTTGA AGCTATCTCG TCAGGGGTAG TGGAGTCAAT CTTGAAATAC CACCCTTGTT	60
TAATTAGGTT TCTAACTTAT AGAAATATGA GGAGAGTGCC AGGTGGGTAG TTTGACTGGG	120
GCGGTCGCTT CCTAAAGAGT AACGGAGGTG CGCAAAGGTT ACCTTAGAGT GGTGGAAT	180
CACTCTGTAA GTGTAAAGGC ATAAGGTAGC TTAAGTGTAA GACTGACAAG TCGAACAGAT	240
ACGAAAGTAG GTCTTAGTGA TCTGGCGGTG GCAAGTGGA GCGCCGTCAC TTAACGAATA	300
AAAGGTACTC CGGGGATAAC AGGCTTATCC TTCCCAAGAG TTCACATCGA CGGAAGGgTT	360
TGGCACcTCG ATGTCGGCTC ATCGCATCCT AGGGcTGGAG CAGgTCCTAA GGGTATGGCT	420
GTTCGCCATT TAAAGCGGTA CCGAGCTGGG TTCAGAACGT CGTGAGACAG TTTGGTCCCT	480
ATCTGCCACA AGCGTTGGAT ATTGAGAGGA GCTATnTTAG TACGAGAGGA CCG	533

(2) INFORMATION FOR SEQ ID NO: 151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 521 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

TGGTTTTGAA GCTTTTTTAG TAGGCTTAGA AGAAATTTTT AGTGAATTTT TAAGAATTTT	60
ATTTTCATTT AGCACATTTT GATAATCTTG AAATAGTTTG AGCATAAAAT CCATGTTGAA	120

1112

ATTATTTAAA TTA [~] AATAAT TATTAGTGTT CATAAAATCC TCTCCTTGAA GGTGTTACTT	180
TTAAATTAAG TAAAAGTAAT AAAAATAGAT AAAAATAGTA ATTTATATTG TACCAAAAAC	240
GAAAAATTTT AGTCAAATTT TGTGAGTTCT CATTGCATGA GAAATTTGGG TTGTAGGGAG	300
GCTGTTATAA ATAGAATGGG CATTTTCTGA GGGTGTCGGC TAAGAAAGAC TACATACTTT	360
AGCTAATATA TAGCAAAGAC TTTGAAATTT AATTGTATG TGT [~] TTATAG TCTTTTGTA	420
TGAGTAGTGC ATTTGCAATG GAGAGATTTT GGGGAGTTGT TTAAAATTAC ATTTGCGTTT	480
TGTTAAAATG TAACAGCTGA ATGTAACAAA ATTATATATT T	521

(2) INFORMATION FOR SEQ ID NO: 152:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 501 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

GTTCTCAAAT TTTTATAAAT CTTGTTTAGG AATTTTCTTT TTTTCTTTCA ATTGACTTTT	60
CTAATTTACG CTTTATGTAA CTTAGaTCGC TATATTTATG ATTTTCAATA ATAAAGTGGG	120
GTTTATATTT GTAATTTTCG TATATTTTTT GAAAATTGT TTCTAATTGT TCTGAATTGT	180
ATCCACTTTT TTCTAATTCT TTTTGAGTGT TGCATAGAAT TTTCTTTAAT TTTTCTTGTT	240
TTTCTTTACT GCAAGATTTA GGAAAGTAAA TATTTTATT TTTTGCTTTA ATATCAGTTC	300
TTTTTATGGT TTTAATTATT TTGATCATAG TATCTTatCA ACATTTAAAT TTAATAAAAT	360
TGAAAGAATT tCTTTACATG AAAAGTTGCA TTtATtGAAA TAATTTATtA CTGATACTTT	420
CTATTcATTA AcCTTCTTCT cTTTATAtAt TTTATTACTA TTACAGGAnT CACACGTACA	480
CTACCCATTT TGAACCGAAT T	501

(2) INFORMATION FOR SEQ ID NO: 153:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 488 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

GTTCCnChTT ATCAAGGAAA TTAACGACAT CTTTCATTAT GGTTCATTT GCAAATTTAA	60
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1113

CAAAATTGTC TTTTCTTTT TCTAATCTTT TTCTGAAGTT TTCAAATTCT GCTTGTTTTTC	120
TTAAATACAA ATCTTTAAGA TTGGAGATTT CATTTTCAAG TTCAGCAATT TTTTATCAG	180
AATTTACTAA ATTTAAGTTT TCTTTTTTTT GAGATTTTGT ATTTTATTA TCTTGTTGT	240
TGTTTTTTTC AGATTGCTT TTAGTTTCTT TTTTTCCAT TTTTCCTCCT kTGATAAAGC	300
ATTTTATCTT TAAAAAAAT ATTTTACAAA TTTTnTTCTT TCytGAAATT TAAnAAAATG	360
GAGTCATTTT GnGGCATTG TAAGATGTAG ATTTTCTTA AGCTTTCAGT AAGAGTGTTA	420
TATGnATACA TAGGTTATTT AGTnAAAATG TTCGTGTGTA TTTTGTGTCA AAAGAAAAA	480
TTTAAGTT	488

(2) INFORMATION FOR SEQ ID NO: 154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

GGAGAGGCGG TTTGCGTATT GGGCGCTCTT CCGCTTCCTC GCTCACTGAC TCGCTGCGCT	60
CGGTGCTTCG GCTGCGGCGA GCGGTATCAG CTCACTCAA GCGGTAATA CGGTATCCA	120
CAGAATCAGG ATAACGCAGA AAGAACATGT GAGCAAAAGG CCAGCAAAAG GCCAGGAACC	180
GTA AAAAGGC CGCGTTGCTG GCGTTTTTCC ATAGGCTCCG CCCCCTGAC GAGCATCACA	240
AAAATCGACG CTCAAGTCAG AGGTGGCGAA ACCCGACAGG ACTATAAAGA TACCAGGCGT	300
TTCCCCCTGG AAGCTCCCTC GTGCGCTCTC CTGTTCCGAC CCTGCCGCTT ACCGGATACC	360
TGTCCGCCTT TCTCCCTTCG GGAAGCGTGG CGCTTCTCA TAGCTCACGC TGTAGTATCT	420
CAGTTCGGTG TAGTCGTTTC CTCCAAGCTG GGCTGTGTG	459

(2) INFORMATION FOR SEQ ID NO: 155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:


GAACAAGAGT CGAAAGTAGG TGTTAGTGAT sTGCGGTGG CAAGTGAAG CGCCGTCAC	60
TAACGAATAA AAGGTACTCC GGGGATAACA GGCTTATCCT TCCCAAGAGT TCACATCGAC	120

1114

GGAAGGGTTT GGCACCTCGA TGTCGGCTCA TCGCATCCTA GGGCTGGAGC AGGTCCTAAG	180
GGTATGGCTG TTCGCCATTT AAAGCGGTAC GCrAGCTGGG TTCAGAACGT CGTGAGACAG	240
TTTGGTCCCT ATCTGCCACA AGCGTTGGAT ATTTGAGAGG AnCTATCTTT AGTACGAGAG	300
GACCGAGATG GACGAACCTC TAGTGTGCCA GTTATCCTGC CAAGGGTAAG TGCTGGGTAG	360
CTACnTTC	368

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>8</u> . line <u>23</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet: <u> </u>	
Name of depositary institution <p style="text-align: center;">American Type Culture Collection</p>	
Address of depositary institution (including postal code and country) <p>12301 Parklawn Drive Rockville, Maryland 20852 United States of America</p>	
Date of deposit <u>August 8, 1997</u>	Accession Number <u>202012</u>
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <u> </u>	
EUROPE In respect of those designations in which a European Patent is sought a sample of the deposited microorganism will be available until the publication of the mention of the grant of the European patent or until the date on which the application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28(4)EPC).	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	
<div>For receiving Office use only</div> <div><input checked="" type="checkbox"/> This sheet was received with the international application</div> <div>Authorized officer  International Division BO/US 703/995 8887</div>	<div>For International Bureau use only</div> <div><input type="checkbox"/> This sheet was received by the International Bureau on: <u> </u></div> <div>Authorized officer</div>

CANADA

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

NORWAY

The applicant hereby requests that the application has been laid open to public inspection (by the Norwegian Patent Office), or has been finally decided upon by the Norwegian Patent Office without having been laid open inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Norwegian Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Norwegian Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on the list of recognized experts drawn up by the Norwegian Patent Office or any person approved by the applicant in the individual case.

AUSTRALIA

The applicant hereby gives notice that the furnishing of a sample of a microorganism shall only be effected prior to the grant of a patent, or prior to the lapsing, refusal or withdrawal of the application, to a person who is a skilled addressee without an interest in the invention (Regulation 3.25(3) of the Australian Patents Regulations).

FINLAND

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Regulations), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

UNITED KINGDOM

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for the international publication of the application.

Page 2

DENMARK

The applicant hereby requests that, until the application has been laid open to public inspection (by the Danish Patent Office), or has been finally decided upon by the Danish Patent office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Danish Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Danish Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Danish Patent Office or any person by the applicant in the individual case.

SWEDEN

The applicant hereby requests that, until the application has been laid open to public inspection (by the Swedish Patent Office), or has been finally decided upon by the Swedish Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the International Bureau before the expiration of 16 months from the priority date (preferably on the Form PCT/RO/134 reproduced in annex Z of Volume I of the PCT Applicant's Guide). If such a request has been filed by the applicant any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Swedish Patent Office or any person approved by a applicant in the individual case.

NETHERLANDS

The applicant hereby requests that until the date of a grant of a Netherlands patent or until the date on which the application is refused or withdrawn or lapsed, the microorganism shall be made available as provided in the 31F(1) of the Patent Rules only by the issue of a sample to an expert. The request to this effect must be furnished by the applicant with the Netherlands Industrial Property Office before the date on which the application is made available to the public under Section 22C or Section 25 of the Patents Act of the Kingdom of the Netherlands, whichever of the two dates occurs earlier.

What Is Claimed Is:

1. An isolated nucleic acid molecule comprising a polynucleotide having a nucleotide sequence selected from the group consisting of:
 - (a) any one nucleotide sequence of SEQ ID NOS:1-155; or
 - (b) a nucleotide sequence complementary to any one of the nucleotide sequences in (a).
 - (c) a nucleotide sequence at least 95% identical to any one of the nucleotide sequences of SEQ ID NOS:1-155; or,
 - (d) a nucleotide sequence at least 95% identical to a nucleotide sequence complementary to any one of the nucleotide sequences of SEQ ID NOS:1-155.
2. An isolated nucleic acid molecule of claim 1 comprising a polynucleotide which hybridizes under stringent hybridization conditions to a polynucleotide having a nucleotide sequence identical to a nucleotide sequence in (a) or (b) of claim 1.
3. An isolated nucleic acid molecule of claim 1 comprising a polynucleotide which encodes an epitope-bearing portion of a polypeptide in (a) of claim 1.
4. Computer readable medium having recorded thereon the nucleotide sequence depicted in SEQ ID NOS:1-155, a representative fragment thereof or a nucleotide sequence at least 95% identical to a nucleotide sequence depicted in SEQ ID NOS:1-155.
5. A method for making a recombinant vector comprising the step of inserting an isolated nucleic acid molecule of claim 1 into a vector.
6. A recombinant vector produced by the method of claim 5.
7. A host cell comprising the vector of claim 6.
8. A method of producing a polypeptide comprising:
 - (a) growing the host cell of claim 7 such that the protein is expressed by the cell; and
 - (b) recovering the expressed polypeptide.
9. An isolated polypeptide comprising a polypeptide selected from the group consisting of:
 - (a) a polypeptide encoded by an ORF of any one sequence of SEQ ID NOS:1-155;
 - (b) a polypeptide encoded by an ORF of any one sequence of SEQ ID NOS:1-155 except the N-terminal residue;

- (c) a fragment of the polypeptide of (a) having biological activity; and
(d) an epitope-bearing fragment of the polypeptide of (a).
10. An isolated antibody specific for the polypeptide of claim 9.
11. A polypeptide produced according to the method of claim 8.
12. An isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence selected from the group consisting of an amino acid sequence of any one of the polypeptides in Table 1.
13. An isolated polypeptide antigen comprising an amino acid sequence of an *B. burgdorferi* epitope shown in Table 4.
14. An isolated nucleic acid molecule comprising a polynucleotide with a nucleotide sequence encoding a polypeptide of claim 9.
15. A host cell which produces an antibody of claim 10.
16. A vaccine, comprising:
(1) one or more *B. burgdorferi* polypeptides selected from the group consisting of a polypeptide of claim 9; and
(2) a pharmaceutically acceptable diluent, carrier, or excipient;
wherein said polypeptide is present, in an amount effective to elicit protective antibodies in an animal to a member of the *Borrelia* genus.
17. A method of preventing or attenuating an infection caused by a member of the *Borrelia* genus in an animal, comprising administering to said animal a polypeptide of claim 9, wherein said polypeptide is administered in an amount effective to prevent or attenuate said infection.
18. A method of detecting *Borrelia* nucleic acids in a biological sample comprising:
(a) contacting the sample with one or more nucleic acids of claim 1, under conditions such that hybridization occurs, and
(b) detecting hybridization of said nucleic acids to the one or more *Borrelia* nucleic acid sequences present in the biological sample.
19. A method of detecting *Borrelia* nucleic acids in a biological sample obtained from an animal, comprising:

- (a) amplifying one or more *Borrelia* nucleic acid sequences in said sample using polymerase chain reaction, and
- (b) detecting said amplified *Borrelia* nucleic acid.

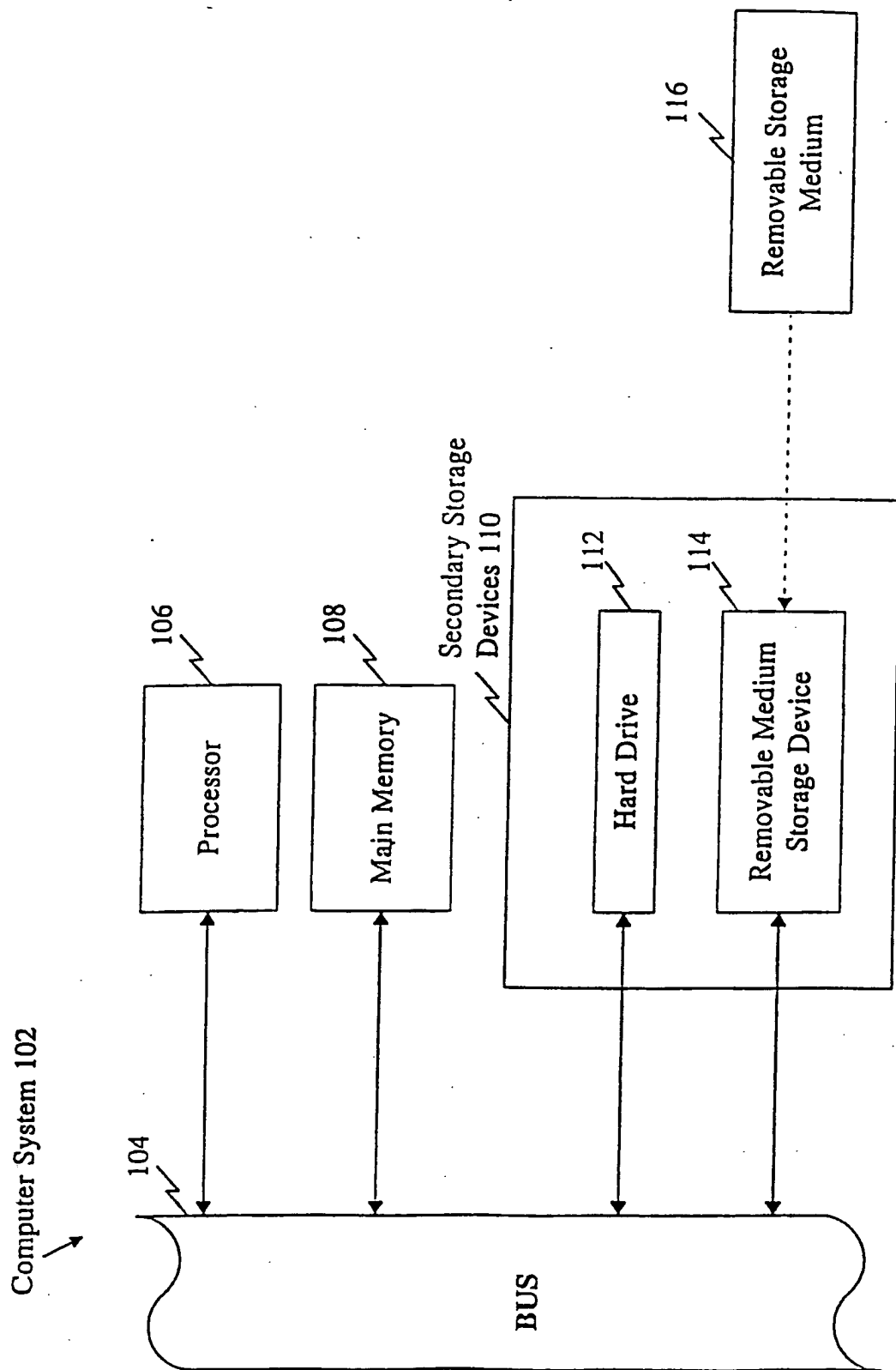
20. A kit for detecting *Borrelia* antibodies in a biological sample obtained from an animal, comprising

- (a) a polypeptide of claim 9 attached to a solid support; and
- (b) detecting means.

21. A method of detecting *Borrelia* antibodies in a biological sample obtained from an animal, comprising

- (a) contacting the sample with a polypeptide of claim 9; and
- (b) detecting antibody-antigen complexes.

Figure 1



2/2
Figure 2